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(54) Title: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT

(57) Abstract: Isolated nucleic acid molecules, designated MCT nucleic acid molecules, which encode novel MCT proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MCT nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated MCT proteins, mutated MCT proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MCT genes in this organism.

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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS
INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE TRANSPORT**

5 Related Applications

This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999. This application also claims priority to German Patent Application No. 19931454.3, filed July 8, 1999, German Patent Application No. 19931478.0, filed July 8, 1999, German Patent Application No. 19931563.9, filed July 8, 1999, German Patent Application No. 19932122.1, filed July 9, 1999, German Patent Application No. 19932124.8, filed 99709, German Patent Application No. 19932125.6, filed July 9, 1999, German Patent Application No. 19932128.0, filed July 9, 1999, German Patent Application No. 19932180.9, filed July 9, 1999, German Patent Application No. 19932182.5, filed July 9, 1999, German Patent Application No. 19932190.6, filed July 9, 1999, German Patent Application No. 19932191.4, filed July 9, 1999, German Patent Application No. 19932209.0, filed July 9, 1999, German Patent Application No. 19932212.0, filed July 9, 1999, German Patent Application No. 19932227.9, filed July 9, 1999, German Patent Application No. 19932228.7, filed July 9, 1999, German Patent Application No. 19932229.5, filed 99070, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent Application No. 19932927.3, filed July 14, 1999, German Patent Application No. 19933005.0, filed July 14, 1999, German Patent Application No. 19933006.9, filed July 14, 1999, German Patent Application No. 19940764.9, filed August 27, 1999, German Patent Application No. 19940765.7, filed August 27, 1999, German Patent Application No. 19940766.5, filed August 27, 1999, German Patent Application No. 19940830.0, filed August 27, 1999, German Patent Application No. 19940831.9, filed August 27, 1999, German Patent Application No. 19940832.7, filed August 27, 1999, German Patent Application No. 19940833.5, filed August 27, 1999, German Patent Application No. 19941378.9 filed August 31, 1999, German Patent Application No. 19941379.7, filed August 31, 1999, German Patent Application No. 19941395.9, filed August 31, 1999, German Patent Application No. 19942077.7, filed September 3, 1999, German Patent Application No. 19942078.5, filed September 3, 1999, German Patent

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Application No. 19942079.3, filed September 3, 1999, and German Patent Application No. 19942088.2, filed September 3, 1999. The entire contents of all of the above referenced applications are hereby expressly incorporated herein by this reference.

5 Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

20 Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as membrane construction and membrane transport (MCT) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MCT nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by

fermentation processes. Modulation of the expression of the MCT nucleic acids of the invention, or modification of the sequence of the MCT nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (e.g., to improve the yield or production of one or more fine chemicals
5 from a *Corynebacterium* or *Brevibacterium* species).

The MCT nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C.*
10 *glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium*
15 *diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The MCT nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for
20 genetically engineered *Corynebacterium* or *Brevibacterium* species.

The MCT proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the metabolism (e.g., the biosynthesis or degradation) of compounds necessary for membrane biosynthesis, or of assisting in the transmembrane transport of one or more compounds either into or out of
25 the cell. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen.*
30 *Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of

production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an MCT protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. Those MCT proteins involved in the export of fine chemical molecules from the cell may be increased in number or activity such that greater quantities of these compounds are secreted to the extracellular medium, from which they are more readily recovered. Similarly, those MCT proteins involved in the import of nutrients necessary for the biosynthesis of one or more fine chemicals (e.g., phosphate, sulfate, nitrogen compounds, etc.) may be increased in number or activity such that these precursors, cofactors, or intermediate compounds are increased in concentration within the cell. Further, fatty acids and lipids themselves are desirable fine chemicals; by optimizing the activity or increasing the number of one or more MCT proteins of the invention which participate in the biosynthesis of these compounds, or by impairing the activity of one or more MCT proteins which are involved in the degradation of these compounds, it may be possible to increase the yield, production, and/or efficiency of production of fatty acid and lipid molecules from *C. glutamicum*.

The mutagenesis of one or more MCT genes of the invention may also result in MCT proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, MCT proteins of the invention involved in the export of waste products may be increased in number or activity such that the normal metabolic wastes of the cell (possibly increased in quantity due to the overproduction of the desired fine chemical) are efficiently exported before they are able to damage nucleotides and proteins within the cell (which would decrease the viability of the cell) or to interfere with fine chemical biosynthetic pathways (which would decrease the yield, production, or efficiency of production of the desired fine chemical). Further, the relatively large intracellular quantities of the desired fine chemical may in itself be toxic to the cell, so by increasing the activity or number of transporters able to export this compound from the cell, one may increase the viability of the cell in culture, in turn leading to a greater number of cells in the culture producing the desired fine chemical. The MCT proteins of the invention may also be manipulated

such that the relative amounts of different lipid and fatty acid molecules are produced. This may have a profound effect on the lipid composition of the membrane of the cell. Since each type of lipid has different physical properties, an alteration in the lipid composition of a membrane may significantly alter membrane fluidity. Changes in
5 membrane fluidity can impact the transport of molecules across the membrane, as well as the integrity of the cell, both of which have a profound effect on the production of fine chemicals from *C. glutamicum* in large-scale fermentative culture.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as MCT proteins, which are capable of, for example, participating in
10 the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Nucleic acid molecules encoding an MCT protein are referred to herein as MCT nucleic acid molecules. In a preferred embodiment, the MCT protein participates in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*,
15 or in the transport of molecules across these membranes. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MCT protein or biologically active portions thereof, as well as nucleic acid fragments
20 suitable as primers or hybridization probes for the detection or amplification of MCT-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), forth as the odd-numbered SEQ ID NOs in the
25 Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and
30 even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion

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thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8...). The preferred MCT proteins of the present invention also preferably possess at least one of the MCT activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an MCT activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown in the corresponding odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7...)).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MCT fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and is able to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MCT protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MCT protein by culturing the host cell in a suitable medium. The MCT protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MCT gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MCT sequence as a transgene. In another embodiment, an endogenous MCT gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MCT gene. In another embodiment, an endogenous or introduced MCT gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MCT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MCT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MCT gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the

sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 676) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MCT protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MCT protein or portion thereof can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In another preferred embodiment, the isolated MCT protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes.

The invention also provides an isolated preparation of an MCT protein. In preferred embodiments, the MCT protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated MCT protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MCT protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under

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stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98,%, or 99% or more homologous, to a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred
5 that the preferred forms of MCT proteins also have one or more of the MCT bioactivities described herein.

The MCT polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MCT polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MCT
10 protein alone. In other preferred embodiments, this fusion protein participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

15 In another aspect, the invention provides methods for screening molecules which modulate the activity of an MCT protein, either by interacting with the protein itself or a substrate or binding partner of the MCT protein, or by modulating the transcription or translation of an MCT nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine
20 chemical. This method involves the culturing of a cell containing a vector directing the expression of an MCT nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MCT nucleic acid. In another preferred embodiment, this
25 method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an
30 agent which modulates MCT protein activity or MCT nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum*

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metabolic pathways for cell membrane components or is modulated for the transport of compounds across such membranes, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MCT protein activity can be an agent which stimulates MCT protein activity or MCT nucleic acid expression. Examples of agents which stimulate MCT protein activity or MCT nucleic acid expression include small molecules, active MCT proteins, and nucleic acids encoding MCT proteins that have been introduced into the cell. Examples of agents which inhibit MCT activity or expression include small molecules and antisense MCT nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant MCT gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides MCT nucleic acid and protein molecules which are involved in the metabolism of cellular membrane components in *C. glutamicum* or in the transport of compounds across such membranes. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of a fatty acid biosynthesis protein has a direct impact on the yield, production, and/or efficiency of production of the fatty acid from modified *C. glutamicum*), or may have an indirect impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of the metabolism of cell membrane components results in alterations in the yield, production,

and/or efficiency of production or the composition of the cell membrane, which in turn may impact the production of one or more fine chemicals). Aspects of the invention are further explicated below.

5 I. Fine Chemicals

 The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both
10 proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates
15 (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and
20 Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine
25 chemicals are further explicated below.

 A. *Amino Acid Metabolism and Uses*

 Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-
30 recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in

proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins.

Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids
5 have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways
10 to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are
15 interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout
20 the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino acids –
25 technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH:
30 Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial

- amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-
- 5 step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase.
- 10 Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-
- 15 step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine
- 20 from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. *Biochemistry* 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted

25 amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways,

30 see Stryer, L. *Biochemistry*, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of

compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)- β -alanine) can be produced
5 either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β -alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β -alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5
10 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthanol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in
15 microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate
20 dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

25 Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrines belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are
30 also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language “purine” or “pyrimidine” includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term “nucleotide” includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language “nucleoside” includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) “Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents.” *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) “Enzymes in nucleotide synthesis.” *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine,

folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-562). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α , α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S.

Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from
5 which it can be collected using methods known in the art.

II. Membrane Biosynthesis and Transmembrane Transport

Cellular membranes serve a variety of functions in a cell. First and foremost, a membrane differentiates the contents of a cell from the surrounding environment, thus
10 giving integrity to the cell. Membranes may also serve as barriers to the influx of hazardous or unwanted compounds, and also to the efflux of desired compounds. Cellular membranes are by nature impervious to the unfacilitated diffusion of hydrophilic compounds such as proteins, water molecules and ions due to their structure: a bilayer of lipid molecules in which the polar head groups face outwards (towards the
15 exterior and interior of the cell, respectively) and the nonpolar tails face inwards at the center of the bilayer, forming a hydrophobic core (for a general review of membrane structure and function, see Gennis, R.B. (1989) *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg). This barrier enables cells to maintain a relatively higher concentration of desired compounds and a relatively lower concentration of
20 undesired compounds than are contained within the surrounding medium, since the diffusion of these compounds is effectively blocked by the membrane.

However, the membrane also presents an effective barrier to the import of desired compounds and the export of waste molecules. To overcome this difficulty, cellular membranes incorporate many kinds of transporter proteins which are able to facilitate
25 the transmembrane transport of different kinds of compounds. There are two general classes of these transport proteins: pores or channels and transporters. The former are integral membrane proteins, sometimes complexes of proteins, which form a regulated hole through the membrane. This regulation, or 'gating' is generally specific to the molecules to be transported by the pore or channel, rendering these transmembrane
30 constructs selectively permeable to a specific class of substrates; for example, a potassium channel is constructed such that only ions having a like charge and size to that of potassium may pass through. Channel and pore proteins tend to have discrete

hydrophobic and hydrophilic domains, such that the hydrophobic face of the protein may associate with the interior of the membrane while the hydrophilic face lines the interior of the channel, thus providing a sheltered hydrophilic environment through which the selected hydrophilic molecule may pass. Many such pores/channels are
5 known in the art, including those for potassium, calcium, sodium, and chloride ions.

This pore and channel-mediated system of facilitated diffusion is limited to very small molecules, such as ions, because pores or channels large enough to permit the passage of whole proteins by facilitated diffusion would be unable to prevent the passage of smaller hydrophilic molecules as well. Transport of molecules by this process
10 is sometimes termed 'facilitated diffusion' since the driving force of a concentration gradient is required for the transport to occur. Permeases also permit facilitated diffusion of larger molecules, such as glucose or other sugars, into the cell when the concentration of these molecules on one side of the membrane is greater than that on the other (also called 'uniport'). In contrast to pores or channels, these integral membrane
15 proteins (often having between 6-14 membrane-spanning α -helices) do not form open channels through the membrane, but rather bind to the target molecule at the surface of the membrane and then undergo a conformational shift such that the target molecule is released on the opposite side of the membrane.

However, cells frequently require the import or export of molecules against the
20 existing concentration gradient ('active transport'), a situation in which facilitated diffusion cannot occur. There are two general mechanisms used by cells for such membrane transport: symport or antiport, and energy-coupled transport such as that mediated by the ABC transporters. Symport and antiport systems couple the movement of two different molecules across the membrane (via permeases having two separate
25 binding sites for the two different molecules); in symport, both molecules are transported in the same direction, while in antiport, one molecule is imported while the other is exported. This is possible energetically because one of the two molecules moves in accordance with a concentration gradient, and this energetically favorable event is permitted only upon concomitant movement of a desired compound against the
30 prevailing concentration gradient. Single molecules may be transported across the membrane against the concentration gradient in an energy-driven process, such as that utilized by the ABC transporters. In this system, the transport protein located in the

membrane has an ATP-binding cassette; upon binding of the target molecule, the ATP is converted to ADP + Pi, and the resulting release of energy is used to drive the movement of the target molecule to the opposite face of the membrane, facilitated by the transporter. For more detailed descriptions of all of these transport systems, see:

- 5 Bamberg, E. *et al.*, (1993) "Charge transport of ion pumps on lipid bilayer membranes", *Q. Rev. Biophys.* 26: 1-25; Findlay, J.B.C. (1991) "Structure and function in membrane transport systems", *Curr. Opin. Struct. Biol.* 1:804-810; Higgins, C.F. (1992) "ABC transporters from microorganisms to man", *Ann. Rev. Cell Biol.* 8: 67-113; Gennis, R.B. (1989) "Pores, Channels and Transporters", in: *Biomembranes, Molecular Structure and*
10 *Function*, Springer: Heidelberg, p. 270-322; and Nikaido, H. and Saier, H. (1992) "Transport proteins in bacteria: common themes in their design", *Science* 258: 936-942, and references contained within each of these references.

The synthesis of membranes is a well-characterized process involving a number of components, the most important of which are lipid molecules. Lipid synthesis may
15 be divided into two parts: the synthesis of fatty acids and their attachment to sn-glycerol-3-phosphate, and the addition or modification of a polar head group. Typical lipids utilized in bacterial membranes include phospholipids, glycolipids, sphingolipids, and phosphoglycerides. Fatty acid synthesis begins with the conversion of acetyl CoA either to malonyl CoA by acetyl CoA carboxylase, or to acetyl-ACP by
20 acetyltransacylase. Following a condensation reaction, these two product molecules together form acetoacetyl-ACP, which is converted by a series of condensation, reduction and dehydration reactions to yield a saturated fatty acid molecule having a desired chain length. The production of unsaturated fatty acids from such molecules is catalyzed by specific desaturases either aerobically, with the help of molecular oxygen,
25 or anaerobically (for reference on fatty acid synthesis, see F.C. Neidhardt *et al.* (1996) *E. coli* and *Salmonella*. ASM Press: Washington, D.C., p. 612-636 and references contained therein; Lengeler *et al.* (eds) (1999) *Biology of Prokaryotes*. Thieme: Stuttgart, New York, and references contained therein; and Magnuson, K. *et al.*, (1993) *Microbiological Reviews* 57: 522-542, and references contained therein). The
30 cyclopropane fatty acids (CFA) are synthesized by a specific CFA-synthase using SAM as a cosubstrate. Branched chain fatty acids are synthesized from branched chain amino acids that are deaminated to yield branched chain 2-oxo-acids (see Lengeler *et al.*, eds.

(1999) Biology of Procaryotes. Thieme: Stuttgart, New York, and references contained therein). Another essential step in lipid synthesis is the transfer of fatty acids onto the polar head groups by, for example, glycerol-phosphate-acyltransferases. The combination of various precursor molecules and biosynthetic enzymes results in the production of different fatty acid molecules, which has a profound effect on the composition of the membrane.

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MCT nucleic acid and protein molecules, which control the production of cellular membranes in *C. glutamicum* and govern the movement of molecules across such membranes. In one embodiment, the MCT molecules participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. In a preferred embodiment, the activity of the MCT molecules of the present invention to regulate membrane component production and membrane transport has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MCT molecules of the invention are modulated in activity, such that the *C. glutamicum* metabolic pathways which the MCT proteins of the invention regulate are modulated in yield, production, and/or efficiency of production and the transport of compounds through the membranes is altered in efficiency, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "MCT protein" or "MCT polypeptide" includes proteins which participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Examples of MCT proteins include those encoded by the MCT genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "MCT gene" or "MCT nucleic acid sequence" include nucleic acid sequences encoding an MCT protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MCT genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation

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product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound.

In another embodiment, the MCT molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an MCT protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. Those MCT proteins involved in the export of fine chemical molecules from the cell may be increased in number or activity such that greater quantities of these compounds are secreted to the extracellular medium, from which they are more readily recovered. Similarly, those MCT proteins involved in the import of nutrients necessary for the biosynthesis of one or more fine chemicals (*e.g.*, phosphate, sulfate, nitrogen compounds, etc.) may be increased in number or

activity such that these precursor, cofactor, or intermediate compounds are increased in concentration within the cell. Further, fatty acids and lipids themselves are desirable fine chemicals; by optimizing the activity or increasing the number of one or more MCT proteins of the invention which participate in the biosynthesis of these compounds, or by
5 impairing the activity of one or more MCT proteins which are involved in the degradation of these compounds, it may be possible to increase the yield, production, and/or efficiency of production of fatty acid and lipid molecules from *C. glutamicum*.

The mutagenesis of one or more MCT genes of the invention may also result in MCT proteins having altered activities which indirectly impact the production of one or
10 more desired fine chemicals from *C. glutamicum*. For example, MCT proteins of the invention involved in the export of waste products may be increased in number or activity such that the normal metabolic wastes of the cell (possibly increased in quantity due to the overproduction of the desired fine chemical) are efficiently exported before they are able to damage nucleotides and proteins within the cell (which would decrease
15 the viability of the cell) or to interfere with fine chemical biosynthetic pathways (which would decrease the yield, production, or efficiency of production of the desired fine chemical). Further, the relatively large intracellular quantities of the desired fine chemical may in itself be toxic to the cell, so by increasing the activity or number of transporters able to export this compound from the cell, one may increase the viability of
20 the cell in culture, in turn leading to a greater number of cells in the culture producing the desired fine chemical. The MCT proteins of the invention may also be manipulated such that the relative amounts of different lipid and fatty acid molecules are produced. This may have a profound effect on the lipid composition of the membrane of the cell. Since each type of lipid has different physical properties, an alteration in the lipid
25 composition of a membrane may significantly alter membrane fluidity. Changes in membrane fluidity can impact the transport of molecules across the membrane, as well as the integrity of the cell, both of which have a profound effect on the production of fine chemicals from *C. glutamicum* in large-scale fermentative culture.

The isolated nucleic acid sequences of the invention are contained within the
30 genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MCT DNAs and the predicted amino acid sequences of the *C.*

glutamicum MCT proteins are shown in the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins involved in the metabolism of cellular membrane components or proteins involved in the transport of compounds across such membranes.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing).. As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The MCT protein or a biologically active portion or fragment thereof of the invention can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode MCT polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MCT-encoding nucleic acid (*e.g.*, MCT DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about

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20 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MCT nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g., a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

15 A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* MCT DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsch, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA

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can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the

5 nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding

10 to an MCT nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing correspond to the

15 *Corynebacterium glutamicum* MCT DNAs of the invention. This DNA comprises sequences encoding MCT proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the

20 coding region of any of the nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, RXS, or RXC number having the designation "RXA", "RXN", "RXS" or "RXC" followed by 5 digits (*i.e.*, RXA02099, RXN03097, RXS00148, or RXC01748). Each of

25 the nucleic acid sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, RXS, or RXC designation to eliminate confusion. The recitation "one of the odd-numbered sequences in of the Sequence Listing", then, refers to any of the nucleic acid sequences in the Sequence Listing, which may also be distinguished by

30 their differing RXA, RXN, RXS, or RXC designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also set forth in the Sequence Listing, as an even-numbered SEQ ID NO: immediately following

the corresponding nucleic acid sequence. For example, the coding region for RXA03097 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, RXS, or RXC designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequences designated RXA02099, RXN03097, RXS00148, and RXC01748 are translations of the coding region of the nucleotide sequences of nucleic acid molecules RXA02099, RXN03097, RXS00148, and RXC01748, respectively. The correspondence between the RXA, RXN, RXS, and RXC nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1. For example, as set forth in Table 1, the nucleotide sequence of RXA00104 is SEQ ID NO:5, and the amino acid sequence of RXA00104 is SEQ ID NO:6.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, RXS, or RXC designation. For example, SEQ ID NO:11, designated, as indicated on Table 1, as "F RXA02581", is an F-designated gene, as are SEQ ID NOs: 31, 33, and 43 (designated on Table 1 as "F RXA02487", "F RXA02490", and "F RXA02809", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the *dapD* gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can

hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%,
5 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the
10 invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended
15 to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a
20 portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MCT protein. The nucleotide sequences determined from the cloning of the MCT genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning
25 MCT homologues in other cell types and organisms, as well as MCT homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a
30 sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing), an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a

nucleotide sequence of the invention can be used in PCR reactions to clone MCT homologues. Probes based on the MCT nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MCT protein, such as by measuring a level of an MCT-encoding nucleic acid in a sample of cells, *e.g.*, detecting MCT mRNA levels or determining whether a genomic MCT gene has been mutated or deleted.

10 In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to participate in the metabolism of compounds necessary for the
15 construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered
20 SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the protein or portion thereof is able to participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. Protein members of such membrane component metabolic pathways or membrane transport systems, as
25 described herein, may play a role in the production and secretion of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an MCT protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MCT protein activities are set forth in Table 1.

30 In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino

acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing).

Portions of proteins encoded by the MCT nucleic acid molecules of the invention are preferably biologically active portions of one of the MCT proteins. As used herein, the term "biologically active portion of an MCT protein" is intended to include a portion, *e.g.*, a domain/motif, of an MCT protein that participates in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has an activity as set forth in Table 1. To determine whether an MCT protein or a biologically active portion thereof can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an MCT protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the MCT protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MCT protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same MCT protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:). In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (e.g., a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 38% identical to the nucleotide sequence designated RXA01420 (SEQ ID NO:7), a nucleotide sequence which is greater than and/or at least 43% identical to the nucleotide sequence designated RXA00104 (SEQ ID NO:5), and a nucleotide sequence which is greater than and/or at least 45% identical to the nucleotide sequence designated RXA02173 (SEQ ID NO:25). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (e.g., at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* MCT nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MCT proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the MCT gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MCT protein, preferably a *C. glutamicum* MCT protein.

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Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MCT gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MCT that are the result of natural variation and that do not alter the functional activity of MCT proteins are intended to be within the scope of the invention.

- 5 Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MCT DNA of the invention can be isolated based on their homology to the *C. glutamicum* MCT nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in
- 10 another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent
- 15 conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such
- 20 stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated
- 25 nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C.*
- 30 *glutamicum* MCT protein.

In addition to naturally-occurring variants of the MCT sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be

introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded MCT protein, without altering the functional ability of the MCT protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a
5 nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MCT proteins (*e.g.*, an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said MCT protein, whereas an "essential" amino acid residue is required for MCT protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved
10 or only semi-conserved in the domain having MCT activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MCT activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MCT proteins that contain changes in amino acid residues that are not essential for MCT activity. Such MCT proteins differ in amino acid sequence from a
15 sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the MCT activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of participate in the metabolism of compounds
20 necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one
25 of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention..

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic
30 acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding

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amino acid positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are

5 homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an MCT protein homologous to a

10 protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of

15 the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side

20 chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains

25 (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MCT protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MCT coding sequence, such as by saturation

30 mutagenesis, and the resultant mutants can be screened for an MCT activity described herein to identify mutants that retain MCT activity. Following mutagenesis of the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing,

the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding MCT proteins described
5 above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can
10 hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MCT coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MCT protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are
15 translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO:5 (RXA00104) comprises nucleotides 1 to 756). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MCT. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*,
20 also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MCT disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the
25 entire coding region of MCT mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MCT mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MCT mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An
30 antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized

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using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified

5 nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine,

10 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-

15 methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from

20 the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MCT protein to thereby inhibit expression of the

25 protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a

30 selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve

sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention
5 is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a
10 chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes
15 (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave MCT mRNA transcripts to thereby inhibit translation of MCT mRNA. A ribozyme having specificity for an MCT-encoding nucleic acid can be designed based upon the nucleotide sequence of an MCT DNA disclosed herein (*i.e.*, SEQ ID NO. 5 (RXA00104)). For example, a derivative of a *Tetrahymena* L-19 IVS
20 RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MCT-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, MCT mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and
25 Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, MCT gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MCT nucleotide sequence (*e.g.*, an MCT promoter and/or enhancers) to form triple helical structures that prevent transcription of an MCT gene in target cells. See generally, Helene, C. (1991)
30 *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

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B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MCT protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185,

Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-,
5 trp-tet-, lpp-, lac-, lpp-lac-, lacI^q-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, army, SPO2, λ -P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MF α , AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use
10 artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described
15 herein (e.g., MCT proteins, mutant forms of MCT proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MCT proteins in prokaryotic or eukaryotic cells. For example, MCT genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.*
20 (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics
25 of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology*:
30 *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the MCT protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MCT protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89 ; and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by

host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 *gn1* gene under the transcriptional control of the *lacUV 5* promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming

5 Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of *Bacillus* species. Several plasmids of use in the transfer of genetic information into *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the

10 protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those

15 preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the MCT protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1

20 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J.

25 (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York (ISBN 0 444 904018).

Alternatively, the MCT proteins of the invention can be expressed in insect cells

30 using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.*

(1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the MCT proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the
5 spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+,
10 pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC
15 (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F.,
20 and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed.*, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type
25 (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and
30 Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477),

pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to MCT mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MCT protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other

suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via
5 conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid,
10 transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring*
15 *Harbor Laboratory Press, Cold Spring Harbor, NY, 1989*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is
20 generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MCT protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic
25 acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MCT gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the MCT gene.
30 Preferably, this MCT gene is a *Corynebacterium glutamicum* MCT gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous

recombination, the endogenous MCT gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MCT gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous MCT protein). In the homologous recombination vector, the altered portion of the MCT gene is flanked at its 5' and 3' ends by additional nucleic acid of the MCT gene to allow for homologous recombination to occur between the exogenous MCT gene carried by the vector and an endogenous MCT gene in a microorganism. The additional flanking MCT nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced MCT gene has homologously recombined with the endogenous MCT gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an MCT gene on a vector placing it under control of the lac operon permits expression of the MCT gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous MCT gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced MCT gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MCT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MCT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MCT gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MCT gene and protein modifications may be readily

produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an MCT protein. Accordingly, the invention further provides methods for producing MCT proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MCT protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered MCT protein) in a suitable medium until MCT protein is produced. In another embodiment, the method further comprises isolating MCT proteins from the medium or the host cell.

C. Isolated MCT Proteins

Another aspect of the invention pertains to isolated MCT proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of MCT protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MCT protein having less than about 30% (by dry weight) of non-MCT protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-MCT protein, still more preferably less than about 10% of non-MCT protein, and most preferably less than about 5% non-MCT protein. When the MCT protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MCT protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or

other chemicals" includes preparations of MCT protein having less than about 30% (by dry weight) of chemical precursors or non-MCT chemicals, more preferably less than about 20% chemical precursors or non-MCT chemicals, still more preferably less than about 10% chemical precursors or non-MCT chemicals, and most preferably less than about 5% chemical precursors or non-MCT chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the MCT protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* MCT protein in a microorganism such as *C. glutamicum*.

10 An isolated MCT protein or a portion thereof of the invention can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to
15 an amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes. The portion of the protein is preferably a biologically active portion as
20 described herein. In another preferred embodiment, an MCT protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing.. In yet another preferred embodiment, the MCT protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of the invention (e.g., a sequence of
25 an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the MCT protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%,
30 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention, or a

portion thereof. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. The preferred MCT proteins of the present invention also preferably possess at least one of the MCT activities described herein. For example, a preferred MCT protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of the invention, and which can participate in the metabolism of compounds necessary for the construction of cellular membranes in *C. glutamicum*, or in the transport of molecules across these membranes, or which has one or more of the activities set forth in Table 1.

In other embodiments, the MCT protein is substantially homologous to an amino acid sequence of the invention (e.g., a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MCT protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the MCT activities described herein. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention.

Biologically active portions of an MCT protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MCT protein, *e.g.*, the amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an MCT protein, which include
5 fewer amino acids than a full length MCT protein or the full length protein which is homologous to an MCT protein, and exhibit at least one activity of an MCT protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an MCT protein. Moreover, other
10 biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MCT protein include one or more selected domains/motifs or portions thereof having biological activity.

MCT proteins are preferably produced by recombinant DNA techniques. For
15 example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the MCT protein is expressed in the host cell. The MCT protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MCT protein,
20 polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MCT protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-MCT antibody, which can be produced by standard techniques utilizing an MCT protein or fragment thereof of this invention.

The invention also provides MCT chimeric or fusion proteins. As used herein,
25 an MCT "chimeric protein" or "fusion protein" comprises an MCT polypeptide operatively linked to a non-MCT polypeptide. An "MCT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an MCT protein, whereas a "non-MCT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MCT protein,
30 *e.g.*, a protein which is different from the MCT protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MCT polypeptide and the non-MCT polypeptide are fused

- 50 -

in-frame to each other. The non-MCT polypeptide can be fused to the N-terminus or C-terminus of the MCT polypeptide. For example, in one embodiment the fusion protein is a GST-MCT fusion protein in which the MCT sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of

5 recombinant MCT proteins. In another embodiment, the fusion protein is an MCT protein containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells), expression and/or secretion of an MCT protein can be increased through use of a heterologous signal sequence.

Preferably, an MCT chimeric or fusion protein of the invention is produced by

10 standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid

15 undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric

20 gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). An MCT-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MCT protein.

25 Homologues of the MCT protein can be generated by mutagenesis, e.g., discrete point mutation or truncation of the MCT protein. As used herein, the term "homologue" refers to a variant form of the MCT protein which acts as an agonist or antagonist of the activity of the MCT protein. An agonist of the MCT protein can retain substantially the same, or a subset, of the biological activities of the MCT protein. An antagonist of the

30 MCT protein can inhibit one or more of the activities of the naturally occurring form of the MCT protein, by, for example, competitively binding to a downstream or upstream member of the cell membrane component metabolic cascade which includes the MCT

protein, or by binding to an MCT protein which mediates transport of compounds across such membranes, thereby preventing translocation from taking place.

In an alternative embodiment, homologues of the MCT protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MCT protein for MCT protein agonist or antagonist activity. In one embodiment, a variegated library of MCT variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of MCT variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MCT sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MCT sequences therein. There are a variety of methods which can be used to produce libraries of potential MCT homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential MCT sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the MCT protein coding can be used to generate a variegated population of MCT fragments for screening and subsequent selection of homologues of an MCT protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an MCT coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MCT protein.

- Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of
- 5 MCT homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in
- 10 whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MCT homologues (Arkin and Yourvan (1992) *PNAS* 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).
- 15 In another embodiment, cell based assays can be exploited to analyze a variegated MCT library, using methods well known in the art.

D. Uses and Methods of the Invention

- The nucleic acid molecules, proteins, protein homologues, fusion proteins,
- 20 primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of MCT protein regions required for function; modulation of an MCT protein activity; modulation of the
- 25 metabolism of one or more cell membrane components; modulation of the transmembrane transport of one or more compounds; and modulation of cellular production of a desired compound, such as a fine chemical.

- The MCT nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a
- 30 close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the

extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to
5 pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the
10 body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria
15 in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in
20 the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

25 The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated
30 with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the

localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that
5 these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MCT nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic and transport processes in which the molecules of the invention participate are utilized by a wide variety of
10 prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein
15 which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MCT nucleic acid molecules of the invention may result in the production of MCT proteins having functional differences from the wild-type MCT
20 proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an MCT protein, either by interacting with the protein itself or a substrate or binding partner of the MCT protein, or by modulating the transcription or translation of
25 an MCT nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MCT proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the MCT protein is assessed.

There are a number of mechanisms by which the alteration of an MCT protein of
30 the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. Recovery of fine chemical compounds from large-scale cultures of *C. glutamicum* is

significantly improved if *C. glutamicum* secretes the desired compounds, since such compounds may be readily purified from the culture medium (as opposed to extracted from the mass of *C. glutamicum* cells). By either increasing the number or the activity of transporter molecules which export fine chemicals from the cell, it may be possible to

5 increase the amount of the produced fine chemical which is present in the extracellular medium, thus permitting greater ease of harvesting and purification. Conversely, in order to efficiently overproduce one or more fine chemicals, increased amounts of the cofactors, precursor molecules, and intermediate compounds for the appropriate biosynthetic pathways are required. Therefore, by increasing the number and/or activity

10 of transporter proteins involved in the import of nutrients, such as carbon sources (*i.e.*, sugars), nitrogen sources (*i.e.*, amino acids, ammonium salts), phosphate, and sulfur, it may be possible to improve the production of a fine chemical, due to the removal of any nutrient supply limitations on the biosynthetic process. Further, fatty acids and lipids are themselves desirable fine chemicals, so by optimizing the activity or increasing the

15 number of one or more MCT proteins of the invention which participate in the biosynthesis of these compounds, or by impairing the activity of one or more MCT proteins which are involved in the degradation of these compounds, it may be possible to increase the yield, production, and/or efficiency of production of fatty acid and lipid molecules from *C. glutamicum*.

20 The engineering of one or more MCT genes of the invention may also result in MCT proteins having altered activities which indirectly impact the production of one or more desired fine chemicals from *C. glutamicum*. For example, the normal biochemical processes of metabolism result in the production of a variety of waste products (*e.g.*, hydrogen peroxide and other reactive oxygen species) which may actively interfere with

25 these same metabolic processes (for example, peroxynitrite is known to nitrate tyrosine side chains, thereby inactivating some enzymes having tyrosine in the active site (Groves, J.T. (1999) *Curr. Opin. Chem. Biol.* 3(2): 226-235). While these waste products are typically excreted, the *C. glutamicum* strains utilized for large-scale fermentative production are optimized for the overproduction of one or more fine

30 chemicals, and thus may produce more waste products than is typical for a wild-type *C. glutamicum*. By optimizing the activity of one or more MCT proteins of the invention which are involved in the export of waste molecules, it may be possible to improve the

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viability of the cell and to maintain efficient metabolic activity. Also, the presence of high intracellular levels of the desired fine chemical may actually be toxic to the cell, so by increasing the ability of the cell to secrete these compounds, one may improve the viability of the cell.

5 Further, the MCT proteins of the invention may be manipulated such that the relative amounts of various lipid and fatty acid molecules produced are altered. This may have a profound effect on the lipid composition of the membrane of the cell. Since each type of lipid has different physical properties, an alteration in the lipid composition of a membrane may significantly alter membrane fluidity. Changes in membrane fluidity
10 can impact the transport of molecules across the membrane, which, as previously explicated, may modify the export of waste products or the produced fine chemical or the import of necessary nutrients. Such membrane fluidity changes may also profoundly affect the integrity of the cell; cells with relatively weaker membranes are more vulnerable in the large-scale fermentor environment to mechanical stresses which may
15 damage or kill the cell. By manipulating MCT proteins involved in the production of fatty acids and lipids for membrane construction such that the resulting membrane has a membrane composition more amenable to the environmental conditions extant in the cultures utilized to produce fine chemicals, a greater proportion of the *C. glutamicum* cells should survive and multiply. Greater numbers of *C. glutamicum* cells in a culture
20 should translate into greater yields, production, or efficiency of production of the fine chemical from the culture.

The aforementioned mutagenesis strategies for MCT proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art.
25 Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MCT nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C.*
30 *glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do

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not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents,
5 published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: GENES IN THE APPLICATION

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXN03097	VV0062	3	557	AMMONIUM TRANSPORT SYSTEM
3	4	RXA02099	GR00630	6198	6470	AMMONIUM TRANSPORT SYSTEM
5	6	RXA00104	GR00014	15895	16650	CYSQ PROTEIN, ammonium transport protein

Polyketide Synthesis						
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
7	8	RXA01420	GR00416	775	17	4"-MYCAROSYL ISOVALERYL-COA TRANSFERASE (EC 2.---)
9	10	RXN02581	VV0098	30482	28623	POLYKETIDE SYNTHASE
11	12	F RXA02581	GR00741	1	1527	POLYKETIDE SYNTHASE
13	14	RXA02582	GR00741	1890	6719	PROBABLE POLYKETIDE SYNTHASE CY338.20
15	16	RXA01138	GR00318	1656	2072	ACTINORHODIN POLYKETIDE DIMERASE (EC ----)
17	18	RXA01980	GR00573	1470	838	POLYKETIDE CYCLASE
19	20	RXN01007	VV0021	2572	866	FRNA
21	22	RXN00784	VV0103	27531	28265	FRNE

Fatty acid and lipid synthesis						
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
23	24	RXA02335	GR00672	550	2322	BIOTIN CARBOXYLASE (EC 6.3.4.14)
25	26	RXA02173	GR00641	7473	8924	ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT BETA (EC 6.4.1.2)
27	28	RXA01764	GR00500	2178	3110	3-OXOACYL-ACYL-CARRIER PROTEIN REDUCTASE (EC 1.1.1.100)
29	30	RXN02487	VV0007	6367	4664	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
31	32	F RXA02487	GR00718	4937	4650	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
33	34	F RXA02490	GR00720	817	5	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
35	36	RXA01467	GR00422	920	1210	ACYL CARRIER PROTEIN
37	38	RXA00796	GR00212	202	5	Acyl carrier protein phosphodiesterase
39	40	RXA01897	GR00544	617	1159	Acyl carrier protein phosphodiesterase
41	42	RXN02809	VV0342	380	6	Acyl carrier protein phosphodiesterase
43	44	F RXA02809	GR00790	277	5	Acyl carrier protein phosphodiesterase
45	46	RXN00113	VV0129	103	5724	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41;
47	48	F RXA00113	GR00017	2	3295	FATTY-ACID SYNTHASE (EC 2.3.1.85)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
49	50	RXN03111	VW0084	6040	5	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
51	52	F RXA00158	GR00024	2088	4	FATTY ACID SYNTHASE (EC 2.3.1.85)
53	54	F RXA00572	GR00155	2	3832	FATTY ACID SYNTHASE (EC 2.3.1.85)
55	56	RXA02582	GR00741	1890	6719	PROBABLE POLYKETIDE SYNTHASE CY338.20
57	58	RXA02691	GR00754	15347	14541	FATTY ACYL RESPONSIVE REGULATOR
59	60	RXA00880	GR00242	6213	8057	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
61	62	RXA01060	GR00296	9566	10489	OMEGA-3 FATTY ACID DESATURASE (EC 1.14.99.-)
63	64	RXN01722	VW0036	2938	1214	MEDIUM-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.-)
65	66	F RXA01722	GR00488	5746	4022	MEDIUM-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.-)
67	68	RXA01644	GR00456	9854	8577	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE (EC 2.1.1.79)
69	70	RXA02029	GR00618	356	1669	CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE (EC 2.1.1.79)
71	72	RXA01801	GR00509	3396	2380	ENOYL-COA HYDRATASE (EC 4.2.1.17)
73	74	RXN02512	VW0171	16147	15185	LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (EC 2.3.1.-)
75	76	F RXA02512	GR00721	3303	4259	LIPID A BIOSYNTHESIS LAUROYL ACYLTRANSFERASE (EC 2.3.1.-)
77	78	RXA00899	GR00245	1599	2864	CARDIOLIPIN SYNTHETASE (EC 2.7.8.-)
79	80	RXN00819	VW0054	18127	19455	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
81	82	F RXA00819	GR00221	18	1007	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
83	84	F RXA01766	GR00500	4081	4371	ACYL-COA DEHYDROGENASE (EC 1.3.99.-)
85	86	RXN01762	VW0054	15318	13783	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
87	88	F RXA01762	GR00500	1272	10	LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
89	90	RXA00881	GR00179	3405	2662	3-OXOACYL-ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
91	92	RXA00802	GR00214	3803	4516	3-OXOACYL-ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
93	94	RXA02133	GR00639	3	308	3-OXOACYL-ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100)
95	96	RXN01114	VW0182	9118	10341	3-KETOACYL-COA THIOLASE (EC 2.3.1.16)
97	98	F RXA01114	GR00308	2	793	3-KETOACYL-COA THIOLASE (EC 2.3.1.16)
99	100	RXA01894	GR00542	1622	2476	PHOSPHATIDYLGLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.7.7.41)
101	102	RXA02599	GR00742	3179	3655	PHOSPHATIDYLGLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.7.7.41)
103	104	RXN02638	VW0098	54531	53656	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
105	106	F RXA02638	GR00749	8	511	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
107	108	RXA00856	GR00232	720	1256	CDP-DIACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
109	110	RXA02511	GR00721	2621	3277	CDP-DIACYLGLYCEROL-GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
111	112	RXN02836	VW0102	32818	33372	PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
113	114	F RXA02836	GR00827	106	411	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
115	116	RXA02578	GR00740	2438	3541	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
117	118	RXA02150	GR00639	18858	19658	PUTATIVE ACYLTRANSFERASE
119	120	RXA00607	GR00160	1869	2249	1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.51)
121	122	RXA02397	GR00698	1888	2583	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.-)
123	124	RXN03110	VW0083	16568	17929	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.-)
125	126	F RXA00660	GR00171	1027	5	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
127	128	RXA00801	GR00214	3138	3770	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
129	130	RXA00821	GR00221	1469	2311	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
131	132	RXN02966	VW0143	12056	13462	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
133	134	F RXA01833	GR00517	1666	260	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
135	136	RXA01853	GR00525	5561	5010	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
137	138	RXN02424	VV0116	10570	11169	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
139	140	F RXA02424	GR00706	808	428	HYDROXYACYLGLUTATHIONE HYDROLASE (EC 3.1.2.6)
141	142	RXN00419	VV0112	1024	266	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
143	144	F RXA00419	GR00095	3	464	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
145	146	F RXA00421	GR00096	565	723	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
147	148	RXN02923	VV0088	3301	2564	ACETOACETYL-COA REDUCTASE (EC 1.1.1.36)
149	150	RXN02922	VV0321	11407	10328	ACYL-COA DEHYDROGENASE, SHORT-CHAIN SPECIFIC (EC 1.3.99.2)
151	152	RXN03065	VV0038	6237	6629	Holo-(acyl-carrier protein) synthase (EC 2.7.8.7)
153	154	RXN03132	VV0127	39053	39472	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (EC 2.3.1.-)
155	156	RXN03157	VV0188	1607	1170	LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN KDTB (AE000805) LPS biosynthesis RbU related protein [Methanobacterium thermoautotrophicum]
157	158	RXN00934	VV0171	15181	14099	LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN KDTB (AE000805) LPS biosynthesis RbU related protein [Methanobacterium thermoautotrophicum]
159	160	RXN00792	VV0321	10328	9132	ACYL-COA DEHYDROGENASE, SHORT-CHAIN SPECIFIC (EC 1.3.99.2)
161	162	RXN00931	VV0171	13011	12166	ACYL-COA THIOESTERASE II (EC 3.1.2.-)
163	164	F RXA00931	GR00253	4959	4114	thioesterase II
165	166	RXN01421	VV0122	16024	15638	ACYLTRANSFERASE (EC 2.3.1.-)
167	168	RXN02342	VV0078	3460	4266	BIOTIN-(ACETYL-COA-CARBOXYLASE) SYNTHETASE (EC 6.3.4.15)
169	170	RXN00563	VV0038	1	2739	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
171	172	RXN02168	VV0100	2894	81	FATTY ACID SYNTHASE (EC 2.3.1.85) [INCLUDES: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]
173	174	RXN01090	VV0155	6483	5686	KETOACYL REDUCTASE HETN (EC 1.3.1.-)
175	176	RXN02062	VV0222	3159	1990	Lipopolysaccharide N-acetylglucosaminyltransferase
177	178	RXN02148	VV0300	16561	17703	Lipopolysaccharide N-acetylglucosaminyltransferase
179	180	RXN02595	VV0098	11098	9935	Lipopolysaccharide N-acetylglucosaminyltransferase
181	182	RXN00148	VV0167	9849	12059	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
183	184	RXN00149	VV0167	7995	9842	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)
185	186	RXN02106	VV0123	22649	21594	LIPOATE-PROTEIN LIGASE A (EC 6.---)
187	188	RXN01746	VV0185	934	1686	LIPOATE-PROTEIN LIGASE B (EC 6.---)
189	190	RXN01747	VV0185	1826	2869	LIPOIC ACID SYNTHETASE
191	192	RXN01748	VV0185	3001	3780	protein involved in lipid metabolism
193	194	RXC00354	VV0135	33604	32792	Cytosolic Protein involved in lipid metabolism
195	196	RXC01749	VV0185	3953	5569	Membrane Spanning Protein involved in lipid metabolism
Fatty acid degradation						
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
197	198	RXA02268	GR00655	2182	3081	LIPASE (EC 3.1.1.3)
199	200	RXA02269	GR00655	3094	4065	LIPASE (EC 3.1.1.3)
201	202	RXA01614	GR00449	8219	7197	LYSOPHOSPHOLIPASE L2 (EC 3.1.1.5)
203	204	RXA01983	GR00573	3559	3053	LIPASE (EC 3.1.1.3)
205	206	RXN02947	VV0078	1319	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
207	208	F RXA02320	GR00667	593	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
209	210	F RXA02851	GR00851	524	6	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
211	212	RXN02321	VV0078	3291	1663	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
213	214	F RXA02321	GR00667	1380	937	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
215	216	F RXA02343	GR00675	1403	1816	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
217	218	F RXA02850	GR00850	2	493	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
219	220	RXA02583	GR00741	6743	8290	PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
221	222	RXA00870	GR00239	809	2320	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE (ACYLATING) (EC 1.2.1.27) 2-Methyl-3-oxopropanoate:NAD+ oxidoreductase (CoA-propanoylating)
223	224	RXA01260	GR00367	2381	1200	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
225	226	RXA01261	GR00367	2607	2437	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
227	228	RXA01136	GR00318	685	1116	ISOVALERYL-COA DEHYDROGENASE (EC 1.3.99.10)
229	230	RXN00559	VW0103	7568	6552	PROTEIN VDLD
231	232	F RXA00559	GR00149	218	6	PROTEIN VDLD
233	234	RXA01580	GR00440	707	6	Glycerophosphoryl diester phosphodiesterase
235	236	RXA02677	GR00754	3119	3877	GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46)
237	238	RXS01166	VW0117	18142	16838	EXTRACELLULAR LIPASE PRECURSOR (EC 3.1.1.3)

Terpenoid biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
239	240	RXA00875	GR00241	2423	1857	ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (EC 5.3.3.2)
241	242	RXA01292	GR00373	1204	2388	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
243	244	RXA01293	GR00373	2370	2696	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
245	246	RXA02310	GR00665	1132	2394	GERANYLGERANYL HYDROGENASE
247	248	RXA02718	GR00758	18539	19585	GERANYLGERANYL PYROPHOSPHATE SYNTHASE (EC 2.5.1.1)
249	250	RXA01067	GR00298	1453	2181	undecaprenyl-diphosphate synthase (EC 2.5.1.31)
251	252	RXA01269	GR00367	20334	19894	UNDECAPRENYL-PHOSPHATE GALACTOSEPHOSPHOTRANSFERASE (EC 2.7.8.6)
253	254	RXA01205	GR00346	3	533	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
255	256	RXA01576	GR00438	8053	8811	DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE (EC 2.4.1.117)
257	258	RXN02309	VW0025	28493	29542	OCTAPRENYL-DIPHOSPHATE SYNTHASE (EC 2.5.1.-)
259	260	F RXA02309	GR00665	978	4	OCTAPRENYL-DIPHOSPHATE SYNTHASE (EC 2.5.1.-)
261	262	RXN00477	VW0086	38905	37262	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
263	264	F RXA00477	GR00119	13187	11544	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
265	266	RXA00478	GR00119	14020	13190	PHYTOENE DEHYDROGENASE (EC 1.3.-.-)
267	268	RXA01291	GR00373	345	1277	PHYTOENE SYNTHASE (EC 2.5.1.-)
269	270	RXA00480	GR00119	17444	16329	FARNESYL DIPHOSPHATE SYNTHASE (EC 2.5.1.1) (EC 2.5.1.10)
271	272	RXS01879	VW0105	1505	573	isopentenyl-phosphate kinase (EC 2.7.4.-)
273	274	RX02023	VW0160	3234	4001	P450 cytochrome isopentenyltransf, ferridox
275	276	RXS00948	VW0107	4266	5384	12-oxophytodienoate reductase (EC 1.3.1.42)
277	278	RXS02228	VW0068	1876	2778	TRNA DELTA(2)-ISOPENTENYL PYROPHOSPHATE TRANSFERASE (EC 2.5.1.8)
279	280	RXC01971	VW0105	4545	3715	Metal-Dependent Hydrolase involved in metabolism of terpenoids
281	282	RXC02697	VW0017	31257	32783	Membrane protein involved in metabolism of terpenoids

Table 1 (continued)

ABC-Transporter

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
283	284	RXN01946	VW0228	2	1276	Hypothetical ABC Transporter ATP-Binding Protein
285	286	F RXA01946	GR00559	1849	575	(AL021184) ABC transporter ATP-binding protein [Mycobacterium tuberculosis]
287	288	RXN00164	VW0232	1782	94	Hypothetical ABC Transporter ATP-Binding Protein
289	290	F RXA00164	GR00025	1782	94	, P, G, R ATPase subunits of ABC transporters
291	292	RXN00243	VW0057	28915	27899	, P, G, R ATPase subunits of ABC transporters
293	294	F RXA00243	GR00037	930	4	, P, G, R ATPase subunits of ABC transporters
295	296	RXA00259	GR00039	8469	6268	, P, G, R ATPase subunits of ABC transporters
297	298	RXN00410	VW0086	51988	51323	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
299	300	F RXA00410	GR00092	829	164	, P, G, R ATPase subunits of ABC transporters
301	302	RXN00456	VW0076	6780	8156	, P, G, R ATPase subunits of ABC transporters
303	304	F RXA00456	GR00114	316	5	, P, G, R ATPase subunits of ABC transporters
305	306	F RXA00459	GR00115	1231	245	, P, G, R ATPase subunits of ABC transporters
307	308	RXN01604	VW0137	8117	7470	, P, G, R ATPase subunits of ABC transporters
309	310	F RXA01604	GR00448	2	607	, P, G, R ATPase subunits of ABC transporters
311	312	RXN02547	VW0057	27726	25588	, P, G, R ATPase subunits of ABC transporters
313	314	F RXA02547	GR00726	22055	19932	, P, G, R ATPase subunits of ABC transporters
315	316	RXN02571	VW0101	12331	13359	MALTOSE/MALTODEXTRIN TRANSPORT ATP-BINDING PROTEIN MALK
317	318	F RXA02571	GR00736	1469	2497	, P, G, R ATPase subunits of ABC transporters
319	320	RXN02074	VW0318	12775	11153	TRANSPORT ATP-BINDING PROTEIN CYDD
321	322	F RXA02074	GR00628	5798	4176	, P, G, R ATPase subunits of ABC transporters
323	324	RXA02095	GR00629	14071	15474	, P, G, R ATPase subunits of ABC transporters
325	326	RXA02225	GR00652	3156	2275	, P, G, R ATPase subunits of ABC transporters
327	328	RXA02253	GR00654	20480	21406	, P, G, R ATPase subunits of ABC transporters
329	330	RXN01881	VW0105	529	95	Hypothetical ABC Transporter ATP-Binding Protein
331	332	F RXA01881	GR00537	3092	3532	ATPase components of ABC transporters with duplicated ATPase domains
333	334	RXA00526	GR00136	1353	664	Hypothetical ABC Transporter ATP-Binding Protein
335	336	RXN00733	VW0132	1647	2531	Hypothetical ABC Transporter ATP-Binding Protein
337	338	F RXA00733	GR00197	411	4	Hypothetical ABC Transporter ATP-Binding Protein
339	340	RXA00735	GR00198	849	181	Hypothetical ABC Transporter ATP-Binding Protein
341	342	RXA00878	GR00242	3733	1871	Hypothetical ABC Transporter ATP-Binding Protein
343	344	RXN01191	VW0169	10478	12067	Hypothetical ABC Transporter ATP-Binding Protein
345	346	F RXA01191	GR00341	1571	165	Hypothetical ABC Transporter ATP-Binding Protein
347	348	RXN01212	VW0169	3284	4207	Hypothetical ABC Transporter ATP-Binding Protein
349	350	F RXA01212	GR00350	1	813	Hypothetical ABC Transporter ATP-Binding Protein
351	352	RXA02749	GR00764	4153	5028	Hypothetical ABC Transporter ATP-Binding Protein
353	354	RXA02224	GR00652	2271	475	Hypothetical ABC Transporter ATP-Binding Protein
355	356	RXN01602	VW0229	1109	2638	Hypothetical ABC Transporter ATP-Binding Protein
357	358	RXN02515	VW0087	962	1717	Hypothetical ABC Transporter ATP-Binding Protein
359	360	RXN00525	VW0079	26304	27566	Hypothetical ABC Transporter Pemease Protein
361	362	RXN02096	VW0126	20444	22135	Hypothetical ABC Transporter Pemease Protein
363	364	RXN00412	VW0086	53923	52844	Hypothetical Amino Acid ABC Transporter ATP-Binding Protein
365	366	RXN00411	VW0086	52844	52170	Hypothetical Amino Acid ABC Transporter Pemease Protein
367	368	RXN02614	VW0313	5964	5236	TAURINE TRANSPORT ATP-BINDING PROTEIN TAUB
369	370	RXN02613	VW0313	5223	4267	TAURINE-BINDING PERIPLASMIC PROTEIN PRECURSOR

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
371		RXN00368	VW0226	2300	726	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
372		F RXA00368	GR00076	1	579	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
373	374	F RXA00370	GR00077	6	803	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA
375	376	RXN01285	VW0215	1780	1055	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
377	378	RXN00523	VW0194	1363	338	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
379	380	RXN01142	VW0077	5805	6302	NITRATE TRANSPORT PROTEIN NRTD
381	382	RXN01141	VW0077	4644	5468	NITRATE TRANSPORT PROTEIN NRTA
383	384	RXN01002	VW0106	8858	8055	PHOSPHONATES TRANSPORT ATP-BINDING PROTEIN PHNC
385	386	RXN01000	VW0106	7252	6407	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
387	388	RXN01732	VW0106	9944	8895	PHOSPHONATES-BINDING PERIPLASMIC PROTEIN PRECURSOR
389	390	RXN03080	VW0045	1670	2449	FERRIC ENTEROBACTIN TRANSPORT ATP-BINDING PROTEIN FEPC
391	392	RXN03081	VW0045	2476	2934	FERRIC ENTEROBACTIN-BINDING PERIPLASMIC PROTEIN PRECURSOR
393	394	RXN03082	VW0045	3131	3451	FERRIC ENTEROBACTIN-BINDING PERIPLASMIC PROTEIN PRECURSOR
395	396					

Other transporters

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
397	398	RXA02261	GR00654	30536	32291	AMMONIUM TRANSPORT SYSTEM
399	400	RXA02020	GR00613	1015	5	AROMATIC AMINO ACID TRANSPORT PROTEIN AROP
401	402	RXA00281	GR00043	4721	5404	BACTRACIN TRANSPORT ATP-BINDING PROTEIN BCRA
403	404	RXN00570	VW0147	855	4	BENZOATE MEMBRANE TRANSPORT PROTEIN
405	406	F RXA00570	GR00153	1	498	BENZOATE MEMBRANE TRANSPORT PROTEIN
407	408	RXN00571	VW0173	1298	42	BENZOATE MEMBRANE TRANSPORT PROTEIN
409	410	F RXA00571	GR00154	2	1186	BENZOATE MEMBRANE TRANSPORT PROTEIN
411	412	RXA00962	GR00268	2	667	BENZOATE MEMBRANE TRANSPORT PROTEIN
413	414	RXA02811	GR00792	177	560	BENZOATE MEMBRANE TRANSPORT PROTEIN
415	416	RXA02115	GR00635	2	1198	BENZOATE MEMBRANE TRANSPORT PROTEIN
417	418	RXN00590	VW0178	5043	6230	BENZOATE MEMBRANE TRANSPORT PROTEIN
419	420	F RXA00590	GR00157	178	564	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
421	422	F RXA01538	GR00427	5040	5429	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
423	424	RXA01727	GR00489	1471	194	BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM CARRIER PROTEIN
425	426	RXA00623	GR00163	6525	7862	C4-DICARBOXYLATE TRANSPORT PROTEIN
427	428	RXA01584	GR00441	55	597	CHROMATE TRANSPORT PROTEIN
429	430	RXA00852	GR00231	3137	2448	COBALT TRANSPORT ATP-BINDING PROTEIN CBIQ
431	432	RXA00690	GR00181	1213	68	COBALT TRANSPORT PROTEIN CBIQ
433	434	RXA00827	GR00223	1319	567	COBALT TRANSPORT PROTEIN CBIQ
435	436	RXA00851	GR00231	2448	1840	COBALT TRANSPORT PROTEIN CBIQ
437	438	RX503220				D-XYLOSE-PROTON SYMPORT
439	440	F RXA02762	GR00768	346	630	D-XYLOSE PROTON-SYMPORTER
441	442	RXN00092	VW0129	27509	26844	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
443	444	F RXA00092	GR00014	1	204	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
445	446	RXN03060	VW0030	6227	5376	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
447	448	F RXA02618	GR00745	1914	2351	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ
449	450	F RXA02900	GR10040	2979	2128	GLUTAMINE TRANSPORT ATP-BINDING PROTEIN GLNQ

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
451	452	RXS03212				GLYCINE BETAINES TRANSPORTER BETP
453	454	F RXA01591	GR00446	3	947	GLYCINE BETAINES TRANSPORTER BETP
455	456	RXN00201	VV0096	197	6	HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD
457	458	F RXA00201	GR00032	191	6	HIGH AFFINITY RIBOSE TRANSPORT PROTEIN RBSD
459	460	RXA01221	GR00354	2108	2833	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN BRAG
461	462	RXA01222	GR00354	2844	3542	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT ATP-BINDING PROTEIN LIVF
463	464	RXA01219	GR00354	151	1032	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVH
465	466	RXA01220	GR00354	1032	2108	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVM
467	468	RXA00091	GR00013	7762	8514	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
469	470	RXA00228	GR00032	29232	28642	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
471	472	RXA00346	GR00064	1054	1743	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
473	474	RXA00524	GR00135	779	1111	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
475	476	RXA01823	GR00516	591	1367	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
477	478	RXA02767	GR00770	1032	1814	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
479	480	RXA02792	GR00777	8581	7829	IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE
481	482	RXN02929	VV0090	36837	37874	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
483	484	F RXA01235	GR00358	1165	194	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
485	486	RXA02794	VV0134	10625	9552	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
487	488	F RXA01419	GR00415	888	1151	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
489	490	F RXA02794	GR00777	10172	9552	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
491	492	RXN03079	VV0045	644	1660	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
493	494	F RXA02865	GR10007	3832	2816	IRON(III) DICITRATE TRANSPORT SYSTEM PERMEASE PROTEIN FECD
495	496	RXA00181	GR00028	3954	2383	PROLINE TRANSPORT SYSTEM
497	498	RXA00591	GR00158	229	1581	PROLINE/BETAINE TRANSPORTER
499	500	RXA01629	GR00453	3476	1965	PROLINE/BETAINE TRANSPORTER
501	502	RXA02030	GR00618	3072	1687	PROLINE/BETAINE TRANSPORTER
503	504	RXA00186	GR00028	12242	12988	SHORT-CHAIN FATTY ACIDS TRANSPORTER
505	506	RXA00187	GR00028	13097	13447	SHORT-CHAIN FATTY ACIDS TRANSPORTER
507	508	RXA01667	GR00464	703	1908	SHORT-CHAIN FATTY ACIDS TRANSPORTER
509	510	RXA02171	GR00641	6571	4919	SODIUM/PROLINE SYMPORTER
511	512	RXA00902	GR00245	4643	5875	SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN
513	514	RXA00941	GR00257	1999	683	sodium-dependent phosphate transport protein
515	516	RXN00449	VV0112	30992	32572	Sodium-Dicarboxylate Symport Protein
517	518	F RXA00449	GR00109	2040	1036	Sodium-Dicarboxylate Symport Protein
519	520	F RXA01755	GR00498	352	5	Sodium-Dicarboxylate Symport Protein
521	522	RXA00269	GR00041	1826	1038	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POT
523	524	RXA00369	GR00076	583	1299	SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POT
525	526	RXA02073	GR00628	4176	2647	TRANSPORT ATP-BINDING PROTEIN CYDD
527	528	RXA01399	GR00409	1	1119	TRANSPORT ATP-BINDING PROTEIN CYDD
529	530	RXA01339	GR00389	8408	7164	TYROSINE-SPECIFIC TRANSPORT PROTEIN
531	532	RXA02527	GR00725	5519	6847	2-OXOGLUTARATE/MALATE TRANSLATOR PRECURSOR
533	534	RXN00298	VV0176	40228	42072	HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN
535	536	F RXA00298	GR00048	4459	6303	Ectoine/Proline/Glycine betaine carrier ectp

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
537	538	RXA00596	GR00159	335	787	potassium efflux system protein phaE C4-DICARBOXYLATE-BINDING PERIPLASMIC PROTEIN PRECURSOR, transport protein
539	540	RXA02364	GR00686	841	215	
541	542	RXN01411	VV0050	26015	26779	SHIKIMATE TRANSPORTER
543	544	RXN00960	VV0075	1139	105	PROTON/SODIUM-GLUTAMATE SYMPORT PROTEIN
545	546	RXN02447	VV0107	14297	13203	GALACTOSE-PROTON SYMPORT
547	548	RXN02395	VV0176	16747	14858	GLYCINE BETAIN TRANSPORTER BETP
549	550	RXN02348	VV0078	6027	7910	KUP SYSTEM POTASSIUM UPTAKE PROTEIN
551	552	RXN00297	VV0176	38630	39541	Hypothetical Malonate Transporter
553	554	RXN03103	VV0070	845	1087	GLUTAMATE-BINDING PROTEIN PRECURSOR
555	556	RXN02993	VV0071	736	65	GLUTAMINE-BINDING PROTEIN
557	558	RXN00349	VV0135	35187	36653	Hypothetical Trehalose Transport Protein
559	560	RXN03095	VV0057	4056	4424	CADIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG
561	562	RXN03160	VV0189	5150	5617	CHROMATE TRANSPORT PROTEIN
563	564	RXN02955	VV0176	8666	9187	DICARBOXYLATE TRANSPORTER
565	566	RXN03109	VV0082	659	6	HEMIN TRANSPORT SYSTEM PERMEASE PROTEIN HMLU
567	568	RXN02979	VV0149	2150	2383	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
569	570	RXN02987	VV0234	527	294	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
571	572	RXN03084	VV0048	900	1817	IRON(III) DICITRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
573	574	RXN03183	VV0372	1	417	TREHALOSE/MALTOSE BINDING PROTEIN
575	576	RXN01139	VV0077	2776	1823	CATION EFFLUX SYSTEM PROTEIN CZCD
577	578	RXN00378	VV0223	8027	5418	Cation transport ATPases
579	580	RXN01338	VV0032	2	1903	CATION-TRANSPORTING ATPASE PACS (EC 3.6.1.-)
581	582	RXN00980	VV0149	2635	4428	CATION-TRANSPORTING P-TYPE ATPASE B (EC 3.6.1.-)
583	584	RXN00099	VV0129	18876	17704	CYANATE TRANSPORT PROTEIN CYNX
585	586	RXN02662	VV0315	1461	1724	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
587	588	RXN02442	VV0217	5970	6818	zinc transport system membrane protein
589	590	RXN02443	VV0217	6818	7771	zinc-binding periplasmic protein precursor
591	592	RXN00842	VV0138	8686	7487	BRANCHED CHAIN AMINO ACID TRANSPORT SYSTEM II CARRIER PROTEIN
593	594	F RXA00842	GR00228	3208	2009	Permeases
595	596	RXN00832	VV0180	3133	4182	CALCIUM/PROTON ANTIporter
597	598	RXN00466	VV0086	63271	64266	Ferrichrome transport proteins
599	600	RXN01936	VV0127	40116	41387	MACROLIDE-EFFLUX PROTEIN
601	602	RXN01995	VV0182	2139	3476	PUTATIVE 3-(3-HYDROXYPHENYL) PROPIONATE TRANSPORT PROTEIN
603	604	RXN00661	VV0142	9718	9029	PNUC PROTEIN

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
605	606	RXN02566	VV0154	11823	13031	NUCLEOSIDE PERMEASE NUPG
607	608	F RXA02561	GR00732	664	5	NUCLEOSIDE PERMEASE NUPG
609	610	F RXA02566	GR00733	782	345	NUCLEOSIDE PERMEASE NUPG
611	612	RXA00051	GR00008	5770	7173	PROLINE-SPECIFIC PERMEASE PROY
613	614	RXA01172	GR00334	2687	4141	SULFATE PERMEASE
615	616	RXA02128	GR00637	2906	4600	SULFATE PERMEASE

Permeases

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
617		RXA02634	GR00748	6045	7655	SULFATE PERMEASE
619	620	RXN02233	VW0068	6856	8142	URACIL PERMEASE
621	622	F RXA02233	GR00653	6856	8067	URACIL PERMEASE
623	624	RXN02372	VW0213	9311	11197	XANTHINE PERMEASE
625	626	F RXA02372	GR00688	6	560	XANTHINE PERMEASE
627	628	F RXA02377	GR00689	3336	4526	XANTHINE PERMEASE
629	630	RXA02676	GR00754	2697	1309	GLUCONATE PERMEASE
631	632	RXN00432	VW0112	14751	13267	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
633	634	F RXA00432	GR00100	1	891	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
635	636	F RXA00436	GR00101	45	569	NA(+)-LINKED D-ALANINE GLYCINE PERMEASE
637	638	RXA00847	GR00230	1829	381	OLIGOPEPTIDE-BINDING PROTEIN APPA PRECURSOR (permease)
639	640	RXN01382	VW0119	8670	9761	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR
641	642	F RXA01382	GR00405	1067	6	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR (permease)
643	644	RXA02659	GR00753	2	313	OLIGOPEPTIDE-BINDING PROTEIN OPPA PRECURSOR (permease)
645	646	RXN02933	VW0176	30042	29233	DIPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN DPPC
647	648	RXN02991	VW0072	618	4	GLUTAMINE TRANSPORT SYSTEM PERMEASE PROTEIN GLNP
649	650	RXN02992	VW0072	842	621	GLUTAMINE TRANSPORT SYSTEM PERMEASE PROTEIN GLNP
651	652	RXN02996	VW0069	1980	2648	HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PERMEASE PROTEIN LIVH
653	654	RXN03126	VW0112	9894	9001	TEICHOIC ACID TRANSLOCATION PERMEASE PROTEIN TAGG
655	656	RXN00443	VW0112	21572	20769	MOLYBDATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
657	658	RXN00444	VW0112	20785	19949	MOLYBDENUM TRANSPORT SYSTEM PERMEASE PROTEIN MODB
659	660	RXN00193	VW0371	1	594	POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM PERMEASE PROTEIN AMYD
661	662	RXN01298	VW0116	2071	1142	POTENTIAL STARCH DEGRADATION PRODUCTS TRANSPORT SYSTEM PERMEASE PROTEIN AMYD

Channel Proteins

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
663	664	RXA01737	GR00493	2913	3971	POTASSIUM CHANNEL PROTEIN
665	666	RXN02348	VW0078	6027	7910	KUP SYSTEM POTASSIUM UPTAKE PROTEIN
667	668	RXA02426	GR00707	2165	633	PROBABLE NA(+)/H(+) ANTIPORTER
669	670	RXN03164	VW0277	1586	2455	POTASSIUM CHANNEL BETA SUBUNIT
671	672	RXN00024	VW0127	64219	63275	POTASSIUM CHANNEL BETA SUBUNIT

Lipoprotein and Lipopolysaccharide synthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
673	674	RXN01164	VW0117	15894	14260	DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) / APOLIPOPROTEIN N-ACYLTRANSFERASE (EC 2.3.1.-)
675	676	RXN01168	VW0117	14224	13415	DOLICHOL-PHOSPHATE MANNOSYLTRANSFERASE (EC 2.4.1.83) / APOLIPOPROTEIN N-ACYLTRANSFERASE (EC 2.3.1.-)

TABLE 2 - Excluded Genes

GeneBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the <i>Corynebacterium glutamicum</i> rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinase synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

	Promoter and operator regions of tryptophan operon	
E01377		Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937	Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040	Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041	Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307	Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376	Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377	Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484	Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108	Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112	Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 199724661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of <i>Corynebacterium glutamicum</i> 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in <i>Corynebacterium glutamicum</i> : molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the <i>Corynebacterium glutamicum</i> mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the <i>Corynebacterium diphtheriae</i> dtxR from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthraniolate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; bmQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The <i>Corynebacterium glutamicum</i> aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the bmQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthraniolate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgIIIM; cgIIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cglIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the <i>lysA</i> gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum fda</i> gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the <i>dapA</i> gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambdacorynephage</i> ," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum lysA</i> gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Purative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdaCorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)
X66078	copI	PsI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)

Table 2 (continued)

X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X75084	mirA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)

Table 2 (continued)

	16S rDNA	16S ribosomal RNA	
X82061			Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of <i>C. glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting 'Arthrobacter aureus C70,' <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

Table 2 (continued)

X90360	Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361	Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362	Promoter fragment F37	Patek, M. et al. "Promoters from <i>C. glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90363	Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364	Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365	Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366	Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367	Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368	Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4	Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	Lysine exporter protein; Lysine export regulator protein	Vrjic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of coryneophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum</i> glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site <i>Corynebacterium</i> 304L	
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z29563	thrC	Threonine synthase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z46753	16S rDNA		Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z49822	sigA	Gene for 16S ribosomal RNA SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum</i> ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)
* A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.			

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							
Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NGTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saitama, Japan.

Table 4: Alignment Results

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx00051	1527	GB_HTG3:AC009685	210031	AC009685	Homo sapiens chromosome 15 clone 91_E_13 map 15, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	34,247	29-Sep-99
		GB_HTG3:AC009685	210031	AC009685	Homo sapiens chromosome 15 clone 91_E_13 map 15, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	34,247	29-Sep-99
		GB_HTG7:AC009511	271896	AC009511	Homo sapiens clone RP11-860B13, *** SEQUENCING IN PROGRESS ***, 59 unordered pieces.	Homo sapiens	35,033	09-DEC-1999
rx00091	876	GB_BA1:D50453	146191	D50453	Bacillus subtilis DNA for 25-36 degree region containing the amyE-srfA region, complete cds.	Bacillus subtilis	54,452	10-Feb-99
		GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	36,806	16-Aug-99
rx00092	789	GB_BA1:ECOUW93	338534	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	38,642	17-Apr-96
		GB_BA1:SCH35	45396	AL078610	Streptomyces coelicolor cosmid H35.	Streptomyces coelicolor	49,934	4-Jun-99
		GB_HTG3:AC011498_0	312343	AC011498	Homo sapiens chromosome 19 clone CIT978SKB_50L17, *** SEQUENCING IN PROGRESS ***, 190 unordered pieces.	Homo sapiens	37,117	13-Dec-99
		GB_HTG3:AC011498_0	312343	AC011498	Homo sapiens chromosome 19 clone CIT978SKB_50L17, *** SEQUENCING IN PROGRESS ***, 190 unordered pieces.	Homo sapiens	37,117	13-Dec-99
rx00104	879	GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	36,732	10-Feb-99
		GB_PL2:T24M8	68251	AF077409	Arabidopsis thaliana BAC T24M8.	Arabidopsis thaliana	37,150	3-Aug-98
		GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	42,874	10-Feb-99
rx00113	5745	GB_BA1:MAFASGEN	10520	X87822	B.ammoniaenes FAS gene.	Corynebacterium ammoniagenes	68,381	03-OCT-1996
		GB_BA1:BAFASAA	10549	X64795	B.ammoniaenes FAS gene.	Corynebacterium ammoniagenes	57,259	14-OCT-1997
		GB_BA1:MTCY159	33818	Z83863	Mycobacterium tuberculosis H37Rv complete genome; segment 111/162.	Mycobacterium tuberculosis	39,870	17-Jun-98
rx00164	1812	GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,714	03-DEC-1999
		GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,714	03-DEC-1999
		GB_HTG2:HSJ1153D9	118360	AL109806	Homo sapiens chromosome 20 clone RP5-1153D9, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,334	03-DEC-1999
rx00181	1695	GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	100,000	8-Sep-97
		GB_BA2:U32814	10393	U32814	Haemophilus influenzae Rd section 129 of 163 of the complete genome.	Haemophilus influenzae Rd	36,347	29-MAY-1998
		GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	37,454	8-Sep-97
rx00186	870	GB_PR3:AC004843	136655	AC004843	Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.	Homo sapiens	37,315	5-Nov-98

Table 4 (continued)

GB_HTG2:HS745114	133309	AL033532	Homo sapiens chromosome 1 clone RP4-745114 map q23.1-24.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	38,129	03-DEC-1999
GB_HTG2:HS745114	133309	AL033532	Homo sapiens chromosome 1 clone RP4-745114 map q23.1-24.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	38,129	03-DEC-1999
GB_GSS10:AQ184082	506	AQ184082	HS_3216_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216 Col=15 Row=M, genomic survey sequence.	Homo sapiens	37,297	1-Nov-98
GB_GSS1:CNS008ZZ	1101	AL052951	Drosophila melanogaster genome survey sequence T7 end of BAC # BACR18L01 of RPC1-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	Drosophila melanogaster	34,120	3-Jun-99
GB_GSS10:AQ184082	506	AQ184082	HS_3216_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216 Col=15 Row=M, genomic survey sequence.	Homo sapiens	39,655	1-Nov-98
GB_PR3:HSJ824F16	139330	AL050325	Human DNA sequence from clone 824F16 on chromosome 20, complete sequence.	Homo sapiens	34,520	23-Nov-99
GB_BA1:RCSECA	2724	X89411	R. capsulatus DNA for secA gene.	Rhodobacter capsulatus	38,163	6-Jan-96
GB_EST34:AV122904	242	AV122904	AV122904 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 2610529H07, mRNA sequence.	Mus musculus	38,889	1-Jul-99
GB_EST15:AA486042	515	AA486042	ab40c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:843278 5', mRNA sequence.	Homo sapiens	37,500	06-MAR-1998
GB_EST15:AA486042	515	AA486042	ab40c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:843278 5', mRNA sequence.	Homo sapiens	38,816	06-MAR-1998
GB_PR2:CNS01DS5	101584	AL121655	BAC sequence from the SPG4 candidate region at 2p21.2p22, complete	Homo sapiens	37,001	29-Sep-99
GB_HTG3:AC011408	79332	AC011408	Homo sapiens clone CIT978SKB_65D22, *** SEQUENCING IN PROGRESS ***; 10 unordered pieces.	Homo sapiens	38,040	06-OCT-1999
GB_HTG3:AC011408	79332	AC011408	Homo sapiens clone CIT978SKB_65D22, *** SEQUENCING IN PROGRESS ***; 10 unordered pieces.	Homo sapiens	38,040	06-OCT-1999
GB_HTG1:CEY62E10	254217	AL031580	Caenorhabditis elegans chromosome IV clone Y62E10, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	36,776	6-Sep-99
GB_HTG1:CEY62E10	254217	AL031580	Caenorhabditis elegans chromosome IV clone Y62E10, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	36,776	6-Sep-99
GB_PL2:YSCCHROM1	41988	L22015	Saccharomyces cerevisiae chromosome I centromere and right arm sequence.	Saccharomyces cerevisiae	39,260	05-MAR-1998
GB_HTG4:AC009974	219565	AC009974	Homo sapiens chromosome unknown clone NH045919, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	37,358	29-OCT-1999
GB_HTG4:AC009974	219565	AC009974	Homo sapiens chromosome unknown clone NH045919, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	37,358	29-OCT-1999
GB_BA1:AB017508	32050	AB017508	Bacillus halodurans C-125 genomic DNA, 32 kb fragment, complete cds.	Bacillus halodurans	44,622	14-Apr-99
GB_BA1:SCE8	24700	AL035654	Streptomyces coelicolor cosmid E8.	Streptomyces coelicolor	36,328	11-MAR-1999
GB_BA1:SCU51332	3216	U51332	Streptomyces coelicolor histidine kinase homolog (absA1) and response regulator homolog (absA2) genes, complete cds.	Streptomyces coelicolor	39,089	14-Sep-96
GB_HTG4:AC011122	187123	AC011122	Homo sapiens chromosome 8 clone 23_D_19 map 8, *** SEQUENCING IN PROGRESS ***; 27 ordered pieces.	Homo sapiens	38,658	14-OCT-1999

Table 4 (continued)

rx00298	1968	GB_BA1:CGECTP	2719	AJ001436	Corynebacterium glutamicum ectP gene.	Corynebacterium glutamicum	100,000	20-Nov-98
		GB_BA1:CGECTP	2719	AJ001436	Corynebacterium glutamicum ectP gene.	Corynebacterium glutamicum	100,000	20-Nov-98
		GB_EST24:AI234006	432	AI234006	EST230694 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUCU01 3' end, mRNA sequence.	Rattus sp.	46,552	31-Jan-99
rx00346	813	GB_BA1:SC2E9	20850	AL021530	Streptomyces coelicolor cosmid 2E9.	Streptomyces coelicolor	43,267	28-Jan-98
		GB_BA1:SC9B1	24800	AL049727	Streptomyces coelicolor cosmid 9B1.	Streptomyces coelicolor	44,613	27-Apr-99
		GB_BA1:ECU70214	123171	U70214	Escherichia coli chromosome minutes 4-6.	Escherichia coli	39,490	21-Sep-96
rx00368	1698	GB_BA2:AF065159	35209	AF065159	Bradyrhizobium japonicum putative arylsulfatase (arsA), putative soluble lytic transglycosylase precursor (sltA), dihydroadiponate synthase (dapA), MscL (mscL), SmpB (smpB), BcpB (bcpB), RnpO (rnpO), RelA/SpoT homolog (relA), PdxJ (pdxJ), and acyl carrier protein synthase AcpS (acpS) genes, complete cds; prokaryotic type I signal peptidase SipF (sipF) gene, sipF-sipS allele, complete cds; RNase III (rnc) gene, complete cds; GTP-binding protein Era (era) gene, partial cds; and unknown genes.	Bradyrhizobium japonicum	40,409	27-OCT-1999
		GB_BA1:AEOCHIT1	6861	D63139	Aeromonas sp. gene for chitinase, complete and partial cds.	Aeromonas sp. 10S-24	38,577	13-Feb-99
		GB_EST4:D62996	314	D62996	HUM347G01B Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-347G01 5', mRNA sequence.	Homo sapiens	41,613	29-Aug-95
rx00369	817	GB_BA1:YP102KB	119443	AL031866	Yersinia pestis 102 kbases unstable region: from 1 to 119443.	Yersinia pestis	35,396	4-Jan-99
		GB_GSS8:AQ012142	501	AQ012142	8750H1A037010398 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 8750H1A037010398, genomic survey sequence.	Rhodobacter sphaeroides	54,800	4-Jun-98
		GB_HTG2:AC005081	180096	AC005081	Homo sapiens clone RG270D13, *** SEQUENCING IN PROGRESS *** , 18 unordered pieces.	Homo sapiens	45,785	12-Jun-98
rx00410	789	GB_BA1:ATPLOCC	8870	Z30328	A.tumefaciens Ti plasmid pTiAch5 genes for OccR, OccQ, OccM, OccP, OccT, OoxB, OoxA and ornithine cyclodeaminase.	Agrobacterium tumefaciens	46,490	10-OCT-1994
		GB_BA2:U67591	9829	U67591	Methanococcus jannaschii section 133 of 150 of the complete genome.	Methanococcus jannaschii	45,677	28-Jan-98
		GB_BA1:TIPOCCQMPJ4350	M80607	M80607	Plasmid pTiA6 (from Agrobacterium tumefaciens) periplasmic-type octopine permease (occR, occQ, occM, occP, and occJ) and lysR-type regulatory protein (occR) genes, complete cds.	Plasmid pTiA6	46,490	24-Apr-96
rx00419	882	GB_BA2:MSU46844	16951	U46844	Mycobacterium smegmatis catalase-peroxidase (katG), putative arabinosyl transferase (embC, embA, embB), genes complete cds and putative propionyl-coA carboxylase beta chain (pccB) genes, partial cds.	Mycobacterium smegmatis	57,029	12-MAY-1997
		GB_EST28:AI513245	471	AI513245	GH13311.3prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH13311 3prime, mRNA sequence.	Drosophila melanogaster	37,696	16-MAR-1999
		GB_HTG4:AC010066	187240	AC010066	Drosophila melanogaster chromosome 3L72A4 clone RPC198-2501, *** SEQUENCING IN PROGRESS *** , 70 unordered pieces.	Drosophila melanogaster	39,607	16-OCT-1999
rx00432	1608	GB_BA1:BSUB0015	218410	Z99118	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.	Bacillus subtilis	49,810	26-Nov-97
		GB_PL1:CAC35A5	42565	AL033396	C.albicans cosmid Ca35A5.	Candida albicans	35,041	5-Nov-98
		GB_EST13:AA336266	378	AA336266	EST40981 Endometrial tumor Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	39,733	21-Apr-97

Table 4 (continued)

rx00449	1704	GB_HTG2:AC008199	124050	AC008199	Drosophila melanogaster chromosome 3 clone BACR01K08 (D756) RPCI-98 01.K.8 map 94D-94D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 83 unordered pieces.	Drosophila melanogaster	38,392	2-Aug-99
		GB_HTG2:AC008199	124050	AC008199	Drosophila melanogaster chromosome 3 clone BACR01K08 (D756) RPCI-98 01.K.8 map 94D-94D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 83 unordered pieces.	Drosophila melanogaster	38,392	2-Aug-99
rx00456	1500	GB_RO:RATLNKP2	177	M22337	Rat link protein gene, exon 2.	Rattus sp.	40,678	27-Apr-93
		GB_GSS1:FR0030597	476	AL026966	Fugu rubripes GSS sequence, clone 091C22aF9, genomic survey sequence.	Fugu rubripes	47,407	25-Jun-98
		GB_GSS5:AQ786587	556	AQ786587	HS_3086_B1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3086 Col=9 Row=P, genomic survey sequence.	Homo sapiens	38,406	3-Aug-99
		GB_GSS14:AQ526586	434	AQ526586	HS_5198_B1_B03_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=774 Col=5 Row=D, genomic survey sequence.	Homo sapiens	36,951	11-MAY-1999
rx00477	1767	GB_EST17:AA610489	407	AA610489	np93e05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133888 similar to gb:M11353 HISTONE H3.3 (HUMAN); mRNA sequence.	Homo sapiens	41,791	09-DEC-1997
		GB_PR1:HS333G4	1015	X05857	Human H3.3 gene exon 4.	Homo sapiens	38,182	24-Jan-96
		GB_EST30:AI637667	579	AI637667	tt10g11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240420 3', mRNA sequence.	Homo sapiens	35,417	27-Apr-99
rx00478	954	GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS ***; 12 unordered pieces.	Homo sapiens	38,769	3-Aug-99
		GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS ***; 12 unordered pieces.	Homo sapiens	38,769	3-Aug-99
		GB_HTG3:AC008708	83932	AC008708	Homo sapiens chromosome 5 clone CIT978SKB_78F1, *** SEQUENCING IN PROGRESS ***; 12 unordered pieces.	Homo sapiens	36,797	3-Aug-99
rx00480	1239	GB_HTG1:HSJ575L21	94715	AL096841	Homo sapiens chromosome 1 clone RP4-575L21, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	38,138	23-Nov-99
		GB_HTG1:HSJ575L21	94715	AL096841	Homo sapiens chromosome 1 clone RP4-575L21, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	38,138	23-Nov-99
		GB_RO:AC005960	158414	AC005960	Mus musculus chromosome 17 BAC citb20h22 from the MHC region, complete sequence.	Mus musculus	38,712	01-DEC-1998
rx00524	433	GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid i51.	Streptomyces coelicolor A3(2)	40,284	16-Aug-99
		GB_BA2:AF082879	3434	AF082879	Yersinia enterocolitica ABC transporter enterochelin/enterobactin gene cluster, complete sequence.	Yersinia enterocolitica	55,634	20-OCT-1999
rx00526	813	GB_BA1:BSP132617	5192	AJ132617	Burkholderia sp. P-transporter operon and flanking genes.	Burkholderia sp.	40,793	13-Jul-99
		GB_BA1:BSUB0008	208230	Z99111	Bacillus subtilis complete genome (section 8 of 21): from 1394791 to 1603020.	Bacillus subtilis	54,534	26-Nov-97
		GB_BA2:AF012285	46864	AF012285	Bacillus subtilis mobA-nprE gene region.	Bacillus subtilis	54,534	1-Jul-98
		GB_BA1:D90725	13796	D90725	Escherichia coli genomic DNA. (19.7 - 20.0 min).	Escherichia coli	51,481	7-Feb-99
rx00559	1140	GB_BA2:CAU77910	3385	U77910	Corynebacterium ammoniagenes sequence upstream of the 5-phosphoribosyl-1-pyrophosphate amidotransferase (purF) gene.	Corynebacterium ammoniagenes	39,007	1-Jan-98
		GB_EST4:H34952	382	H34952	EST108261 Rat PC-12 cells, untreated Rattus sp. cDNA clone RPCK07 similar to NADH-ubiquinone oxidoreductase complex 1 23 kDa precursor (iron-sulfur protein), mRNA sequence.	Rattus sp.	39,267	2-Apr-98
		GB_BA2:AE000963	22014	AE000963	Archaeoglobus fulgidus section 144 of 172 of the complete genome.	Archaeoglobus fulgidus	38,338	15-DEC-1997

Table 4 (continued)

rx00570	852	GB_GSS12:AQ422451	563	AQ422451	RPC1-11-185C3 TV RPC1-11	Homo sapiens genomic clone RPC1-11-185C3, genomic survey sequence.	Homo sapiens	38,767	23-MAR-1999
		GB_EST28:A1504741	568	A1504741	vi16c01.x1 Stratagene mouse Tcell 937311	Mus musculus cDNA clone IMAGE:972384 3' similar to gb:Z14044 M.musculus mRNA for valosin-containing protein (MOUSE);, mRNA sequence.	Mus musculus	37,900	11-MAR-1999
		GB_EST18:AA712043	68	AA712043	vu29f10.r1 Barstead mouse myotubes MPLRB5	Mus musculus cDNA clone IMAGE:1182091 5' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A (HUMAN);, mRNA sequence.	Mus musculus	42,647	24-DEC-1997
rx00571	1280	GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv	complete genome; segment 145/162.	Mycobacterium tuberculosis	38,468	17-Jun-98
		GB_PR3:AC005788	36224	AC005788	Homo sapiens chromosome 19, cosmid R26652,	complete sequence.	Homo sapiens	36,911	06-OCT-1998
		GB_PR3:AC005338	34541	AC005338	Homo sapiens chromosome 19, cosmid R31646,	complete sequence.	Homo sapiens	36,911	30-Jul-98
rx00590	1288	GB_HTG6:AC010932	203273	AC010932	Homo sapiens chromosome 15 clone RP11-296E22	map 15, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	37,242	30-Nov-99
		GB_HTG6:AC010932	203273	AC010932	Homo sapiens chromosome 15 clone RP11-296E22	map 15, *** SEQUENCING IN PROGRESS ***, 36 unordered pieces.	Homo sapiens	36,485	30-Nov-99
		GB_BA1:MSGB26CS	37040	L78816	Mycobacterium leprae cosmid B26	DNA sequence.	Mycobacterium leprae	39,272	15-Jun-96
rx00591	1476	GB_IN1:CEK09E9	30098	Z79602	Caenorhabditis elegans cosmid K09E9,	complete sequence.	Caenorhabditis elegans	34,092	2-Sep-99
		GB_PR4:AF135802	4965	AF135802	Homo sapiens thyroid hormone receptor-associated	protein complex component TRAP170 mRNA, complete cds.	Homo sapiens	36,310	9-Apr-99
		GB_PR4:AF104256	4365	AF104256	Homo sapiens transcriptional co-activator CRSP150	(CRSP150) mRNA, complete cds.	Homo sapiens	36,617	4-Feb-99
rx00596	576	GB_PR3:AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17	BAC clone, complete	Homo sapiens	34,321	02-MAY-1998
		GB_PR3:AC004659	129577	AC004659	Homo sapiens chromosome 19, CIT-HSP-87m17	BAC clone, complete	Homo sapiens	35,739	02-MAY-1998
		GB_PR1:HUMCBP2	2047	D83174	Human mRNA for collagen binding protein 2,	complete cds.	Homo sapiens	40,404	6-Feb-99
rx00607	504	GB_BA1:MTV010	3400	AL021186	Mycobacterium tuberculosis H37Rv	complete genome; segment 119/162.	Mycobacterium tuberculosis	40,862	23-Jun-99
		GB_BA1:MTV010	3400	AL021186	Mycobacterium tuberculosis H37Rv	complete genome; segment 119/162.	Mycobacterium tuberculosis	38,833	23-Jun-99
rx00623	1461	GB_BA1:MTCY428	26914	Z81451	Mycobacterium tuberculosis H37Rv	complete genome; segment 107/162.	Mycobacterium tuberculosis	60,552	17-Jun-98
		GB_BA1:RSPNGR234	34010	Z68203	Rhizobium sp. plasmid NGR234a	DNA.	Rhizobium sp.	51,992	8-Aug-96
rx00681		GB_BA2:AE000101	10057	AE000101	Rhizobium sp. NGR234 plasmid pNGR234a,	section 38 of 46 of the complete plasmid sequence.	Rhizobium sp. NGR234	51,992	12-DEC-1997
rx00690	1269	GB_HTG5:AC008338	136685	AC008338	Drosophila melanogaster chromosome X clone	BACR30J04 (D908) RPC1-98 30.J.4 map 19C-19E strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 93 unordered pieces.	Drosophila melanogaster	35,341	15-Nov-99
		GB_HTG4:AC009766	170502	AC009766	Homo sapiens chromosome 11 clone 404_A_03	map 11, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	37,984	19-OCT-1999

Table 4 (continued)

GB_HTG4:AC009766	170502	AC009766	Homo sapiens chromosome 11 clone 404_A_03 map 11, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.	Homo sapiens	37,984	19-OCT-1999
GB_EST30:AU054038	245	AU054038	AU054038 Dictyostelium discoideum SL (H. Urushihara) Dictyostelium discoideum cDNA clone SLK472, mRNA sequence.	Dictyostelium discoideum	43,265	28-Apr-99
GB_EST30:AU054038	245	AU054038	AU054038 Dictyostelium discoideum SL (H. Urushihara) Dictyostelium discoideum cDNA clone SLK472, mRNA sequence.	Dictyostelium discoideum	43,265	28-Apr-99
GB_BA1:MTCY50	36030	Z77137	Mycobacterium tuberculosis H37Rv complete genome; segment 55/162.	Mycobacterium tuberculosis	36,819	17-Jun-98
GB_BA1:D90904	150894	D90904	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448.	Synechocystis sp.	52,585	7-Feb-99
GB_BA1:D90904	150894	D90904	Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448.	Synechocystis sp.	39,699	7-Feb-99
GB_GSS14:AQ579838	651	AQ579838	T135342b shotgun sub-library of BAC clone 31P06 Medicago truncatula genomic clone 31-P-06-C-054, genomic survey sequence.	Medicago truncatula	37,153	27-Sep-99
GB_PR4:AC007625	174701	AC007625	Genomic sequence of Homo sapiens clone 2314F2 from chromosome 18, complete sequence.	Homo sapiens	38,014	30-Jun-99
GB_EST14:AA427576	580	AA427576	zw54b04.s1 Soares, total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773839 3' similar to gb:M86852 PEROXISOME ASSEMBLY FACTOR-1 (HUMAN); mRNA sequence.	Homo sapiens	42,731	16-OCT-1997
GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	59,350	17-Jun-98
GB_RO:AC002109	160048	AC002109	Genomic sequence from Mouse 9, complete sequence.	Mus musculus	39,398	9-Sep-97
GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	36,842	17-Jun-98
GB_GSS14:AQ563349	642	AQ563349	HS_5335_B2_A09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=911 Col=18 Row=B, genomic survey sequence.	Homo sapiens	37,649	29-MAY-1999
GB_BA1:DIHCLPBA	2441	M32229	B.nodulus clpB gene encoding a regulatory subunit of ATP-dependent protease.	Dichelobacter nodosus	41,140	26-Apr-93
GB_GSS3:B61538	698	B61538	T17M17TR TAMU Arabidopsis thaliana genomic clone T17M17, genomic survey sequence.	Arabidopsis thaliana	36,946	21-Nov-97
GB_HTG3:AC008691_1	110000	AC008691	Homo sapiens chromosome 5 clone CIT978SKB_63A22, *** SEQUENCING IN PROGRESS ***, 253 unordered pieces.	Homo sapiens	38,270	3-Aug-99
GB_HTG3:AC008691_1	110000	AC008691	Homo sapiens chromosome 5 clone CIT978SKB_63A22, *** SEQUENCING IN PROGRESS ***, 253 unordered pieces.	Homo sapiens	38,270	3-Aug-99
GB_HTG3:AC009127	186591	AC009127	Homo sapiens chromosome 16 clone RPCI-11_498D10, *** SEQUENCING IN PROGRESS ***, 49 unordered pieces.	Homo sapiens	38,947	3-Aug-99
GB_HTG1:HS32B1	271488	AL023693	Homo sapiens chromosome 6 clone RP1-32B1, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,565	23-Nov-99
GB_HTG1:HS32B1	271488	AL023693	Homo sapiens chromosome 6 clone RP1-32B1, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,565	23-Nov-99
GB_PR3:AC004919	75547	AC004919	Homo sapiens PAC clone DJ0895B23 from UL, complete sequence.	Homo sapiens	34,346	19-Sep-98
GB_EST6:W06539	300	W06539	T2367 MVAT4 bloodstream form of serodeme WRATat1.1 Trypanosoma brucei rhodesiense cDNA 5', mRNA sequence.	Trypanosoma brucei rhodesiense	40,000	12-Aug-96
GB_PR4:AC008179	181745	AC008179	Homo sapiens clone NH0576F01, complete sequence.	Homo sapiens	35,903	28-Sep-99

Table 4 (continued)

rx00860	1968	GB_EST4:H22888	468	H22888	ym54e12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52158 5' mRNA sequence.	Homo sapiens	37,179	6-Jul-95
		GB_GSS13:AQ426858	516	AQ426858	CITBI-E1-2578F1.TF CITBI-E1 Homo sapiens genomic clone 2578F1, genomic survey sequence.	Homo sapiens	38,447	24-MAR-1999
rx00899	1389	GB_PR1:AB002335	6289	AB002335	Human mRNA for KIAA0337 gene, complete cds.	Homo sapiens	35,799	13-Feb-99
		GB_BA1:NGU58849	2401	U58849	Neisseria gonorrhoeae pilS6 silent pilus locus.	Neisseria gonorrhoeae	40,623	20-Jun-96
		GB_BA1:PLPDHOS	3119	L06822	Integron pSa (from Escherichia coli) dihydropteroate synthase gene, 3' end.	Plasmid pSa	38,966	20-MAR-1996
		GB_BA1:PDGINTORF	6747	L06418	Integron In7 (from Plasmid pDGO100 from Escherichia coli) integrase (int), aminoglycoside adenyltransferase (aad), quaternary ammonium compound-resistance protein, dihydrofolate reductase (dhfrX), and dihydropteroate synthase (sulI) genes.	Plasmid pDGO100	38,966	20-MAR-1996
rx00902	1333	GB_GSS15:AQ606873	581	AQ606873	HS_5404_B2_H05_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=980 Col=10 Row=P, genomic survey sequence.	Homo sapiens	37,900	10-Jun-99
		GB_GSS9:AQ163442	658	AQ163442	nbxb0007A07f CUGI Rice BAC Library Oryza saliva genomic clone	Oryza sativa	41,885	12-Sep-98
		GB_PL1:PSST70	4974	X69213	nbxb0007A07f, genomic survey sequence.			
rx00931	969	GB_GSS1:FR0025208	612	AL018047	P.sativum Pst70 gene for heat-shock protein.	Pisum sativum	36,866	3-Jul-96
		GB_GSS1:FR0021844	252	AL014715	F.rubripes GSS sequence, clone 145D10aA8, genomic survey sequence.	Fugu rubripes	37,815	10-DEC-1997
		GB_GSS12:AQ403344	593	AQ403344	F.rubripes GSS sequence, clone 069K22aG5, genomic survey sequence.	Fugu rubripes	37,698	10-DEC-1997
rx00941	1440	GB_BA1:MTCY180	44201	Z97193	HS_2257_B1_B03_TTC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=5 Row=D, genomic survey sequence.	Homo sapiens	31,552	13-MAR-1999
		GB_BA1:MTCY180	44201	Z97193	Mycobacterium tuberculosis H37Rv complete genome; segment 85/162.	Mycobacterium tuberculosis	37,902	17-Jun-98
		GB_BA2:MSGKATG	1745	L14268	Mycobacterium tuberculosis H37Rv complete genome; segment 85/162.	Mycobacterium tuberculosis	39,140	17-Jun-98
rx00962	689	GB_HTG6:AC010998	144338	AC010998	Mycobacterium tuberculosis ethyl methane sulphonate resistance protein (katG) gene, 3'end.	Mycobacterium tuberculosis	42,517	26-Aug-99
		GB_GSS1:GGA340111	990	AJ232089	Homo sapiens clone RP11-95116, *** SEQUENCING IN PROGRESS *** , 17 unordered pieces.	Homo sapiens	39,497	08-DEC-1999
		GB_HTG6:AC010998	144338	AC010998	Gallus gallus anonymous sequence from Cosmid mapping to chromosome 2 (Cosmid 34 - Contig 15), genomic survey sequence.	Gallus gallus	37,970	25-Aug-98
rx01060	1047	GB_BA1:ECTTN7	2280	AJ001816	Homo sapiens clone RP11-95116, *** SEQUENCING IN PROGRESS *** , 17 unordered pieces.	Homo sapiens	38,226	08-DEC-1999
		GB_IN2:AF176377	8220	AF176377	Escherichia coli left end of transposon Tn7 including type 2 integron.	Escherichia coli	38,822	4-Nov-97
		GB_GSS10:AQ196728	429	AQ196728	Caenorhabditis briggsae CES-1 (ces-1) gene, complete cds; and CPN-1 (cpn-1) gene, partial cds.	Caenorhabditis briggsae	39,921	09-DEC-1999
rx01067	852	GB_BA1:U00016	42931	U00016	CIT-HSP-2381F4, TR CIT-HSP Homo sapiens genomic clone 2381F4, genomic survey sequence.	Homo sapiens	39,019	16-Sep-98
		GB_BA1:SYCGROESL	3256	D12677	Mycobacterium leprae cosmid B1937.	Mycobacterium leprae	58,303	01-MAR-1994
					Synechocystis sp. groES and groEL genes.	Synechocystis sp.	34,593	3-Feb-99
rx01114	1347	GB_BA1:D90905	139467	D90905	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915.	Synechocystis sp.	34,593	7-Feb-99
		GB_BA1:PSEFAOAB	3480	D10390	P. fragi faoA and faoB genes, complete cds.	Pseudomonas fragi	51,919	2-Feb-99

Table 4 (continued)

GB_BA1:AB014757	6057	AB014757	Pseudomonas sp. 61-3 genes for PhbR, acetoacetyl-CoA reductase, beta-ketothiolase and PHB synthase, complete cds.	Pseudomonas sp. 61-3	50,573	26-DEC-1998
GB_BA1:SC8D9	38681	AL035569	Streptomyces coelicolor cosmid 8D9.	Streptomyces coelicolor	42,200	26-Feb-99
GB_EST11:AA244557	379	AA244557	mx07a01.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:679464 5', mRNA sequence.	Mus musculus	39,050	10-MAR-1997
GB_EST14:AA407673	306	AA407673	EST01834 Mouse 7.5 dpc embryo ectoplacental cone cDNA library Mus musculus cDNA clone C0014F02 3', mRNA sequence.	Mus musculus	38,562	26-Aug-98
GB_EST26:AI390328	604	AI390328	mx07a01.y1 Soares mouse NML Mus musculus cDNA clone IMAGE:679464 5', mRNA sequence.	Mus musculus	33,136	2-Feb-99
GB_OV:XLXINT1	1278	X13138	Xenopus laevis int-1 mRNA for int-1 protein.	Xenopus laevis	40,038	31-MAR-1995
GB_PR4:AC006054	143738	AC006054	Homo sapiens Xq28 BAC RPC111-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	37,996	1-Apr-99
GB_PR4:AC006054	143738	AC006054	Homo sapiens Xq28 BAC RPC111-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	36,053	1-Apr-99
GB_BA1:SCE39	23550	AL049573	Streptomyces coelicolor cosmid E39.	Streptomyces coelicolor	62,357	31-MAR-1999
GB_BA1:MSU50335	5193	U50335	Mycobacterium smegmatis phage resistance (mpr) gene, complete cds.	Mycobacterium smegmatis	37,853	1-Feb-97
GB_BA1:BACTHRTRN	15467	D84213	Bacillus subtilis genome, trnI-feuABC region.	Bacillus subtilis	53,807	6-Feb-99
GB_PR2:HS1191B2	60828	AL022237	Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.	Homo sapiens	38,366	23-Nov-99
GB_PR2:HS1191B2	60828	AL022237	Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Acyl Transferase gene similar to C. elegans C50D2.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.	Homo sapiens	39,595	23-Nov-99
GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	57,762	17-Jun-98
GB_PL1:ATY12776	38483	Y12776	Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus.	Arabidopsis thaliana	32,971	7-Sep-98
GB_PL2:ATT6K21	99643	AL021889	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSA project).	Arabidopsis thaliana	35,273	16-Aug-99
GB_BA2:SCD25	41622	AL118514	Streptomyces coelicolor cosmid D25.	Streptomyces coelicolor	39,654	21-Sep-99
GB_BA1:SLGLYUB	2576	X65556	S. lividans tRNA-GlyU beta gene.	A3(2)		
GB_BA1:SCH10	39524	AL049754	Streptomyces coelicolor cosmid H10.	Streptomyces lividans	54,493	20-DEC-1993
GB_PAT:A68024	520	A68024	Sequence 19 from Patent WO9743409.	Streptomyces coelicolor	44,638	04-MAY-1999
GB_PAT:A68025	193	A68025	Sequence 20 from Patent WO9743409.	unidentified	42,553	05-MAY-1999
GB_PAT:A68027	193	A68027	Sequence 22 from Patent WO9743409.	unidentified	43,229	05-MAY-1999
				unidentified	38,342	05-MAY-1999

Table 4 (continued)

rx01220	1200	GB_PR3:HS512B11	64356	AL031058	Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs, complete sequence.	Homo sapiens	35,478	23-Nov-99
		GB_EST6:N99239	424	N99239	zb76h11.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:309573 3', mRNA sequence.	Homo sapiens	39,623	20-Aug-96
		GB_EST16:AA554268	400	AA554268	nk36c09.s1 NCL_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1015600 3' similar to gb:X01677 GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); mRNA sequence.	Homo sapiens	36,111	8-Sep-97
rx01221	849	GB_PR4:AF179633	96371	AF179633	Homo sapiens chromosome 16 map 16q23.3-q24.1 sequence.	Homo sapiens	40,199	5-Sep-99
		GB_VI:EHVU20824	184427	U20824	Equine herpesvirus 2, complete genome.	Equine herpesvirus 2	37,001	2-Feb-96
		GB_BA2:AE000407	10601	AE000407	Escherichia coli K-12 MG1655 section 297 of 400 of the complete genome.	Escherichia coli	39,471	12-Nov-98
rx01222	822	GB_PAT:AR068625	28804	AR068625	Sequence 1 from patent US 5854034.	Unknown.	40,574	29-Sep-99
		GB_BA2:SSU51197	28804	U51197	Spingomonas S88 sphingian polysaccharide synthesis (spsG), (spsS), (spsR), glycosyl transferase (spsQ), (spsI), glycosyl transferase (spsK), glycosyl transferase (spsL), (spsJ), (spsF), (spsD), (spsC), (spsE), Urf 32, Urf 26, ATP-binding cassette transporter (atrD), ATP-binding cassette transporter (atrB), glucosyl-isoprenylphosphate transferase (spsB), glucose-1-phosphate thymidyltransferase (hsA), dTDP-6-deoxy-D-glucose -3,5-epimerase (hsC) dTDP-D-glucose-4,6-dehydratase (hsB), dTDP-6-deoxy-L-mannose-dehydrogenase (hsD), Urf 31, and Urf 34 genes, complete cds.	Spingomonas sp. S88	40,574	16-MAY-1996
rx01260	1305	GB_IN1:BBU44918	2791	U44918	Babesia bovis ATP-binding protein (babC) mRNA, complete cds.	Babesia bovis	39,228	9-Aug-97
		GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	99,923	1-Feb-99
		GB_BA1:MTV038	16094	AL021933	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162.	Mycobacterium tuberculosis	59,056	17-Jun-98
		GB_PR3:AC005618	176714	AC005618	Homo sapiens chromosome 5, BAC clone 249h5 (LBNL H149), complete sequence.	Homo sapiens	36,270	5-Sep-98
rx01261	294	GB_BA1:CGLPD	1800	Y16642	Corynebacterium glutamicum lpd gene, complete CDS.	Corynebacterium glutamicum	100,000	1-Feb-99
		GB_HTG4:AC010045	164829	AC010045	Drosophila melanogaster chromosome 3L75A1 clone RPC198-17C17, *** SEQUENCING IN PROGRESS ***; 50 unordered pieces.	Drosophila melanogaster	50,512	16-OCT-1999
		GB_HTG4:AC010045	164829	AC010045	Drosophila melanogaster chromosome-3L75A1 clone RPC198-17C17, *** SEQUENCING IN PROGRESS ***; 50 unordered pieces.	Drosophila melanogaster	50,512	16-OCT-1999
rx01269	564	GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Bacteroides fragilis	56,071	01-DEC-1999
		GB_BA1:AB002668	24907	AB002668	Actinobacillus actinomycetemcomitans DNA for glycosyltransferase, lytic transglycosylase, dTDP-4-rhamnose reductase, complete cds.	Actinobacillus actinomycetemcomitans	46,679	21-Feb-98
		GB_BA1:AB010415	23112	AB010415	Actinobacillus actinomycetemcomitans gene cluster for 6-deoxy-L-talan synthesis, complete cds.	Actinobacillus actinomycetemcomitans	46,679	13-Feb-99
rx01291	1056	GB_STS:AU027820	238	AU027820	Rattus norvegicus, OTSUKA clone, OT78.02/918b07, microsatellite sequence, sequence tagged site.	Rattus norvegicus	34,874	02-MAR-1999
		GB_STS:AU027820	238	AU027820	Rattus norvegicus, OTSUKA clone, OT78.02/918b07, microsatellite sequence, sequence tagged site.	Rattus norvegicus	34,874	02-MAR-1999

Table 4 (continued)

rx01292	1308	GB_HTG3:AC006445	174547	AC006445	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	34,812	15-Sep-99
		GB_BA1:BSUB0017	217420	Z99120	Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.	Bacillus subtilis	37,802	26-Nov-97
		GB_HTG3:AC010580	121119	AC010580	Drosophila melanogaster chromosome 3 clone BACR48J06 (D1102) RPCI-98 48.J.6 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 71 unordered pieces.	Drosophila melanogaster	35,637	01-OCT-1999
		GB_HTG3:AC010580	121119	AC010580	Drosophila melanogaster chromosome 3 clone BACR48J06 (D1102) RPCI-98 48.J.6 map 96F-96F strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 71 unordered pieces.	Drosophila melanogaster	35,637	01-OCT-1999
rx01293	450	GB_GSS8:AQ001809	705	AQ001809	CIT-HSP-2290D17.TF CIT-HSP Homo sapiens genomic clone 2290D17, genomic survey sequence.	Homo sapiens	42,021	26-Jun-98
		GB_GSS8:AQ001809	705	AQ001809	CIT-HSP-2290D17.TF CIT-HSP Homo sapiens genomic clone 2290D17, genomic survey sequence.	Homo sapiens	40,323	26-Jun-98
rx01339	1111	GB_PL1:MGU60290	4614	U60290	Magnaporthe grisea nitrogen regulatory protein (NUT1) gene, complete cds.	Magnaporthe grisea	38,707	3-Jul-96
		GB_HTG3:AC011371	189187	AC011371	Homo sapiens chromosome 5 clone CIT978SKB_107C20, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	39,741	06-OCT-1999
		GB_HTG3:AC011371	189187	AC011371	Homo sapiens chromosome 5 clone CIT978SKB_107C20, *** SEQUENCING IN PROGRESS ***, 31 unordered pieces.	Homo sapiens	39,741	06-OCT-1999
rx01382	1192	GB_HTG4:AC009892	138122	AC009892	Homo sapiens chromosome 19 clone CIT978SKB_83J4, *** SEQUENCING IN PROGRESS ***, 6 ordered pieces.	Homo sapiens	40,154	31-OCT-1999
		GB_HTG4:AC009892	138122	AC009892	Homo sapiens chromosome 19 clone CIT978SKB_83J4, *** SEQUENCING IN PROGRESS ***, 6 ordered pieces.	Homo sapiens	40,154	31-OCT-1999
rx01399	1142	GB_PR3:AC002416	128915	AC002416	Human Chromosome X, complete sequence.	Homo sapiens	37,521	29-Jan-98
		GB_EST9:AA096601	524	AA096601	mo03b09.r1 Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:552473 5' similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 (HUMAN); gb:L04280 Mus musculus ribosomal protein (MOUSE); mRNA pat.pk0074.e9.f 5' similar to H-ATPase B subunit, mRNA sequence.	Mus musculus	40,525	15-Feb-97
		GB_EST37:AI982114	626	AI982114	pat.pk0074.e9.f chicken activated T cell cDNA Gallus gallus cDNA clone pat.pk0074.e9.f 5' similar to H-ATPase B subunit, mRNA sequence.	Gallus gallus	37,785	15-Sep-99
rx01420	1065	GB_OV:GGU20766	1645	U20766	Gallus gallus vacuolar H+-ATPase B subunit gene, complete cds.	Gallus gallus	38,244	07-DEC-1995
		GB_HTG2:AC005690	193424	AC005690	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	37,464	11-Apr-99
		GB_HTG2:AC005690	193424	AC005690	Homo sapiens chromosome 4, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	37,464	11-Apr-99
		GB_HTG2:AC006637	22092	AC006637	Caenorhabditis elegans clone F41B4, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Caenorhabditis elegans	37,488	23-Feb-99
rx01467	414	GB_HTG1:CEY102G3_110000	110000	AL020985	Caenorhabditis elegans chromosome V clone Y102G3, *** SEQUENCING IN GB_HTG1:CEY102G3_110000	Caenorhabditis elegans	35,437	3-Dec-98
		GB_HTG1:CEY102G3_110000	110000	AL020985	Caenorhabditis elegans chromosome V clone Y102G3, *** SEQUENCING IN GB_HTG1:CEY102G3_110000	Caenorhabditis elegans	35,437	3-Dec-98
rx01576	882	GB_HTG1:CEY113G7_110000	110000	AL031113	Caenorhabditis elegans chromosome V clone Y113G7, *** SEQUENCING IN GB_HTG1:CEY113G7_110000	Caenorhabditis elegans	35,437	12-Jan-99
		GB_BA2:AF030975_2511	2511	AF030975	Aeromonas salmonicida chaperonin GroES and chaperonin GroEL genes, complete cds.	Aeromonas salmonicida	41,516	2-Apr-98
		GB_BA2:AF030975_2511	2511	AF030975	Aeromonas salmonicida chaperonin GroES and chaperonin GroEL genes, complete cds.	Aeromonas salmonicida	38,171	2-Apr-98

Table 4 (continued)

GB_EST22:AI068560	965	AI068560	mgae0003aC11f Magnaporthe grisea Appressorium Stage cDNA Library	Pyricularia grisea	40,073	09-DEC-1999
GB_GSS14:AQ554460	681	AQ554460	Pyricularia grisea cDNA clone mgae0003aC11f 5', mRNA sequence.			
GB_IN2:AC005449	85518	AC005449	RPCI-11-419F2-TV RPCI-11 Homo sapiens genomic clone RPCI-11-419F2, genomic survey sequence.	Homo sapiens	36,522	28-MAY-1999
GB_IN2:AC005449	85518	AC005449	Drosophila melanogaster, chromosome 2R, region 44C4-44C5, P1 clone DS06765, complete sequence.	Drosophila melanogaster	36,609	23-DEC-1998
GB_IN2:AC005449	85518	AC005449	Drosophila melanogaster, chromosome 2R, region 44C4-44C5, P1 clone DS06765, complete sequence.	Drosophila melanogaster	33,612	23-DEC-1998
GB_HTG3:AC011352	160167	AC011352	Homo sapiens chromosome 5 clone CIT-HSPC_327F10, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	33,688	06-OCT-1999
GB_HTG3:AC011352	160167	AC011352	Homo sapiens chromosome 5 clone CIT-HSPC_327F10, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Homo sapiens	33,688	06-OCT-1999
GB_HTG3:AC011402	168868	AC011402	Homo sapiens chromosome 5 clone CIT978SKB_38B5, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	33,688	06-OCT-1999
GB_BA1:CGA224946	2408	AJ224946	Corynebacterium glutamicum DNA for L-Malate:quinone oxidoreductase.	Corynebacterium glutamicum	42,284	11-Aug-98
GB_EST17:AA608825	439	AA608825	af03g07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030620 3' similar to TR:G976083 G976083 HISTONE H2A RELATED.; mRNA sequence.	Homo sapiens	40,092	02-MAR-1998
GB_PR4:AC005377	102311	AC005377	Homo sapiens PAC clone DJ1136G02 from 7q32-q34, complete sequence.	Homo sapiens	37,811	28-Apr-99
GB_BA1:CGPROPGEN 2936	2936	Y12537	C.glutamicum proP gene.	Corynebacterium glutamicum	100,000	17-Nov-98
GB_BA1:CGPROPGEN 2936	2936	Y12537	C.glutamicum proP gene.	Corynebacterium glutamicum	100,000	17-Nov-98
GB_PR4:AF191071	88481	AF191071	Homo sapiens chromosome 8 clone BAC 388D06, complete sequence.	Homo sapiens	35,612	11-OCT-1999
GB_BA1:MSG8577CO	37770	L01263	M. leprae genomic dna sequence, cosmid b577.	Mycobacterium leprae	55,604	14-Jun-96
GB_BA1:MLCB2407	35615	AL023596	Mycobacterium leprae cosmid B2407.	Mycobacterium leprae	36,416	27-Aug-99
GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	55,844	24-Jun-99
GB_BA1:CGU43536	3464	U43536	Corynebacterium glutamicum heat shock, ATP-binding protein (clpB) gene, complete cds.	Corynebacterium glutamicum	100,000	13-MAR-1997
GB_HTG4:AC009841	164434	AC009841	Drosophila melanogaster chromosome 3LJ77E1 clone RPCI98-13F11, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	33,205	16-OCT-1999
GB_HTG4:AC009841	164434	AC009841	Drosophila melanogaster chromosome 3LJ77E1 clone RPCI98-13F11, *** SEQUENCING IN PROGRESS ***, 70 unordered pieces.	Drosophila melanogaster	33,205	16-OCT-1999
GB_GSS1:FR0022586	522	AL015452	F.rubripes GSS sequence, clone 077P23aB10, genomic survey sequence.	Fugu rubripes	40,192	10-DEC-1997
GB_GSS1:FR0022584	485	AL015450	F.rubripes GSS sequence, clone 077P23aB11, genomic survey sequence.	Fugu rubripes	35,876	10-DEC-1997
GB_IN1:CET26H2	37569	Z82055	Caenorhabditis elegans cosmid T26H2, complete sequence.	Caenorhabditis elegans	34,759	19-Nov-99

Table 4 (continued)

rx01727	1401	GB_BA2:CORCSLYS	2821	M89931	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake carrier (brnQ) genes, complete cds, and hypothetical protein YhbW (yhbW) gene, partial cds.	Corynebacterium glutamicum	99,929	4-Jun-98
		GB_HTG6:AC011037	167849	AC011037	Homo sapiens clone RP11-7F18, WORKING DRAFT SEQUENCE, 19 unordered pieces.	Homo sapiens	36,903	30-Nov-99
		GB_HTG6:AC011037	167849	AC011037	Homo sapiens clone RP11-7F18, WORKING DRAFT SEQUENCE, 19 unordered pieces.	Homo sapiens	35,642	30-Nov-99
rx01737	1182	GB_BA1:SCGD3	33779	AL096822	Streptomyces coelicolor cosmid GD3.	Streptomyces coelicolor	38,054	8-Jul-99
		GB_HTG1:CNS01DSB	222193	AL121768	Homo sapiens chromosome 14 clone R-976B16, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	35,147	05-OCT-1999
		GB_HTG1:CNS01DSB	222193	AL121768	Homo sapiens chromosome 14 clone R-976B16, *** SEQUENCING IN PROGRESS ***, in ordered pieces.	Homo sapiens	35,147	05-OCT-1999
rx01762	1659	GB_BA1:MTCI28	36300	Z97050	Mycobacterium tuberculosis H37Rv complete genome; segment 10/162.	Mycobacterium tuberculosis	49,574	23-Jun-98
		GB_BA1:SCG610	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	44,049	24-MAR-1999
		GB_BA1:SCE29	26477	AL035707	Streptomyces coelicolor cosmid E29.	Streptomyces coelicolor	40,246	12-MAR-1999
rx01764	1056	GB_PL2:SPAC343	42947	AL109739	S.pombe chromosome I cosmid c343.	Schizosaccharomyces pombe	37,084	6-Sep-99
		GB_PL2:SPAC343	42947	AL109739	S.pombe chromosome I cosmid c343.	Schizosaccharomyces pombe	34,890	6-Sep-99
rx01801	1140	GB_EST38:AW066306	334	AW066306	687009D03.y1 687 - Early embryo from Delaware Zea mays cDNA, mRNA sequence.	Zea mays	46,108	12-OCT-1999
		GB_GSS13:AQ484750	375	AQ484750	RPC1-11-248N4.TV RPC1-11 Homo sapiens genomic clone RPC1-11-248N4, genomic survey sequence.	Homo sapiens	32,000	24-Apr-99
		GB_GSS13:AQ489971	252	AQ489971	RPC1-11-247N23.TV RPC1-11 Homo sapiens genomic clone RPC1-11-247N23, genomic survey sequence.	Homo sapiens	36,111	24-Apr-99
rx01823	900	GB_BA1:SCI51	40745	AL109848	Streptomyces coelicolor cosmid I51.	Streptomyces coelicolor A3(2)	35,779	16-Aug-99
		GB_BA1:ECU82598	136742	U82598	Escherichia coli genomic sequence of minutes 9 to 12.	Escherichia coli	39,211	15-Jan-97
rx01853	675	GB_BA1:BSUB0018	209510	Z99121	Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.	Bacillus subtilis	36,999	26-Nov-97
		GB_BA1:MTCY227	35946	Z77724	Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.	Mycobacterium tuberculosis	37,612	17-Jun-98
		GB_HTG3:AC010189	265962	AC010189	Homo sapiens clone RPC11-296K13, *** SEQUENCING IN PROGRESS ***, 80 unordered pieces.	Homo sapiens	39,006	16-Sep-99
		GB_HTG3:AC010189	265962	AC010189	Homo sapiens clone RPC11-296K13, *** SEQUENCING IN PROGRESS ***, 80 unordered pieces.	Homo sapiens	39,006	16-Sep-99
rx01881	558	GB_HTG4:AC011117	148447	AC011117	Homo sapiens chromosome 4 clone 173_C_09 map 4, *** SEQUENCING IN PROGRESS ***, 10 ordered pieces.	Homo sapiens	39,130	14-OCT-1999
		GB_HTG4:AC011117	148447	AC011117	Homo sapiens chromosome 4 clone 173_C_09 map 4, *** SEQUENCING IN PROGRESS ***, 10 ordered pieces.	Homo sapiens	39,130	14-OCT-1999
		GB_BA1:MTCY2B12	20431	Z81011	Mycobacterium tuberculosis H37Rv complete genome; segment 61/162.	Mycobacterium tuberculosis	37,893	18-Jun-98

Table 4 (continued)

rx01894	978	GB_BA1:MTCY274	39991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	37,229	19-Jun-98
		GB_IN1:CELF46H5	38886	U41543	Caenorhabditis elegans cosmid F46H5.	Caenorhabditis elegans	38,525	29-Nov-96
		GB_HTG3:AC009204	115633	AC009204	Drosophila melanogaster chromosome 2 clone BACR03E19 (D1033) RPCI-98 03.E.19 map 36E-37C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 94 unordered pieces.	Drosophila melanogaster	31,579	18-Aug-99
rx01897	666	GB_HTG1:CEY48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	34,703	1-Apr-99
		GB_HTG1:CEY48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	34,703	1-Apr-99
		GB_HTG1:CEY53F4_2	110000	Z92860	Caenorhabditis elegans chromosome II clone Y53F4, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	33,333	15-Oct-99
rx01946	1298	GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.	Mycobacterium tuberculosis	65,560	17-Jun-98
		GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor	50,648	24-MAY-1999
		GB_BA1:SCARD1GN	2321	X84374	S. capreolus ard1 gene.	Streptomyces capreolus	44,973	23-Aug-95
rx01980	756	GB_PL2:AC008262	99698	AC008262	Genomic sequence for Arabidopsis thaliana BAC F4N2 from chromosome I, complete sequence.	Arabidopsis thaliana	35,310	21-Aug-99
		GB_PL1:AB013388	73428	AB013388	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence.	Arabidopsis thaliana	35,505	20-Nov-99
		GB_PL1:AB013388	73428	AB013388	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E1, complete sequence.	Arabidopsis thaliana	39,973	20-Nov-99
rx01983	630	GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 9 unordered pieces.	Drosophila melanogaster	36,672	27-OCT-1999
		GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 9 unordered pieces.	Drosophila melanogaster	36,672	27-OCT-1999
		GB_HTG4:AC006467	175695	AC006467	Drosophila melanogaster chromosome 2 clone BACR03L08 (D532) RPCI-98 03.L.8 map 40A-40C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 9 unordered pieces.	Drosophila melanogaster	32,367	27-OCT-1999
rx02020	1111	GB_BA1:CGDNAAROP	2612	X85965	C. glutamicum ORF3 and aroP gene.	Corynebacterium glutamicum	100,000	30-Nov-97
		GB_PAT:A58887	1612	A58887	Sequence 1 from Patent WO9701637.	unidentified	100,000	06-MAR-1998
		GB_BA1:STYCARABA	4378	M95047	Salmonella typhimurium transport protein, complete cds, and transfer RNA-Arg.	Salmonella typhimurium	50,547	13-MAR-1996
rx02029	1437	GB_HTG2:AC003023	104768	AC003023	Homo sapiens chromosome 11 clone pDJ363p2, *** SEQUENCING IN PROGRESS ***; 22 unordered pieces.	Homo sapiens	35,820	21-OCT-1997
		GB_HTG2:AC003023	104768	AC003023	Homo sapiens chromosome 11 clone pDJ363p2, *** SEQUENCING IN PROGRESS ***; 22 unordered pieces.	Homo sapiens	35,820	21-OCT-1997
		GB_HTG2:HS118B18	104729	AL034344	Homo sapiens chromosome 6 clone RP1-118B18 map p24.1-25.3, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Homo sapiens	34,355	03-DEC-1999

Table 4 (continued)

rx02030	1509	GB_PR4:AC007695	63247	AC007695	Homo sapiens 12q24 BAC RPC111-124N23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	38,681	1-Sep-99
		GB_PR4:AC006464	99908	AC006464	Homo sapiens BAC clone NH0436C12 from 2, complete sequence.	Homo sapiens	35,445	22-OCT-1999
		GB_PR4:AC006464	99908	AC006464	Homo sapiens BAC clone NH0436C12 from 2, complete sequence.	Homo sapiens	35,968	22-OCT-1999
rx02073	1653	GB_BA1:CGGDHA	2037	X72855	C-glutamicum GDHA gene.	Corynebacterium glutamicum	39,655	24-MAY-1993
		GB_BA1:CGGDH	2037	X59404	Corynebacterium glutamicum, gdh gen for glutamate dehydrogenase.	Corynebacterium glutamicum	44,444	30-Jul-99
rx02074		GB_BA2:SC2H4	25970	AL031514	Streptomyces coelicolor cosmid 2H4.	Streptomyces coelicolor A3(2)	38,452	19-OCT-1999
rx02095	1527	GB_EST18:AA703380	471	AA703380	z12b06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450035 3' similar to contains LTR5.13 LTR5 repetitive element ; mRNA sequence.	Homo sapiens	36,518	24-DEC-1997
		GB_HTG6:AC009769	122911	AC009769	Homo sapiens chromosome 8 clone RP11-202112 map 8, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,473	07-DEC-1999
		GB_EST7:W70175	436	W70175	z052c02.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344258 5' similar to contains LTR5.b2 LTR5 repetitive element; mRNA sequence.	Homo sapiens	34,174	16-OCT-1996
rx02099	373	GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial fsY and srp genes.	Corynebacterium glutamicum	100,000	14-MAY-1999
		GB_HTG3:AC011509	111353	AC011509	Homo sapiens chromosome 19 clone CITB-H1_2189E23, *** SEQUENCING IN PROGRESS ***; 35 unordered pieces.	Homo sapiens	33,423	07-OCT-1999
		GB_HTG3:AC011509	111353	AC011509	Homo sapiens chromosome 19 clone CITB-H1_2189E23, *** SEQUENCING IN PROGRESS ***; 35 unordered pieces.	Homo sapiens	33,423	07-OCT-1999
rx02115	1197	GB_HTG5:AC010126	175986	AC010126	Homo sapiens clone GS502B02, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	36,717	13-Nov-99
		GB_HTG5:AC010126	175986	AC010126	Homo sapiens clone GS502B02, *** SEQUENCING IN PROGRESS ***; 3 unordered pieces.	Homo sapiens	36,092	13-Nov-99
rx02128	1818	GB_PR1:HUMHM145	2214	D10925	Human mRNA for HM145.	Homo sapiens	39,171	3-Feb-99
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	38,682	17-Jun-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	35,746	17-Jun-98
		GB_GSS10:AAQ161109	738	AQ161109	nbxb0006DD03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0006DD03r, genomic survey sequence.	Oryza sativa	38,482	12-Sep-98
rx02133	329	GB_BA2:MPAE000058	28530	AE000058	Mycoplasma pneumoniae section 58 of 63 of the complete genome.	Mycoplasma pneumoniae	32,317	18-Nov-96
		GB_HTG4:AC008308	151373	AC008308	Drosophila melanogaster chromosome 3 clone BACR10M16 (D743) RPC1-98 10.M.16 map 93C-93D strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***; 186 unordered pieces.	Drosophila melanogaster	34,579	20-OCT-1999

Table 4 (continued)

GB_HTG4:AC008308	151373	AC008308	Drosophila melanogaster chromosome 3 clone BACR10M16 (D743) RPC1-98 10.M.16 map 93C-93D strain y; cn bw sp. *** SEQUENCING IN PROGRESS ***, 186 unordered pieces.	Drosophila melanogaster	34,579	20-OCT-1999
GB_EST37:AW012260	358	AW012260	um06e09.y1 Sugano mouse kidney mKia Mus musculus cDNA clone IMAGE:2182312 5' similar to SW:AMPL_BOVIN P00727 CYTOSOL AMINOPEPTIDASE.; mRNA sequence.	Mus musculus	39,385	10-Sep-99
GB_GSS3:B87734	389	B87734	RPC111-30D24.TP RPC1-11 Homo sapiens genomic clone RPC1-11-30D24, genomic survey sequence.	Homo sapiens	37,629	9-Apr-99
GB_PR4:AC005042	192218	AC005042	Homo sapiens clone NH0552E01, complete sequence.	Homo sapiens	36,901	14-Jan-99
GB_BA2:AF010496	189370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	53,714	12-MAY-1998
GB_EST24:AI170522	367	AI170522	EST216450 Normalized rat lung, Bento Soares Rattus sp. cDNA clone RLUC075 3' end, mRNA sequence.	Rattus sp.	44,186	20-Jan-99
GB_PL1:PHVDLECA	1441	K03288	P. vulgaris phytohemagglutinin gene encoding erythroagglutinating phytohemagglutinin (PHA-E), complete cds.	Phaseolus vulgaris	39,103	27-Apr-93
GB_BA1:CGGLTG	3013	X66112	C. glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	44,118	17-Feb-95
GB_BA1:CGGLTG	3013	X66112	C. glutamicum glt gene for citrate synthase and ORF.	Corynebacterium glutamicum	36,189	17-Feb-95
GB_BA2:AE000104	10146	AE000104	Rhizobium sp. NGR234 plasmid pNGR234a, section 41 of 45 of the complete plasmid sequence.	Rhizobium sp. NGR234	38,487	12-DEC-1997
GB_BA2:CXU21300	8990	U21300	Corynebacterium striatum hypothetical protein YhbB gene, partial cds; ABC transporter TetB (tetB), ABC transporter TetA (tetA), transposase, 23S rRNA methyltransferase, and transposase genes, complete cds; and unknown genes.	Corynebacterium striatum	37,264	9-Apr-99
GB_HTG3:AC009185	87184	AC009185	Homo sapiens chromosome 5 clone CIT-HSPC_248O19, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	36,459	07-OCT-1999
GB_HTG3:AC009185	87184	AC009185	Homo sapiens chromosome 5 clone CIT-HSPC_248O19, *** SEQUENCING IN PROGRESS ***; 2 ordered pieces.	Homo sapiens	36,459	07-OCT-1999
GB_BA2:MPAE000058	28530	AE000058	Mycoplasma pneumoniae section 58 of 63 of the complete genome.	Mycoplasma pneumoniae	35,498	18-Nov-96
GB_EST26:AI337275	618	AI337275	tb96h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062245 3' similar to TR:Q15392 Q15392 ORF, COMPLETE CDS.; mRNA sequence.	Homo sapiens	35,589	18-MAR-1999
GB_EST26:AI337275	618	AI337275	tb96h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062245 3' similar to TR:Q15392 Q15392 ORF, COMPLETE CDS.; mRNA sequence.	Homo sapiens	42,786	18-MAR-1999
GB_BA1:ERWPNLB	1291	M65057	Erwinia carotovora pectin lyase (pnI) gene, complete cds.	Erwinia carotovora	37,780	26-Apr-93
GB_EST30:AV021947	313	AV021947	AV021947 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1190024M23, mRNA sequence.	Mus musculus	39,423	28-Aug-99
GB_EST33:AV087117	251	AV087117	AV087117 Mus musculus tongue C57BL/6J adult Mus musculus cDNA clone 2310028C15, mRNA sequence.	Mus musculus	47,410	25-Jun-99
GB_EST11:AA250210	532	AA250210	mx79g10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:692610 5' similar to TR:E236517 E236517 F44G4.1.; mRNA sequence.	Mus musculus	36,136	12-MAR-1997
GB_EST11:AA250210	532	AA250210	mx79g10.r1 Soares mouse NML Mus musculus cDNA clone IMAGE:692610 5' similar to TR:E236517 E236517 F44G4.1.; mRNA sequence.	Mus musculus	36,202	12-MAR-1997

Table 4 (continued)

rx02261	1479	GB_BA1:CGL007732	4460	AJ007732	Corynebacterium glutamicum 3' ppc gene, secG gene, amt gene, ocd gene and 5' soxA gene.	Corynebacterium glutamicum	100,000	7-Jan-99
		GB_BA1:CGAMTGENE 2028		X93513	C. glutamicum amt gene.	Corynebacterium glutamicum	100,000	29-MAY-1996
rx02268	1023	GB_BA1:CORPEPC	4885	M25819	C. glutamicum phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
		GB_PL2:AF087130	3478	AF087130	Neurospora crassa siderophore regulation protein (sre) gene, complete cds.	Neurospora crassa	39,268	22-OCT-1998
		GB_EST30:AI663709	408	AI663709	ud47a06.y1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:1449010 5' similar to TR:075585 O75585 MITOGEN- AND STRESS-ACTIVATED PROTEIN KINASE-2 ; mRNA sequence.	Mus musculus	41,523	10-MAY-1999
		GB_RO:AF074714	3120	AF074714	Mus musculus mitogen- and stress-activated protein kinase-2 (mMSK2) mRNA, complete cds.	Mus musculus	38,347	24-OCT-1998
rx02269	1095	GB_GSS4:AQ742825	847	AQ742825	HS_5482_B2_A04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1058 Col=8 Row=B, genomic survey sequence.	Homo sapiens	37,703	16-Jul-99
		GB_HTG3:AC009293	162944	AC009293	Homo sapiens chromosome 18 clone 53_I_06 map 18, *** SEQUENCING IN PROGRESS ***; 15 unordered pieces.	Homo sapiens	37,006	13-Aug-99
		GB_HTG3:AC009293	162944	AC009293	Homo sapiens chromosome 18 clone 53_I_06 map 18, *** SEQUENCING IN PROGRESS ***; 15 unordered pieces.	Homo sapiens	37,006	13-Aug-99
rx02309	1173	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	52,344	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	52,344	03-DEC-1996
		GB_HTG2:AC007163	186618	AC007163	Homo sapiens clone NH0091M05, *** SEQUENCING IN PROGRESS ***; 1 unordered pieces.	Homo sapiens	37,263	23-Apr-99
rx02310	1386	GB_BA1:MTY25D10	40838	Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	36,861	17-Jun-98
		GB_BA1:MSGY224	40051	AD000004	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	36,861	03-DEC-1996
rx02321	1752	GB_PR3:HS279N11	169998	Z98255	Human DNA sequence from PAC 279N11 on chromosome Xq11.2-13.3.	Homo sapiens	34,516	23-Nov-99
		GB_BA1:AB018531	4961	AB018531	Corynebacterium glutamicum dtsR1 and dtsR2 genes, complete cds.	Corynebacterium glutamicum	99,030	19-OCT-1998
		GB_PAT:E17019	4961	E17019	Brevibacterium lactofermentum dtsR and dtsR2 genes.	Corynebacterium glutamicum	98,973	28-Jul-99
rx02335	1896	GB_BA1:AB018530	2855	AB018530	Corynebacterium glutamicum dtsR gene, complete cds.	Corynebacterium glutamicum	99,030	19-OCT-1998
		GB_BA1:CGU35023	3195	U35023	Corynebacterium glutamicum thiosulfate sulfurtransferase (thtR) gene, partial cds, acyl CoA carboxylase (accBC) gene, complete cds.	Corynebacterium glutamicum	99,947	16-Jan-97
		GB_BA1:U00012	33312	U00012	Mycobacterium leprae cosmid B1308.	Corynebacterium glutamicum	40,247	30-Jan-96
		GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	67,568	10-Feb-99
rx02364	750	GB_BA1:AP000006	319000	AP000006	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).	Pyrococcus horikoshii	36,130	8-Feb-99
		GB_BA1:AP000006	319000	AP000006	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).	Pyrococcus horikoshii	34,543	8-Feb-99

Table 4 (continued)

rx02372	2010	GB_HTG3:AC011461	100974	AC011461	Homo sapiens chromosome 19 clone CIT-HSPC_429L19, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces.	Homo sapiens	36,138	07-OCT-1999
		GB_HTG3:AC011461	100974	AC011461	Homo sapiens chromosome 19 clone CIT-HSPC_429L19, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces.	Homo sapiens	36,138	07-OCT-1999
		GB_EST21:AA992021	279	AA992021	α35c01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1618848 3', mRNA sequence.	Homo sapiens	41,219	3-Jun-98
rx02397	1119	GB_HTG4:AC009273	76175	AC009273	Arabidopsis thaliana chromosome 1 clone T1N6, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Arabidopsis thaliana	38,566	12-OCT-1999
		GB_HTG4:AC009273	76175	AC009273	Arabidopsis thaliana chromosome 1 clone T1N6, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Arabidopsis thaliana	38,566	12-OCT-1999
		GB_BA1:D90826	19493	D90826	E.coli genomic DNA, Kohara clone #335(40.9-41.3 min.).	Escherichia coli	39,600	21-MAR-1997
rx02424	723	GB_EST13:AA334108	275	AA334108	EST38262 Embryo, 9 week Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	38,603	21-Apr-97
		GB_PR3:AC005224	16687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	36,111	14-Aug-98
		GB_PR3:AC005224	16687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	33,427	14-Aug-98
rx02426	1656	GB_PAT:A06664	1350	A06664	B.stearothermophilus lct gene.	Bacillus stearothermophilus	39,936	29-Jul-93
		GB_PAT:A04115	1361	A04115	B.stearothermophilus recombinant lct gene.	synthetic construct	40,042	17-Feb-97
		GB_BA1:BACLDHL	1361	M14788	B.stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds.	Bacillus stearothermophilus	40,338	26-Apr-93
rx02487	1827	GB_BA2:AF007101	32870	AF007101	Streptomyces hygroscopicus putative pteridine-dependent dioxygenase, PKS modules 1, 2, 3 and 4, and putative regulatory protein genes, complete cds and putative hydroxylase gene, partial cds.	Streptomyces hygroscopicus	43,298	13-Jan-98
		GB_BA1:MTIC364	29540	Z93777	Mycobacterium tuberculosis H37Rv complete genome; segment 52/162.	Mycobacterium tuberculosis	44,352	17-Jun-98
		GB_BA2:AF119621	15986	AF119621	Pseudomonas abietaniphila BKME-9 Dtl (ditl), dioxygenase Dita oxygenase component small subunit (ditA2), dioxygenase Dita oxygenase component large subunit (ditA1), DtlH (ditH), DtlG (ditG), DtlF (ditF), DtlE (ditE), DtlD (ditD), aromatic diterpenoid extradiol ring-cleavage dioxygenase (ditC), DtlB (ditB), and dioxygenase Dita ferredoxin component (ditA3) genes, complete cds; and unknown genes.	Pseudomonas abietaniphila	43,611	28-Apr-99
rx02511	780	GB_PR4:AC002470	235395	AC002470	Homo sapiens Chromosome 22q11.2 BAC Clone b135h6 In BCRL2-GGT Region, complete sequence.	Homo sapiens	37,971	30-Nov-99
		GB_PR4:AC002472	147100	AC002472	Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 In BCRL2-GGT Region, complete sequence.	Homo sapiens	38,239	13-Sep-99
		GB_EST34:A1806938	118	A1806938	wf24b07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356501 3' similar to SW:PLZF_HUMAN Q05516 ZINC FINGER PROTEIN PLZF., mRNA sequence.	Homo sapiens	38,983	7-Jul-99
rx02512	1086	GB_BA1:MTCY1A10	25949	Z95387	Mycobacterium tuberculosis H37Rv complete genome; segment 117/162.	Mycobacterium tuberculosis	37,407	17-Jun-98
		GB_BA1:MLCL581	36225	Z96801	Mycobacterium leprae cosmid L581.	Mycobacterium leprae	43,193	24-Jun-97
		GB_OV:GGU43396	2738	U43396	Gallus gallus tropomyosin receptor kinase A (ctrka) mRNA, complete cds.	Gallus gallus	38,789	18-Jan-96
rx02527	1452	GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rnb-dnaB genomic region.	Bacillus subtilis	37,395	4-Feb-98

Table 4 (continued)

GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rnb-dnaB genomic region.	Bacillus subtilis	36,218	4-Feb-98
GB_HTG2:AC005861	112369	AC005861	Arabidopsis thaliana clone F23B24, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.	Arabidopsis thaliana	38,407	29-Apr-99
GB_PL1:AB006530	7344	AB006530	Citrus lanatus Sat gene for serine acetyltransferase, complete cds and 5'-flanking region.	Citrus lanatus	35,449	20-Aug-97
GB_PL1:CNASA	5729	D85624	Citrus vulgaris serine acetyltransferase (Sat) DNA, complete cds.	Citrus lanatus	35,449	6-Feb-99
GB_PL1:AB006530	7344	AB006530	Citrus lanatus Sat gene for serine acetyltransferase, complete cds and 5'-flanking region.	Citrus lanatus	34,646	20-Aug-97
GB_EST32:AI727189	619	AI727189	BNLGH17498 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AB020715) KIAA0908 protein [Homo sapiens], mRNA sequence.	Gossypium hirsutum	35,099	11-Jun-99
GB_BA1:CGPUTP	3791	Y09163	C. glutamicum putP gene.	Corynebacterium glutamicum	38,562	8-Sep-97
GB_PL2:SPAC13G6	33481	Z54308	S. pombe chromosome I cosmid c13G6.	Schizosaccharomyces pombe	35,774	18-OCT-1999
GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	41,872	9-Apr-97
GB_EST35:AI857385	488	AI857385	w155e03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2428828 3', mRNA sequence.	Homo sapiens	39,139	26-Aug-99
GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	38,552	9-Apr-97
GB_PL1:AB016871	79109	AB016871	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16L22, complete sequence.	Arabidopsis thaliana	34,213	20-Nov-99
GB_PL1:AB025602	55790	AB025602	Arabidopsis thaliana genomic DNA, chromosome 5, BAC clone: F14A1, complete sequence.	Arabidopsis thaliana	36,461	20-Nov-99
GB_IN1:CELF36H9	35985	AF016668	Caenorhabditis elegans cosmid F36H9.	Caenorhabditis elegans	35,977	8-Aug-97
GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	38,517	17-Jun-98
GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	39,173	17-Jun-98
GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	38,548	24-Jun-99
GB_BA1:MTCY338	29372	Z74697	Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.	Mycobacterium tuberculosis	46,263	17-Jun-98
GB_BA1:SEERYABS	20444	X62569	S. erythraea eryA gene for 6-deoxyerythronolide B synthase II & III.	Saccharopolyspora erythraea	45,053	28-Feb-92
GB_BA2:AF113605	1593	AF113605	Streptomyces coelicolor propionyl-CoA carboxylase complex B subunit (pccB) gene, complete cds.	Streptomyces coelicolor	58,397	08-DEC-1999
GB_BA1:SC1C2	42210	AL031124	Streptomyces coelicolor cosmid 1C2.	Streptomyces coelicolor	52,916	15-Jan-99
GB_BA1:AB018531	4961	AB018531	Corynebacterium glutamicum dtsR1 and dtsR2 genes, complete cds.	Corynebacterium glutamicum	58,809	19-OCT-1998
GB_BA1:AEMML	2585	X99639	Ralstonia eutropha mmH, mmI, and mmJ genes.	Ralstonia eutropha	35,264	22-Jan-98

Table 4 (continued)

GB_EST15:AA508926	422	AA508926	MBAFCW1C08T3 Brugia malayi adult female cDNA (SAW96MLW-BmAF)	Brugia malayi	43,377	8-Jul-97
GB_BA1:AEMLL	2585	X99639	Brugia malayi cDNA clone AFCW1C08 5', mRNA sequence.	Ralstonia eutropha	41,148	22-Jan-98
GB_BA1:SYNPOO	1964	X17439	Ralstonia eutropha mmH4, mmH1 & mmHJ genes.	Synechocystis PCC6803	38,145	10-Feb-99
GB_GSS9:AAQ101527	184	AQ101527	Synechocystis ndhC, psbG genes for NDH-C, PSII-G and ORF157.	Homo sapiens	38,798	27-Aug-98
GB_IN1:MNE133341	399	AJ133341	HS_2265_A1_E11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2265 Col=21 Row=1, genomic survey sequence.	Melarthape neritoides	39,098	2-Jun-99
GB_BA2:AE001756	10938	AE001756	Melarthape neritoides partial caM gene, exons 1-2.	Thermotoga maritima	40,104	2-Jun-99
GB_GSS12:AAQ423878	689	AQ423878	Thermotoga maritima section 68 of 136 of the complete genome.	Homo sapiens	36,451	23-MAR-1999
GB_HTG2:AC006765	274498	AC006765	CITBI-E1-2575E20.TF CITBI-E1 Homo sapiens genomic clone 2575E20, genomic survey sequence.	Caenorhabditis elegans	39,072	23-Feb-99
GB_EST36:AI900317	436	AI900317	Caenorhabditis elegans clone Y43H11, *** SEQUENCING IN PROGRESS***, 7 unordered pieces.	Glycine max	41,566	06-DEC-1999
GB_GSS12:AAQ342831	683	AQ342831	sc04a02.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:Gm-c1012-1155 5' similar to SW:PRS6_SOLTU P54778 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG. ; mRNA sequence.	Homo sapiens	34,762	07-MAY-1999
GB_EST36:AI900856	779	AI900856	RPC111-122K17.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-122K17, genomic survey sequence.	Glycine max	39,063	06-DEC-1999
GB_IN2:CELB0213	39134	AF039050	sb95c11.y1 Gm-c1012 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1012-429 5' similar to SW:PRS6_SOLTU P54778 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG. ; mRNA sequence.	Caenorhabditis elegans	35,814	2-Jun-99
GB_RO:RNITPR2R	10708	X61677	Caenorhabditis elegans cosmid B0213.	Arabidopsis thaliana	38,462	28-Jun-99
GB_RO:D89728	5002	D89728	Arabidopsis thaliana genome survey sequence SP6 end of BAC F10D11 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Rattus norvegicus	37,543	21-OCT-1991
GB_GSS8:AAQ062004	362	AQ062004	Rat ITPR2 gene for type 2 inositol triphosphate receptor.	Mus musculus	38,829	7-Feb-99
GB_GSS14:AAQ555818	462	AQ555818	Mus musculus mRNA for LOK, complete cds.	Homo sapiens	36,565	31-Jul-98
GB_IN1:DME9736	7411	AJ009736	CIT-HSP-2346O14.TR CIT-HSP Homo sapiens genomic clone 2346O14, genomic survey sequence.	Homo sapiens	36,534	29-MAY-1999
GB_PR4:AC004801	193561	AC004801	HS_5230_B1_G06_SP6E RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=806 Col=11 Row=N, genomic survey sequence.	Drosophila melanogaster	36,522	19-Jan-99
GB_PR4:AC004801	193561	AC004801	Drosophila melanogaster Idefix retroelement: gag, pol and env genes, partial. Homo sapiens 12q13.1 PAC RPC1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	39,341	2-Feb-99
GB_EST34:AV132028	258	AV132028	Homo sapiens 12q13.1 PAC RPC1-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	Homo sapiens	37,037	2-Feb-99
GB_GSS10:AAQ240654	452	AQ240654	AV132028 Mus musculus C57BL/6J 11-day embryo Mus musculus cDNA clone 2700087F01, mRNA sequence.	Mus musculus	43,529	1-Jul-99
GB_GSS11:AAQ309500	576	AQ309500	CIT-HSP-2385D24.TFB.1 CIT-HSP Homo sapiens genomic clone 2385D24, genomic survey sequence.	Homo sapiens	40,044	30-Sep-98
			CIT-HSP-2384D24.TFD CIT-HSP Homo sapiens genomic clone 2384D24, genomic survey sequence.	Homo sapiens	38,869	22-DEC-1998

Table 4 (continued)

	GB	Accession	Size	Gene	Species	Length	Date
rx02749	999	AF086791	37867	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase small subunit (carA), carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), enolase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (mh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes.	Zymomonas mobilis	39,024	4-Nov-98
		GB_BA1:SYCSLRB GB_BA2:AE001306 GB_BA2:AF126953	146271 13316 1638	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999. Chlamydia trachomatis section 33 of 87 of the complete genome. Corynebacterium glutamicum gamma-synthase (metB) gene, complete cds.	Synechocystis sp. Chlamydia trachomatis Corynebacterium glutamicum	34,573 38,940 100,000	13-Feb-99 2-Sep-98 10-Sep-99
	906	GB_BA1:SCI5 GB_PR3:HS90L6	6661 190837	Streptomyces coelicolor cosmid l5. Human DNA sequence from clone 90L6 on chromosome 22q11.21-11.23. Contains an RPL15 (60S Ribosomal Protein L15) pseudogene, ESTs, STSs and GSSs, complete sequence.	Streptomyces coelicolor Homo sapiens	37,486 34,149	16-Jun-99 23-Nov-99
	876	GB_BA2:AF099015	5000	Streptomyces coelicolor strain A3(2) integrase (int), Fe-containing superoxide dismutase II (sofF2), Fe uptake system permease (firE), and Fe uptake system integral membrane protein (firD) genes, complete cds.	Streptomyces coelicolor	36,721	1-Jun-99
		GB_BA1:ECONUW93 GB_HTG3:AC011361	338534 186148	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes. Homo sapiens chromosome 5 clone CIT-HSPC_482N19, *** SEQUENCING IN PROGRESS ***, 69 unordered pieces.	Escherichia coli Homo sapiens	38,787 43,577	17-Apr-96 06-OCT-1999
	1197	GB_PR4:AC005998 GB_PR4:AC006008 GB_PR3:HSDJ73H14	96556 57554 95556	Homo sapiens clone DJ0622E21, complete sequence. Homo sapiens clone DJ0820A21, complete sequence. Human DNA sequence from clone 73H14 on chromosome Xq26.3-28, complete sequence.	Homo sapiens Homo sapiens Homo sapiens	37,298 35,538 39,726	29-Jul-99 17-Jun-99 23-Nov-99
	375	GB_RO:MUSSPCTLT GB_RO:MUSGRC GB_RO:RNU57062 GB_GSS6:AQ832862	3172 894 880 476	Mouse cytotoxic T lymphocyte-specific serine protease CCPIL gene, complete mouse granzyme C serine esterase mRNA, complete cds. Rattus norvegicus natural killer cell protease 4 (RNKP-4) mRNA, complete cds. HS_5261_A2_E10_SP65 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=837 Col=20 Row=I, genomic survey sequence.	Mus musculus Mus musculus Rattus norvegicus Homo sapiens	47,518 44,939 41,554 35,610	19-Jan-96 12-Jun-93 31-Jul-96 27-Aug-99
		GB_GSS5:AQ784593 GB_GSS13:AQ473140	515 397	HS_3248_A2_F02 TTC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3248 Col=4 Row=K, genomic survey sequence. CITBI-E1-2589G6.TF CITBI-E1 Homo sapiens genomic clone 2589G6, genomic survey sequence.	Homo sapiens Homo sapiens	38,956 34,761	3-Aug-99 23-Apr-99
	678	GB_EST18:AA696785 GB_EST18:AA696785	316 316	GM08392.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM08392 5prime, mRNA sequence. GM08392.5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM08392 5prime, mRNA sequence.	Drosophila melanogaster Drosophila melanogaster	40,604 38,281	28-Nov-98 28-Nov-98
	1452	GB_BA1:CG8ETPGEN GB_BA1:SC5F2A	2339 40105	C.glutamicum betP gene. Streptomyces coelicolor cosmid 5F2A.	Corynebacterium glutamicum Streptomyces coelicolor A3(2)	99,931 57,557	8-Sep-97 24-MAY-1999

Table 4 (continued)

αs03220 725	GB_BA2:AF008220	220060	AF008220	Bacillus subtilis rmB-dnaB genomic region.	Bacillus subtilis Chlorella kessleri Mus musculus	40,000 45,328 41,758 38,106	4-Feb-98 17-Feb-97 18-Sep-99 17-Feb-97
	GB_PL1:CKHUP2	2353	X66855	C.kessleri HUP2 mRNA.			
	GB_EST38:AW048153	383	AW048153	UI-M-BH1-alc-h-05-Q-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-alc-h-05-Q-UI 3', mRNA sequence.			
	GB_PL1:CKHUP2	2353	X66855	C.kessleri HUP2 mRNA.			

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

- 5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
- 10 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$, 500 mg/l complexing agent
- 15 (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
- 20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca. 18 h at 37°C. The DNA was purified by
- 25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
- 30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

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min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

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Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Loris6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

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Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (*see e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

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Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g.* *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

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the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer,

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A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to
5 use an *Mcr*-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980)
10 *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other
15 *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by
20 sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in
25 Winnacker, E.L. (1987) *From Genes to Clones – Introduction to Gene Technology*. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on
30 the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene

product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is
5 extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.*
10 (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) *Current Protocols in Molecular Biology*, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a
15 matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

20

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and
25 readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as
30 mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex

compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials
5 which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the
10 chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as
15 vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information
20 about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and
25 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can
30 be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers

such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods,

- applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) *Enzymes*. Longmans: London; Fersht, (1985) *Enzyme Structure and Mechanism*. Freeman: New York; Walsh, (1979) *Enzymatic Reaction Mechanisms*. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) *Fundamentals of Enzymology*. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) *The Enzymes*, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) *Enzymkinetik*, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) *Methods of Enzymatic Analysis*, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's
- 10 *Encyclopedia of Industrial Chemistry* (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using

15 reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed

20 according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in *Biomembranes, Molecular Structure and Function*, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired

25 **Product**

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired

30 product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical

- chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.*
- 5 (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of
- 10 Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

- In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the
- 15 production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and
- 20 measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

25 **Example 10: Purification of the Desired Product from *C. glutamicum* Culture**

- Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such
- 30 as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA*

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90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MCT nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MCT protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins.* John Wiley and Sons: New York). The gene sequences of the invention

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were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (e.g., a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (e.g., a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label

may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the
5 expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice
10 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide
15 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the
20 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be
25 labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998),
30 *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as

described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18:

1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and
5 include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (e.g., ^{35}S -methionine, ^{35}S -cysteine, ^{14}C -labelled amino acids, ^{15}N -amino acids, $^{15}\text{NO}_3$ or $^{15}\text{NH}_4^+$ or ^{13}C -labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly,
10 fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount
15 of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other
20 standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, e.g., Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

25 The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (e.g., different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications,
30 such as to compare the behavior of various organisms in a given (e.g., metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an
5 MCT protein, or a portion thereof, provided that the nucleic acid molecule does not
consist of any of the F-designated genes set forth in Table 1.
2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule
10 encodes an MCT protein involved in the production of a fine chemical.
3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the
group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the
Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does
15 not consist of any of the F-designated genes set forth in Table 1.
4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected
from the group consisting of those sequences set forth as even-numbered SEQ ID
NOs of the Sequence Listing, provided that the nucleic acid molecule does not
20 consist of any of the F-designated genes set forth in Table 1.
5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant
of a polypeptide selected from the group of amino acid sequences consisting of those
sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing,
25 provided that the nucleic acid molecule does not consist of any of the F-designated
genes set forth in Table 1.
6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least
50% homologous to a nucleotide sequence selected from the group consisting of
30 those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or
a portion thereof, provided that the nucleic acid molecule does not consist of any of
the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the
5 Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
10
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
- 15 10. A vector comprising the nucleic acid molecule of any one of claims 1-9.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
- 20 13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
25
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group
30 consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated

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fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12
5 in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated MCT polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
- 10 19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical production.
20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the
15 Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting
20 of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
22. The isolated polypeptide of any of claims 18-21, further comprising heterologous
25 amino acid sequences.
23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID
30 NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.
28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujiokense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*, *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors,
5 polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
33. The method of claim 32, wherein said amino acid is drawn from the group consisting
10 of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
34. A method for producing a fine chemical, comprising culturing a cell whose genomic
15 DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of SEQ ID NOs 1 through
20 676 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.
36. A host cell comprising a nucleic acid molecule selected from the group consisting
25 of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.
37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs in the Sequence
30 Listing, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing s.

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38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

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INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TRANSPORT

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Gly	Asp	Arg	Ala	Ala	Ile	Leu	Ala	Asn	Asn	Ser	Pro	Glu	Tyr	Ile	Phe	
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Val	Arg	Lys	His	Phe	Ser	Ser	Leu	Pro	Ala	Ala	Glu	Arg	Pro	Arg	Ile	
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Leu	Ser	Val	Asp	Ser	Leu	Pro	Asp	Ser	Leu	Ala	Asp	Ser	Tyr	Glu	Asn	
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Pro	Met	Leu	Thr	Glu	Ala	Gly	Arg	Arg	Leu	Ala	Ala	Leu	Arg	Gln	Ser	
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Ala	Pro	Ile	Asp	Leu	Thr	Ala	Phe	Leu	Gln	Tyr	Thr	Ser	Gly	Ser	Thr	
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Arg	Thr	Pro	Ala	Gly	Val	Val	Leu	Thr	Asn	Arg	Ser	Ile	Leu	Thr	Asn	
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Val	Ser	Trp	Leu	Pro	Leu	His	His	Asp	Met	Gly	Ile	Ile	Leu	Ala	Ala	
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Phe	Val	Thr	Met	Leu	Gly	Leu	Asp	Asn	Glu	Phe	Met	Asn	Pro	Arg	Asp	
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ttc	gtg	cag	cag	cct	tcc	cgc	tgg	att	aag	cag	ctc	aac	cgt	cgc	gaa	979
Phe	Val	Gln	Pro	Ser	Arg	Trp	Ile	Lys	Gln	Leu	Asn	Arg	Arg	Arg	Glu	
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agc	gac	gtg	gac	gtt	aac	gtc	tac	acc	gtg	gtt	cct	aac	ttc	gcc	ctc	1027
Ser	Asp	Val	Asp	Val	Asn	Val	Tyr	Thr	Val	Val	Pro	Asn	Phe	Ala	Leu	
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Leu Ser Ala Leu Asp Ala Ile Ile Ile Gly Ser Glu Pro Val Thr Glu	
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Asn Ala Leu Thr Thr Phe Arg Glu Ala Phe Glu Pro Tyr Gly Leu Pro	
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Val Gln Thr Leu Arg Pro Ser Tyr Gly Leu Ala Glu Ala Ser Leu Leu	
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Val Thr Thr Pro Gln Thr Glu Asn Arg Pro Leu Ile Ser Tyr Phe Asp	
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Gln Leu Val Ile Val Asp Ser Glu Thr Gly Thr Glu Leu Ala Asp Gly	
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Gln Ile Gly Glu Ile Trp Thr His Gly Glu Asn Thr Ala Ala Gly Tyr	
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Thr Arg Leu Glu Glu Asn Ser Arg Ala Glu Gly Ala Ala Asp Asp Asn	
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Tyr Trp Met Ala Thr Gly Asp Leu Gly Val Ile Val Asp Asn Glu Leu	
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Tyr Ile Thr Gly Arg Leu Lys Asp Leu Ile Val Val Ala Gly Arg Asn	
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His Tyr Pro Gln Asp Ile Glu Tyr Thr Val Gln Ala Ala Ser Ala His	
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Ile Arg Ala Asp Ser Val Ala Ala Phe Ala Val Pro Gly Asp Asp Ile	
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 His Gly Val Val Pro Glu Glu Ile Arg Ile Leu Ala Pro Asp Glu Ile
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 Pro Glu Tyr Ile Phe Ser Phe Leu Gly Ala Ile Tyr Ala Gly Met Val
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 Pro Val Pro Leu Tyr Asp Pro Asn Glu Pro Gly His Ala Asp His Leu
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 Asn Ala Val Phe Ala Asp Ser Glu Pro Val Val Val Leu Thr Asn Ser
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 Glu Arg Pro Arg Ile Leu Ser Val Asp Ser Leu Pro Asp Ser Leu Ala
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 Asp Ser Tyr Glu Asn Pro Met Leu Thr Glu Ala Gly Arg Arg Leu Ala

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Pro Gly Asp Asp Ile Glu Lys Leu Ile Ile Leu Ala Glu Arg Asp Thr
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Thr Ala Asn Glu Ala Asp Asp Ala Ala Ala Glu Glu Ala Ile Arg Ser
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 Ser Lys Ser Ala Gly Ala Val Arg Lys His Phe Ser Ser Leu Pro Ala
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 Ala Glu Arg Pro Arg Ile Leu Ser Val Asp Ser Leu Pro Asp Ser Leu
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 Ala Asp Ser Tyr Glu Asn Pro Met Leu Thr Glu Ala Gly Arg Arg Leu
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gct gct ctg cgc cag tcc gcg ccc att gat ctg acc gca ttc ctg cag 288
 Ala Ala Leu Arg Gln Ser Ala Pro Ile Asp Leu Thr Ala Phe Leu Gln
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 Tyr Thr Ser Gly Ser Thr Arg Thr Pro Ala Gly Val Val Leu Thr Asn
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cgc tcc atc ctg acc aac gtc ttg cag atc ttc agc gcc gca cag ctg	384
Arg Ser Ile Leu Thr Asn Val Leu Gln Ile Phe Ser Ala Ala Gln Leu	
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Lys Thr Pro Leu Arg Leu Val Ser Trp Leu Pro Leu His His Asp Met	
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Gly Ile Ile Leu Ala Ala Phe Val Thr Met Leu Gly Leu Asp Asn Glu	
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Phe Met Asn Pro Arg Asp Phe Val Gln Gln Pro Ser Arg Trp Ile Lys	
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Gln Leu Asn Arg Arg Glu Ser Asp Val Asp Val Asn Val Tyr Thr Val	
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Val Pro Asn Phe Ala Leu Glu Leu Ala Ala Arg Tyr Ala Lys Pro Ala	
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Glu Gly Glu Thr Leu Asp Leu Ser Ala Leu Asp Ala Ile Ile Ile Gly	
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Ser Glu Pro Val Thr Glu Asn Ala Leu Thr Thr Phe Arg Glu Ala Phe	
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Glu Pro Tyr Gly Leu Pro Val Gln Thr Leu Arg Pro Ser Tyr Gly Leu	
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Ala Glu Ala Ser Leu Leu Val Thr Thr Pro Gln Thr Glu Asn Arg Pro	
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Leu Val Glu Lys Gly Asn Asn Lys Ala Val Ala Phe Val Ser Asn Gly	
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Gln Val Ala Ala Pro Gln Gln Leu Val Ile Val Asp Ser Glu Thr Gly	
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Thr Glu Leu Ala Asp Gly Gln Ile Gly Glu Ile Trp Thr His Gly Glu	
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 Gln Ala Ala Ser Ala His Ile Arg Ala Asp Ser Val Ala Ala Phe Ala
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 Leu Ala Pro Asp Glu Ile Ala Arg Ser Ser Ser Gly Lys Ile Ala Arg
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 Tyr Thr Ser Gly Ser Thr Arg Thr Pro Ala Gly Val Val Leu Thr Asn
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 Gln Leu Asn Arg Arg Glu Ser Asp Val Asp Val Asn Val Tyr Thr Val
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 Val Pro Asn Phe Ala Leu Glu Leu Ala Ala Arg Tyr Ala Lys Pro Ala
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 Glu Gly Glu Thr Leu Asp Leu Ser Ala Leu Asp Ala Ile Ile Ile Gly
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Ser	Ser	Asp	Gln	Lys	Met	Thr	Val	Glu	Gln	Val	Arg	Thr	Trp	Leu	Arg															
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Asp	Trp	Val	Val	Arg	Thr	Thr	Gly	Ile	Pro	Val	Glu	Glu	Val	Thr	Asp															
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Asp	Lys	Ala	Met	Glu	Thr	Phe	Gly	Leu	Ser	Ser	Arg	Asp	Val	Val	Val															
t	t	g	t	g	a	a	a	c	c	t	g	a	a	c	c	a	a	t	c	c	a	a	t	c	c	a	a	t	c	307
Leu	Ser	Gly	Glu	Leu	Glu	Asn	Leu	Leu	Asp	Thr	Ser	Leu	Asp	Ala	Thr															
a	t	c	g	t	a	t	a	g	a	t	c	a	a	c	a	a	t	c	c	a	a	t	c	c	a	a	t	c	355	
Ile	Ala	Tyr	Glu	Tyr	Pro	Thr	Ile	Arg	Ser	Leu	Ala	Gln	Arg	Leu	Val															

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Glu Gly Glu Pro Arg Arg Ala His Thr Gln Arg Glu Leu Asn Phe Ser	
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Ala Val Ser Asp Ser Pro Gly Ser His Asp Ile Ala Val Val Gly Met	
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Ala Ala Arg Tyr Pro Gly Ala Glu Ser Leu Glu Asp Met Trp Lys Leu	
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Leu Val Glu Gly Arg Asp Gly Ile Ser Asp Leu Pro Ile Gly Arg Trp	
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Ser Glu Tyr Ala Gly Asp Glu Val Met Ser Arg Lys Met Glu Glu Phe	
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Ser Thr Ile Gly Gly Tyr Leu Ser Asp Ile Ser Ser Phe Asp Ala Glu	
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Phe Phe Gly Leu Ser Pro Leu Glu Ala Ala Asn Met Asp Pro Gln Gln	
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Arg Ile Leu Leu Glu Leu Thr Trp Glu Ala Leu Glu Tyr Ala Arg Ile	
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Ser Asn Asn Asp Tyr Gly Met Met Ile Ala Ala Asp Pro Ala Glu Ala	
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His Pro Tyr Ala Leu Thr Gly Thr Ser Ser Ala Ile Val Ala Asn Arg	
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Ile Asn Tyr Ala Phe Asp Phe Arg Gly Pro Ser Val Asn Val Asp Thr	
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Ala Cys Ser Ser Ser Leu Val Ala Val His Gln Ala Val Arg Ala Leu	
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Arg Asn Gly Glu Ala Asp His Ala Ile Ala Gly Gly Val Asn Ile Leu	
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Pro Thr Gly Lys Ile His Ala Phe Ser Asp Asp Ala Asp Gly Phe Val	
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Ile Arg Asp Gly Asp Lys Ile Ile Gly Val Ile Lys Gly Ser Ala Val	
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375 380 385	
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Gln Val Asp Val Leu Gln Arg Ala Tyr Val Asp Ala Gln Val Asp Pro	
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Thr Thr Val Asp Tyr Val Glu Ala His Gly Thr Gly Thr Ile Leu Gly	
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Asp Pro Ile Glu Ala Thr Ala Leu Gly Ala Val Leu Gly Tyr Gly Arg	
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His Thr Glu Ser Ala Ala Gly Ile Ala Gly Val Ile Lys Val Leu Leu	
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Pro Arg Glu Trp Pro Glu Tyr Asn Gly His Ala Val Ala Gly Val Ser	
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Asp Gln Gln Val Ala Leu Pro Val Ser Gly His Leu Pro Ser Arg Arg	
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Arg Gln Ala Ala Ala Asp Leu Ala Asp Phe Leu Glu Gly Arg Lys Asp	

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Cys	Asp	Leu	Thr	Pro	Val	Ala	Arg	Ala	Leu	Ala	Gly	Arg	Asn	His	Gly														
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cgc	tcc	cgc	gca	gtc	gtg	ctt	gca	agc	act	atc	gag	gaa	gcc	gta	aag														
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cgc	ctg	cgc	cag	gtc	gca	gaa	ggc	aag	gtc	agc	gtc	ggg	atc	tcc	gca														
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Glu	Gly	Glu	Lys	Ser	Leu	Ala	Glu	Asp	Gln	Leu	Gly	Ala	Met	Ala	Val														
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Thr	Val	Gly	Gly	Pro	Arg	Asp	Ala	Val	Val	Gln	Phe	Val	Glu	Lys	Leu														
				810					815					820															

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His Thr Ser Ala Val Glu Pro Leu Leu Gly Glu Leu Ala Gly Glu Ile	
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Ala Gly Ile Glu Pro Leu Pro Leu Gln Ile Pro Leu Phe Ser Ser Val	
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Asp Gln Gly Val Thr Tyr Pro Val Gly Ala Val Val His Asp Ala Asp	
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Ile Ser Arg Lys Asn			
1610			

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Arg Asp Val Val Val Leu Ser Gly Glu Leu Glu Asn Leu Leu Asp Thr			
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Ser Leu Asp Ala Thr Ile Ala Tyr Glu Tyr Pro Thr Ile Arg Ser Leu			
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Ala Gln Arg Leu Val Glu Gly Glu Pro Arg Arg Ala His Thr Gln Arg			
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Glu Leu Asn Phe Ser Ala Val Ser Asp Ser Pro Gly Ser His Asp Ile			
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Ala Val Val Gly Met Ala Ala Arg Tyr Pro Gly Ala Glu Ser Leu Glu			
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Asp Met Trp Lys Leu Leu Val Glu Gly Arg Asp Gly Ile Ser Asp Leu			
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Pro Ile Gly Arg Trp Ser Glu Tyr Ala Gly Asp Glu Val Met Ser Arg			
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Lys Met Glu Glu Phe Ser Thr Ile Gly Gly Tyr Leu Ser Asp Ile Ser			
165	170	175	
Ser Phe Asp Ala Glu Phe Phe Gly Leu Ser Pro Leu Glu Ala Ala Asn			
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 Glu Tyr Ala Arg Ile Ala Pro Asn Thr Leu Arg Gly Glu Ala Val Gly
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Gly Arg Asn His Gly Arg Ser Arg Ala Val Val Leu Ala Ser Thr Ile 595 600 605		
Glu Glu Ala Val Lys Arg Leu Arg Gln Val Ala Glu Gly Lys Val Ser 610 615 620		
Val Gly Ile Ser Ala Ala Asp Ser Pro Ala Ala Asn Gly Pro Val Phe 625 630 635 640		
Val Tyr Ser Gly Phe Gly Ser Gln His Arg Leu Met Ile Lys Glu Leu 645 650 655		
Cys Ser Ile Ser Pro Gln Phe Arg Glu Arg Ile Glu Glu Leu Asp Glu 660 665 670		
Met Val Lys Phe Glu Ser Gly Trp Ser Ile Met Lys Leu Val Leu Asp 675 680 685		
Asp Glu Gln Thr Tyr Asp Thr Glu Thr Ala Gln Val Val Ile Thr Ala 690 695 700		
Ile Gln Ile Ala Leu Thr Asp Leu Leu Ala Ser Phe Gly Val Lys Pro 705 710 715 720		
Ala Ala Val Met Gly Met Ser Met Gly Glu Ile Ala Ala Ala Tyr Ala 725 730 735		
Ala Gly Gly Leu Ser Asp Arg Asp Thr Met Leu Ile Ala Ser His Arg 740 745 750		
Ser Arg Leu Met Gly Glu Gly Glu Lys Ser Leu Ala Glu Asp Gln Leu 755 760 765		
Gly Ala Met Ala Val Val Glu Phe Ala Ala Ala Asp Leu Asp Lys Phe 770 775 780		
Ile Glu Glu Asn Pro Glu Tyr Lys Gly Ile Glu Pro Ala Val Tyr Ala 785 790 795 800		
Gly Pro Gly Met Thr Thr Val Gly Gly Pro Arg Asp Ala Val Val Gln 805 810 815		
Phe Val Glu Lys Leu Glu Ser Glu Asp Lys Phe Ala Arg Leu Leu Asn 820 825 830		
Val Lys Gly Ala Gly His Thr Ser Ala Val Glu Pro Leu Leu Gly Glu 835 840 845		

Leu Ala Gly Glu Ile Ala Gly Ile Glu Pro Leu Pro Leu Gln Ile Pro
 850 855 860
 Leu Phe Ser Ser Val Asp Gln Gly Val Thr Tyr Pro Val Gly Ala Val
 865 870 875 880
 Val His Asp Ala Asp Tyr Met Leu Arg Cys Thr Arg Gln Ser Val Tyr
 885 890 895
 Phe Gln Asp Ser Thr Glu Ala Ala Phe Ala Ala Gly His Asn Thr Leu
 900 905 910
 Val Glu Ile Ser Pro Asn Pro Val Ala Leu Met Gly Met Met Asn Thr
 915 920 925
 Ala Phe Thr Val Gly Lys Pro Asp Ala Gln Leu Leu Phe Ser Leu Lys
 930 935 940
 Arg Lys Val Pro Glu Ala Glu Ser Leu Arg Asp Leu Leu Ala Lys Leu
 945 950 955 960
 Tyr Val Asn Gly Ala Asn Val Asp Phe Ser Ala Leu Tyr Gly Glu Gly
 965 970 975
 Glu Thr Ile Asp Pro Pro His Ile Thr Trp Lys His Gln Arg Phe Trp
 980 985 990
 Thr Ser Ala Arg Pro Ser Ser Gly Ala Ser Leu Asp Leu Pro Gly Phe
 995 1000 1005
 Arg Val Asn Leu Pro Asn Asn Thr Val Ala Phe Ser Thr Ala Ala Glu
 1010 1015 1020
 Leu Ala Pro Ser Ala Val Ala Ile Met Glu Ala Ala Ala Met Ala Val
 1025 1030 1035 1040
 Thr Pro Gly Ser Ser Val Asp Ala Val Asp Glu Arg Asp Met Leu Pro
 1045 1050 1055
 Pro Ser Gly Glu Ile Thr Thr Ile Val Thr Arg Ser Leu Gly Gly Leu
 1060 1065 1070
 Ser Leu Ser Val Tyr Lys Ile Glu Gly Thr Thr Ser Thr Leu Val Ala
 1075 1080 1085
 Glu Gly Phe Ala Ala Asn Pro Gly Phe Ala Ala Ala Ser Ser Phe Asp
 1090 1095 1100
 Gly Pro Gly Tyr Asp Gly Phe Asn Thr Asp Tyr Ser Asp Gln Pro Asp
 1105 1110 1115 1120
 Pro Arg Ser Asp Leu Pro Leu Asp Ile Glu Ala Val Arg Trp Asp Pro
 1125 1130 1135
 Ala Thr Glu Thr Val Glu Glu Arg Met Arg Ala Ile Val Ser Glu Ala
 1140 1145 1150
 Met Gly Tyr Asp Val Asp Asp Leu Pro Arg Glu Leu Pro Leu Ile Asp
 1155 1160 1165

Leu Gly Leu Asp Ser Leu Met Gly Met Arg Ile Lys Asn Arg Ile Glu
 1170 1175 1180
 Asn Asp Phe Gln Ile Pro Pro Leu Gln Val Gln Ala Leu Arg Asp Ala
 1185 1190 1195 1200
 Ser Val Ala Asp Val Val Ile Met Val Glu Asn Met Val Ala Gly Arg
 1205 1210 1215
 Ser Ser Glu Thr Leu Val Asp Ala Thr Pro Gln Val Pro Ala Glu Ala
 1220 1225 1230
 Ala Gly Glu Ala Gln Ala Ala Glu Ser Ser Ala Ser Gly Glu Asp Val
 1235 1240 1245
 Gln Gly Val Gly Val Ala Pro Arg Asp Ala Ser Glu Arg Met Val Phe
 1250 1255 1260
 Gly Thr Trp Ala Gly Leu Thr Gly Ala Ala Ala Ala Gly Val Thr Ser
 1265 1270 1275 1280
 Lys Leu Pro Gln Ile Asp Val Asp Thr Ala Thr Ala Ile Ala Glu Arg
 1285 1290 1295
 Leu Thr Glu Arg Ser Gly Ile Glu Ile Ser Thr Glu Gln Val Leu Ala
 1300 1305 1310
 Ala Glu Thr Leu Glu Pro Leu Ser Asp Leu Val Arg Glu Gly Leu Glu
 1315 1320 1325
 Thr Glu Val Gln Gly Asn Ile Arg Val Leu Arg Gly Arg Ala Glu Gly
 1330 1335 1340
 Ser Thr Lys Pro Ala Val Phe Met Phe His Pro Ala Gly Gly Ser Ser
 1345 1350 1355 1360
 Val Val Tyr Gln Pro Leu Met Arg Arg Leu Pro Glu Asp Val Pro Val
 1365 1370 1375
 Tyr Gly Val Glu Arg Leu Glu Gly Asp Leu Ala Asp Arg Ala Ala Ala
 1380 1385 1390
 Tyr Val Asp Asp Ile Lys Lys Tyr Ser Asp Gly Phe Pro Val Val Leu
 1395 1400 1405
 Gly Gly Trp Ser Phe Gly Gly Ala Val Ala Phe Glu Val Ala His Gln
 1410 1415 1420
 Leu Val Gly Ser Asp Val Glu Val Ala Thr Val Ala Leu Leu Asp Thr
 1425 1430 1435 1440
 Val Gln Pro Ser Asn Pro Ala Pro Asp Thr Ala Glu Glu Thr Arg Ala
 1445 1450 1455
 Arg Trp Thr Arg Tyr Ala Asp Phe Ala Lys Lys Thr Tyr Gly Leu Asp
 1460 1465 1470
 Phe Glu Val Pro Phe Glu Ile Leu Asp Thr Ile Gly Glu Asp Gly Met
 1475 1480 1485
 Leu Ser Met Met Thr Asp Phe Leu Ala Asn Thr Asp Ala Ser Glu His

1490	1495	1500
Gly Leu Ser Ala Gly Val Leu Glu His Gln Arg Ala Ser Phe Val Asp 1505	1510	1515 1520
Asn Arg Ile Leu Ala Lys Leu Asn Phe Ala Asp Trp Ala Asn Val Glu 1525	1530	1535
Ala Pro Val Ile Leu Phe Arg Ala Glu Arg Met His Asp Gly Ala Ile 1540	1545	1550
Glu Leu Glu Pro Asn Tyr Ala Lys Ile Asp Gln Asp Gly Gly Trp Ser 1555	1560	1565
Gly Ile Val Asn Asp Leu Glu Ile Val Gln Leu Asn Gly Asp His Leu 1570	1575	1580
Ala Val Val Asp Glu Pro Glu Ile Gly Thr Val Gly Ala His Leu Ser 1585	1590	1595 1600
Arg Arg Ile Asp Glu Ile Ser Arg Lys Asn 1605	1610	

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(517)
 <223> RXA01138

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 gctgcgagac actgtcggat cgttccttc aggtgtcacg gtg gtc acc act acc 115
 Val Val Thr Thr Thr
 1 5
 gat ggg gaa gtg gac cac ggg ttg act gtg agt gcg ttc gtg tcc ttg 163
 Asp Gly Glu Val Asp His Gly Leu Thr Val Ser Ala Phe Val Ser Leu
 10 15 20
 tcg ttg gag cct gcc atg gtg ttg gtg agt atc gat aag aaa tca agc 211
 Ser Leu Glu Pro Ala Met Val Leu Val Ser Ile Asp Lys Lys Ser Ser
 25 30 35
 gtt gtg ccg ttt ttg gag cag ggt tca cca gtt gct gtg tct gtg tta 259
 Val Val Pro Phe Leu Glu Gln Gly Ser Pro Val Ala Val Ser Val Leu
 40 45 50
 tcg gaa gag cag agc gat ttg gcc atc aca ttt ggc cgt cat ctg gaa 307
 Ser Glu Glu Gln Ser Asp Leu Ala Ile Thr Phe Gly Arg His Leu Glu
 55 60 65
 aac aaa ttc gac gcc gtt tcc att aag cgt tca aca aac agg gca gcg 355
 Asn Lys Phe Asp Gly Val Ser Ile Lys Arg Ser Thr Asn Arg Ala Ala
 70 75 80 85

gtc ttg gaa ggt gcg tca gca tgg ttg agt ggc gct gtg gtg gat aaa 403
 Val Leu Glu Gly Ala Ser Ala Trp Leu Ser Gly Ala Val Val Asp Lys
 90 95 100

tac cca ggt gga gat cac ttt att atc acc att gcc gtg gaa gag tgt 451
 Tyr Pro Gly Gly Asp His Phe Ile Ile Thr Ile Ala Val Glu Glu Cys
 105 110 115

gct cac gac gag gag caa aag cca ctt ctt tac cac cgt ggc agg ctt 499
 Ala His Asp Glu Glu Gln Lys Pro Leu Leu Tyr His Arg Gly Arg Leu
 120 125 130

ttt cag tgg caa gaa gat taattctcca ccccttcatt ttc 540
 Phe Gln Trp Gln Glu Asp
 135

<210> 16
 <211> 139
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 16
 Val Val Thr Thr Thr Asp Gly Glu Val Asp His Gly Leu Thr Val Ser
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Ala Phe Val Ser Leu Ser Leu Glu Pro Ala Met Val Leu Val Ser Ile
 20 25 30

Asp Lys Lys Ser Ser Val Val Pro Phe Leu Glu Gln Gly Ser Pro Val
 35 40 45

Ala Val Ser Val Leu Ser Glu Glu Gln Ser Asp Leu Ala Ile Thr Phe
 50 55 60

Gly Arg His Leu Glu Asn Lys Phe Asp Gly Val Ser Ile Lys Arg Ser
 65 70 75 80

Thr Asn Arg Ala Ala Val Leu Glu Gly Ala Ser Ala Trp Leu Ser Gly
 85 90 95

Ala Val Val Asp Lys Tyr Pro Gly Gly Asp His Phe Ile Ile Thr Ile
 100 105 110

Ala Val Glu Glu Cys Ala His Asp Glu Glu Gln Lys Pro Leu Leu Tyr
 115 120 125

His Arg Gly Arg Leu Phe Gln Trp Gln Glu Asp
 130 135

<210> 17
 <211> 756
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(733)
 <223> RXA01980

<400> 17

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gccgccctag aattcactaa gtttccgata tctttaaccc atg cag atc att gat 115
 Met Gln Ile Ile Asp
 1 5

ctc tct cat gcg ttc gcg ccc gga caa ccc cac tac cct ggg gat cca 163
 Leu Ser His Ala Phe Ala Pro Gly Gln Pro His Tyr Pro Gly Asp Pro
 10 15 20

gat caa gaa att aag acg gtc tcc acg att gaa aac gat ggc ttt tta 211
 Asp Gln Glu Ile Lys Thr Val Ser Thr Ile Glu Asn Asp Gly Phe Leu
 25 30 35

atg cat caa tac aga ctt gtt ggt ccc tgg gga acg cat gta gat gca 259
 Met His Gln Tyr Arg Leu Val Gly Pro Trp Gly Thr His Val Asp Ala
 40 45 50

cct gca cat ttc gat cca caa ggt cgg acg ctt gat cag atc cct gtg 307
 Pro Ala His Phe Asp Pro Gln Gly Arg Thr Leu Asp Gln Ile Pro Val
 55 60 65

gag gaa acg cat tta ccc ctt tat tgc ctg agg ttt tct cgc ccc gat 355
 Glu Glu Thr His Leu Pro Leu Tyr Cys Leu Arg Phe Ser Arg Pro Asp
 70 75 80 85

cta tgt act gct gct gat ata gaa gcg ttt gaa cat aca cac ggg aaa 403
 Leu Cys Thr Ala Ala Asp Ile Glu Ala Phe Glu His Thr His Gly Lys
 90 95 100

atc gaa cca gga tcc ttc gtc gca ctc cac act gga tgg gaa tgg ggt 451
 Ile Glu Pro Gly Ser Phe Val Ala Leu His Thr Gly Trp Glu Trp Gly
 105 110 115

aaa caa ggg atc gca ccc ggc tgg tct atc gag gct tta gaa atc ctc 499
 Lys Gln Gly Ile Ala Pro Gly Trp Ser Ile Glu Ala Leu Glu Ile Leu
 120 125 130

cat gcc cgt gga gtc att gcc att ggc cac gat ctt ccc gat aca gat 547
 His Ala Arg Gly Val Ile Ala Ile Gly His Asp Leu Pro Asp Thr Asp
 135 140 145

cct tca ctg gag gca cag cgc tgg tgg ctg tgc cgt gac cat tgg cag 595
 Pro Ser Leu Glu Ala Gln Arg Trp Trp Leu Cys Arg Asp His Trp Gln
 150 155 160 165

att gaa aac ctc acc aat ttg gac aag gtt cct gca acg ggt gcg atg 643
 Ile Glu Asn Leu Thr Asn Leu Asp Lys Val Pro Ala Thr Gly Ala Met
 170 175 180

att gct tgt cct tgg cca gtt cca aaa gat ggt gct agt ttc cca gtg 691
 Ile Ala Cys Pro Trp Pro Val Pro Lys Asp Gly Ala Ser Phe Pro Val
 185 190 195

cgt cca att gct ctc gtc cca gag cac cta tcc cct act cgc 733
 Arg Pro Ile Ala Leu Val Pro Glu His Leu Ser Pro Thr Arg
 200 205 210

taaagcgaac ggcagcacct tct 756

<210> 18
 <211> 211
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 18
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 Tyr Pro Gly Asp Pro Asp Gln Glu Ile Lys Thr Val Ser Thr Ile Glu
 20 25 30
 Asn Asp Gly Phe Leu Met His Gln Tyr Arg Leu Val Gly Pro Trp Gly
 35 40 45
 Thr His Val Asp Ala Pro Ala His Phe Asp Pro Gln Gly Arg Thr Leu
 50 55 60
 Asp Gln Ile Pro Val Glu Glu Thr His Leu Pro Leu Tyr Cys Leu Arg
 65 70 75 80
 Phe Ser Arg Pro Asp Leu Cys Thr Ala Ala Asp Ile Glu Ala Phe Glu
 85 90 95
 His Thr His Gly Lys Ile Glu Pro Gly Ser Phe Val Ala Leu His Thr
 100 105 110
 Gly Trp Glu Trp Gly Lys Gln Gly Ile Ala Pro Gly Trp Ser Ile Glu
 115 120 125
 Ala Leu Glu Ile Leu His Ala Arg Gly Val Ile Ala Ile Gly His Asp
 130 135 140
 Leu Pro Asp Thr Asp Pro Ser Leu Glu Ala Gln Arg Trp Trp Leu Cys
 145 150 155 160
 Arg Asp His Trp Gln Ile Glu Asn Leu Thr Asn Leu Asp Lys Val Pro
 165 170 175
 Ala Thr Gly Ala Met Ile Ala Cys Pro Trp Pro Val Pro Lys Asp Gly
 180 185 190
 Ala Ser Phe Pro Val Arg Pro Ile Ala Leu Val Pro Glu His Leu Ser
 195 200 205
 Pro Thr Arg
 210

<210> 19
 <211> 1830
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1807)
 <223> RXN01007

<400> 19

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acacgtaaag taacttaaag attcactgga ggtaagccta gtg ttt aaa aag cac 115
Val Phe Lys Lys His
1 5

aga cac ggt ctc ggc tcc ccc gaa acc aaa cca cgc tca ata acc cgc 163
Arg His Gly Leu Gly Ser Pro Glu Thr Lys Pro Arg Ser Ile Thr Arg
10 15 20

cgg ttt ttc acc gcg gcc gcc gct acg ctg gca gga ttg gca gtc ctg 211
Arg Phe Phe Thr Ala Ala Ala Ala Thr Leu Ala Gly Leu Ala Val Leu
25 30 35

tcc ggc tgc aca gca caa ccc tca caa gca gaa gac aac acg ctc act 259
Ser Gly Cys Thr Ala Gln Pro Ser Gln Ala Glu Asp Asn Thr Leu Thr
40 45 50

tac tta gag cca cag ttc ttc cgc acc ctg tac cca cca tca gcg ggc 307
Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr Pro Pro Ser Ala Gly
55 60 65

ttt tac ccc aac ggc agt gtg gtg aac aac att gca gac cgc ttg ctc 355
Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile Ala Asp Arg Leu Leu
70 75 80 85

tac cag gat cct gaa acc ttg gaa ctc aag ccg tgg atc gcc acc gaa 403
Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro Trp Ile Ala Thr Glu
90 95 100

ctc cca gaa gta aac gaa gac gcc acg gaa ttt acc ttc aac atc cgc 451
Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe Thr Phe Asn Ile Arg
105 110 115

acc gat gtc acc tac tcc gat ggc acc ccg ctg acg gct gaa aac gtg 499
Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu Thr Ala Glu Asn Val
120 125 130

gtg aaa aac ttc gat ctc tat ggc ctc ggc gat caa gat cga cgc ctc 547
Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp Gln Asp Arg Arg Leu
135 140 145

acc atc tct gag cag atc acc aac tac gac cac ggc gaa gta gta gat 595
Thr Ile Ser Glu Gln Ile Thr Asn Tyr Asp His Gly Glu Val Val Asp
150 155 160 165

gag gac acc gtc cga ttc cac ttc tct gag cct gca cct ggt ttt gct 643
Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro Ala Pro Gly Phe Ala
170 175 180

cag gcc acc agc tcc ttc aac gct ggc ctt tat gcc gat tcc acc ttg 691
Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr Ala Asp Ser Thr Leu
185 190 195

gag ttc gcc aat gag gat ttc gcg cca ggc aac gcc caa aac gtc atc 739
Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn Ala Gln Asn Val Ile
200 205 210

ggc tcc ggt cct ttc gtg atc acc gat gaa acc cta ggc acc aac ctc 787
Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr Leu Gly Thr Asn Leu
215 220 225

acc ttg act gcg cgt gag gat tac gat tgg gca cca cca tca cgc gaa	835
Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala Pro Pro Ser Arg Glu	
230 235 240 245	
cat caa ggt cgc gcg aag ctt gac gcc gtc aat tat gtc ctc gcg ggt	883
His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn Tyr Val Leu Ala Gly	
250 255 260	
gaa gaa tcc gtc cgc atc gga gcc atc gtt gct ggc caa ggt gat atc	931
Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala Gly Gln Gly Asp Ile	
265 270 275	
gcc cgc cag atc gaa gcg cca gtg gag gca cac ctg aag gat gca ggc	979
Ala Arg Gln Ile Glu Ala Pro Val Glu Ala His Leu Lys Asp Ala Gly	
280 285 290	
atc ccg atc atc tcc gca gcc acc aac ggt gtg aac aac agc ttc aac	1027
Ile Pro Ile Ile Ser Ala Ala Thr Asn Gly Val Asn Asn Ser Phe Asn	
295 300 305	
ttc cgc ttc aaa aac gag ctg ctc tca gac atc cgt gtt cgc caa gct	1075
Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile Arg Val Arg Gln Ala	
310 315 320 325	
ctg atc cac gcg atc gac cgc gaa aag atc atg cgt gtg ctg ttt agt	1123
Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met Arg Val Leu Phe Ser	
330 335 340	
gat tcc tat ccg ctg gca act tct gtg ctt gcg caa aat gca ctg ggc	1171
Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala Gln Asn Ala Leu Gly	
345 350 355	
tac aaa gaa caa gta gat gcc tat gtc tac gac cta gac aaa gca aca	1219
Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp Leu Asp Lys Ala Thr	
360 365 370	
gct ctg ctt gac gaa gcc ggc tgg acc ctt gat agc gac ggc atg cgt	1267
Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp Ser Asp Gly Met Arg	
375 380 385	
cgc aag gac ggt gaa ctt cta gag ctc acc ttc aac gaa gcc ctc cca	1315
Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe Asn Glu Ala Leu Pro	
390 395 400 405	
cag cct cgt tca cgc gaa gtt gtc acc atg gtc caa gaa cag ctc ggt	1363
Gln Pro Arg Ser Arg Glu Val Val Thr Met Val Gln Glu Gln Leu Gly	
410 415 420	
gat ctg ggc atc aag gtc aac ctc aac cca ggt gac caa gca gcc cag	1411
Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly Asp Gln Ala Ala Gln	
425 430 435	
gac gct gac tcc aag gat ctc aac aag atc cag gtt cgc cac acc atg	1459
Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln Val Arg His Thr Met	
440 445 450	
gtg ggt cgc gca gac tat gac gtg ctg aaa tcc cag ctg tac tcc acc	1507
Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser Gln Leu Tyr Ser Thr	
455 460 465	

aac cgc aac gag ctg ttg aac atg acc gtg gaa ggg gag acc gcc gat 1555
 Asn Arg Asn Glu Leu Leu Asn Met Thr Val Glu Gly Glu Thr Ala Asp
 470 475 480 485

 att ggc gat cct cat ttg gag gaa ctc ctc atg gct att gca tcc agc 1603
 Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met Ala Ile Ala Ser Ser
 490 495 500

 cca cgc gaa gag gac cgt gca gca gca tct gcc gca gca cag gat tac 1651
 Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala Ala Ala Gln Asp Tyr
 505 510 515

 atc acc gag cag gca tat gtt ctt cca ctg ttt gaa gag cca gtt gtc 1699
 Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe Glu Glu Pro Val Val
 520 525 530

 tac ggc gtg cag cct tac gtg aag ggc ttt agc ccc gaa gtg atc ggc 1747
 Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser Pro Glu Val Ile Gly
 535 540 545

 cgc ccc agc ttc tat gag acc tac att gac cat tcc agc gac cat tcc 1795
 Arg Pro Ser Phe Tyr Glu Thr Tyr Ile Asp His Ser Ser Asp His Ser
 550 555 560 565

 agt gag gag gac taaatgacta cctcgcatat tct 1830
 Ser Glu Glu Asp

<210> 20

<211> 569

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 20

Val Phe Lys Lys His Arg His Gly Leu Gly Ser Pro Glu Thr Lys Pro
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 Arg Ser Ile Thr Arg Arg Phe Phe Thr Ala Ala Ala Ala Thr Leu Ala
 20 25 30

 Gly Leu Ala Val Leu Ser Gly Cys Thr Ala Gln Pro Ser Gln Ala Glu
 35 40 45

 Asp Asn Thr Leu Thr Tyr Leu Glu Pro Gln Phe Phe Arg Thr Leu Tyr
 50 55 60

 Pro Pro Ser Ala Gly Phe Tyr Pro Asn Gly Ser Val Val Asn Asn Ile
 65 70 75 80

 Ala Asp Arg Leu Leu Tyr Gln Asp Pro Glu Thr Leu Glu Leu Lys Pro
 85 90 95

 Trp Ile Ala Thr Glu Leu Pro Glu Val Asn Glu Asp Ala Thr Glu Phe
 100 105 110

 Thr Phe Asn Ile Arg Thr Asp Val Thr Tyr Ser Asp Gly Thr Pro Leu
 115 120 125

 Thr Ala Glu Asn Val Val Lys Asn Phe Asp Leu Tyr Gly Leu Gly Asp
 130 135 140

Gln Asp Arg Arg Leu Thr Ile Ser Glu Gln Ile Thr Asn Tyr Asp His
 145 150 155 160
 Gly Glu Val Val Asp Glu Asp Thr Val Arg Phe His Phe Ser Glu Pro
 165 170 175
 Ala Pro Gly Phe Ala Gln Ala Thr Ser Ser Phe Asn Ala Gly Leu Tyr
 180 185 190
 Ala Asp Ser Thr Leu Glu Phe Ala Asn Glu Asp Phe Ala Pro Gly Asn
 195 200 205
 Ala Gln Asn Val Ile Gly Ser Gly Pro Phe Val Ile Thr Asp Glu Thr
 210 215 220
 Leu Gly Thr Asn Leu Thr Leu Thr Ala Arg Glu Asp Tyr Asp Trp Ala
 225 230 235 240
 Pro Pro Ser Arg Glu His Gln Gly Arg Ala Lys Leu Asp Ala Val Asn
 245 250 255
 Tyr Val Leu Ala Gly Glu Glu Ser Val Arg Ile Gly Ala Ile Val Ala
 260 265 270
 Gly Gln Gly Asp Ile Ala Arg Gln Ile Glu Ala Pro Val Glu Ala His
 275 280 285
 Leu Lys Asp Ala Gly Ile Pro Ile Ile Ser Ala Ala Thr Asn Gly Val
 290 295 300
 Asn Asn Ser Phe Asn Phe Arg Phe Lys Asn Glu Leu Leu Ser Asp Ile
 305 310 315 320
 Arg Val Arg Gln Ala Leu Ile His Ala Ile Asp Arg Glu Lys Ile Met
 325 330 335
 Arg Val Leu Phe Ser Asp Ser Tyr Pro Leu Ala Thr Ser Val Leu Ala
 340 345 350
 Gln Asn Ala Leu Gly Tyr Lys Glu Gln Val Asp Ala Tyr Val Tyr Asp
 355 360 365
 Leu Asp Lys Ala Thr Ala Leu Leu Asp Glu Ala Gly Trp Thr Leu Asp
 370 375 380
 Ser Asp Gly Met Arg Arg Lys Asp Gly Glu Leu Leu Glu Leu Thr Phe
 385 390 395 400
 Asn Glu Ala Leu Pro Gln Pro Arg Ser Arg Glu Val Val Thr Met Val
 405 410 415
 Gln Glu Gln Leu Gly Asp Leu Gly Ile Lys Val Asn Leu Asn Pro Gly
 420 425 430
 Asp Gln Ala Ala Gln Asp Ala Asp Ser Lys Asp Leu Asn Lys Ile Gln
 435 440 445
 Val Arg His Thr Met Val Gly Arg Ala Asp Tyr Asp Val Leu Lys Ser
 450 455 460

Gln Leu Tyr Ser Thr Asn Arg Asn Glu Leu Leu Asn Met Thr Val Glu
 465 470 475 480

Gly Glu Thr Ala Asp Ile Gly Asp Pro His Leu Glu Glu Leu Leu Met
 485 490 495

Ala Ile Ala Ser Ser Pro Arg Glu Glu Asp Arg Ala Ala Ala Ser Ala
 500 505 510

Ala Ala Gln Asp Tyr Ile Thr Glu Gln Ala Tyr Val Leu Pro Leu Phe
 515 520 525

Glu Glu Pro Val Val Tyr Gly Val Gln Pro Tyr Val Lys Gly Phe Ser
 530 535 540

Pro Glu Val Ile Gly Arg Pro Ser Phe Tyr Glu Thr Tyr Ile Asp His
 545 550 555 560

Ser Ser Asp His Ser Ser Glu Glu Asp
 565

<210> 21
 <211> 858
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(835)
 <223> RXN00784

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atctattcca actacgcgta aaacgaggac gtttaaagct atg tct att gaa ttc 115
 Met Ser Ile Glu Phe
 1 5

tcc gca cca gca aaa atg aaa atc gaa gtg tgg agc gac atc atg tgc 163
 Ser Ala Pro Ala Lys Met Lys Ile Glu Val Trp Ser Asp Ile Met Cys
 10 15 20

ccc ttc tgc tac atc ggc aaa aag cgc ctc gac gac gcc cta agt acc 211
 Pro Phe Cys Tyr Ile Gly Lys Lys Arg Leu Asp Asp Ala Leu Ser Thr
 25 30 35

ttt gac cag gcc gga cgc atc gaa gtg gaa tac aag agc ttc gaa ctc 259
 Phe Asp Gln Ala Gly Arg Ile Glu Val Glu Tyr Lys Ser Phe Glu Leu
 40 45 50

atg cca ggc cta gaa acc cac cca ctg cgt tcc gac gtt gaa tac ctc 307
 Met Pro Gly Leu Glu Thr His Pro Leu Arg Ser Asp Val Glu Tyr Leu
 55 60 65

gcc gac gcc aag ggc atg agc ctc gag cag gcc cgc caa atg aac ggc 355
 Ala Asp Ala Lys Gly Met Ser Leu Glu Gln Ala Arg Gln Met Asn Gly
 70 75 80 85

caa gtc caa gca atg gca caa gcc acc gga ctt gaa atg aat cct gac 403
 Gln Val Gln Ala Met Ala Gln Ala Thr Gly Leu Glu Met Asn Pro Asp

90										95					100					
gaa acc atc gcg gcc aac acc atc aac gcg cac cgc ctt acc cac ttc	451																			
Glu Thr Ile Ala Ala Asn Thr Ile Asn Ala His Arg Leu Thr His Phe																				
105 110 115																				
gcg aaa gcc cac ggc aag caa caa gaa gtg gcg cag gaa ctc ttc aag	499																			
Ala Lys Ala His Gly Lys Gln Gln Glu Val Ala Gln Glu Leu Phe Lys																				
120 125 130																				
gct cac ttc gta gac ggc aag aac gtt gat gac ctc gat gtg ctg gtc	547																			
Ala His Phe Val Asp Gly Lys Asn Val Asp Asp Leu Asp Val Leu Val																				
135 140 145																				
tcc att gct gca gag gtt ggt ctc gat gcc agt gca gcc cgc gaa gct	595																			
Ser Ile Ala Ala Glu Val Gly Leu Asp Ala Ser Ala Ala Arg Glu Ala																				
150 155 160 165																				
ctc gaa tcc gac gtg tac acc aac gaa gtc caa caa gac gtc cac gaa	643																			
Leu Glu Ser Asp Val Tyr Thr Asn Glu Val Gln Gln Asp Val His Glu																				
170 175 180																				
gcc cgc caa ctc ggc gtc caa ggt gtg ccc ttc ttt gta ttc gac cgc	691																			
Ala Arg Gln Leu Gly Val Gln Gly Val Pro Phe Phe Val Phe Asp Arg																				
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Lys Tyr Ala Ile Asn Gly Ala Gln Gln Glu Glu Val Phe Thr Gly Thr																				
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Val Glu Lys Ala Phe Glu Glu Trp Ala Ala Glu Asn Pro Val Ser Pro																				
215 220 225																				
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Lys Ser Phe Glu Leu Met Pro Gly Leu Glu Thr His Pro Leu Arg Ser	
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Asp Val Glu Tyr Leu Ala Asp Ala Lys Gly Met Ser Leu Glu Gln Ala	
65 70 75 80	

39

Tyr	Ala	Glu	Pro	Asp	Ala	Asp	Ala	Pro	Phe	Val	Ser	Tyr	Ala	Asp	Glu	
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gct	ttt	gcc	ctc	ggt	ggc	caa	aca	tcc	gct	gag	tcc	tac	ctt	gtc	att	307
Ala	Phe	Ala	Leu	Gly	Gly	Gln	Thr	Ser	Ala	Glu	Ser	Tyr	Leu	Val	Ile	
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Asp	Lys	Ile	Ile	Asp	Ala	Ala	Arg	Lys	Ser	Gly	Ala	Asp	Ala	Ile	His	
	70				75					80					85	
ccc	ggc	tac	ggc	ttc	ctc	gca	gaa	aac	gct	gac	ttc	gca	gaa	gca	gtc	403
Pro	Gly	Tyr	Gly	Phe	Leu	Ala	Glu	Asn	Ala	Asp	Phe	Ala	Glu	Ala	Val	
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Ile	Asn	Glu	Gly	Leu	Ile	Trp	Ile	Gly	Pro	Ser	Pro	Glu	Ser	Ile	Arg	
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Ser	Leu	Gly	Asp	Lys	Val	Thr	Ala	Arg	His	Ile	Ala	Asp	Thr	Ala	Lys	
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gct	cca	atg	gct	cct	ggc	acc	aag	gaa	cca	gta	aaa	gac	gca	gca	gaa	547
Ala	Pro	Met	Ala	Pro	Gly	Thr	Lys	Glu	Pro	Val	Lys	Asp	Ala	Ala	Glu	
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Val	Val	Ala	Phe	Ala	Glu	Glu	Phe	Gly	Leu	Pro	Ile	Ala	Ile	Lys	Ala	
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Ala	Phe	Gly	Gly	Gly	Gly	Arg	Gly	Met	Lys	Val	Ala	Tyr	Lys	Met	Glu	
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Glu	Val	Ala	Asp	Leu	Phe	Glu	Ser	Ala	Thr	Arg	Glu	Ala	Thr	Ala	Ala	
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Phe	Gly	Arg	Gly	Glu	Cys	Phe	Val	Glu	Arg	Tyr	Leu	Asp	Lys	Ala	Arg	
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cac	gtt	gag	gct	cag	gtc	atc	gcc	gat	aag	cac	ggc	aac	gtt	gtt	gtc	787
His	Val	Glu	Ala	Gln	Val	Ile	Ala	Asp	Lys	His	Gly	Asn	Val	Val	Val	
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gcc	gga	acc	cgt	gac	tgc	tcc	ctg	cag	cgc	cgt	ttc	cag	aag	ctc	gtc	835
Ala	Gly	Thr	Arg	Asp	Cys	Ser	Leu	Gln	Arg	Arg	Phe	Gln	Lys	Leu	Val	
	230				235					240				245		
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Glu	Glu	Ala	Pro	Ala	Pro	Phe	Leu	Thr	Asp	Asp	Gln	Arg	Glu	Arg	Leu	
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cac	tcc	tcc	gcg	aag	gct	atc	tgt	aag	gaa	gct	ggc	tac	tac	ggt	gca	931
His	Ser	Ser	Ala	Lys	Ala	Ile	Cys	Lys	Glu	Ala	Gly	Tyr	Tyr	Gly	Ala	
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Gly	Thr	Val	Glu	Tyr	Leu	Val	Gly	Ser	Asp	Gly	Leu	Ile	Ser	Phe	Leu	

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Glu Val Asn Thr Arg Leu Gln Val Glu His Pro Val Thr Glu Glu Thr																				
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acc ggc atc gac ctg gtc cgc gaa atg ttc cgc atc gca gaa ggc cac	1075																			
Thr Gly Ile Asp Leu Val Arg Glu Met Phe Arg Ile Ala Glu Gly His																				
310 315 320 325																				
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Glu Leu Ser Ile Lys Glu Asp Pro Ala Pro Arg Gly His Ala Phe Glu																				
330 335 340																				
ttc cgc atc aac ggc gaa gac gct ggc tcc aac ttc atg cct gca cca	1171																			
Phe Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn Phe Met Pro Ala Pro																				
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Gly Lys Ile Thr Ser Tyr Arg Glu Pro Gln Gly Pro Gly Val Arg Met																				
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Asp Ser Gly Val Val Glu Gly Ser Glu Ile Ser Gly Gln Phe Asp Ser																				
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Met Leu Ala Lys Leu Ile Val Trp Gly Asp Thr Arg Glu Gln Ala Leu																				
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Gln Arg Ser Arg Arg Ala Leu Ala Glu Tyr Val Val Glu Gly Met Pro																				
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Thr Val Ile Pro Phe His Gln His Ile Val Glu Asn Pro Ala Phe Val																				
425 430 435																				
ggc aac gac gaa ggc ttc gag atc tac acc aag tgg atc gaa gag gtt	1459																			
Gly Asn Asp Glu Gly Phe Glu Ile Tyr Thr Lys Trp Ile Glu Glu Val																				
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Trp Asp Asn Pro Ile Ala Pro Tyr Val Asp Ala Ser Glu Leu Asp Glu																				
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gat gag gac aag acc cca gca cag aag gtt gtt gtg gag atc aac ggc	1555																			
Asp Glu Asp Lys Thr Pro Ala Gln Lys Val Val Val Glu Ile Asn Gly																				
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Arg Arg Val Glu Val Ala Leu Pro Gly Asp Leu Ala Leu Gly Gly Thr																				
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Ala Gly Val Ser Gly Asp Ala Val Ala Ala Pro Met Gln Gly Thr Val																				
520 525 530																				

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 Ile Lys Val Asn Val Glu Glu Gly Ala Glu Val Asn Glu Gly Asp Thr
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 gtt gtt gtc ctc gag gct atg aag atg gaa aac cct gtg aag gct cat 1795
 Val Val Val Leu Glu Ala Met Lys Met Glu Asn Pro Val Lys Ala His
 550 555 560 565
 aag tcc gga acc gta acc ggc ctt act gtc gct gca ggc gag ggt gtc 1843
 Lys Ser Gly Thr Val Thr Gly Leu Thr Val Ala Ala Gly Glu Gly Val
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 agt 1896

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 35 40 45
 Ser Tyr Ala Asp Glu Ala Phe Ala Leu Gly Gly Gln Thr Ser Ala Glu
 50 55 60
 Ser Tyr Leu Val Ile Asp Lys Ile Ile Asp Ala Ala Arg Lys Ser Gly
 65 70 75 80
 Ala Asp Ala Ile His Pro Gly Tyr Gly Phe Leu Ala Glu Asn Ala Asp
 85 90 95
 Phe Ala Glu Ala Val Ile Asn Glu Gly Leu Ile Trp Ile Gly Pro Ser
 100 105 110
 Pro Glu Ser Ile Arg Ser Leu Gly Asp Lys Val Thr Ala Arg His Ile
 115 120 125
 Ala Asp Thr Ala Lys Ala Pro Met Ala Pro Gly Thr Lys Glu Pro Val
 130 135 140
 Lys Asp Ala Ala Glu Val Val Ala Phe Ala Glu Glu Phe Gly Leu Pro
 145 150 155 160
 Ile Ala Ile Lys Ala Ala Phe Gly Gly Gly Gly Arg Gly Met Lys Val
 165 170 175
 Ala Tyr Lys Met Glu Glu Val Ala Asp Leu Phe Glu Ser Ala Thr Arg
 180 185 190

Glu Ala Thr Ala Ala Phe Gly Arg Gly Glu Cys Phe Val Glu Arg Tyr
 195 200 205
 Leu Asp Lys Ala Arg His Val Glu Ala Gln Val Ile Ala Asp Lys His
 210 215 220
 Gly Asn Val Val Val Ala Gly Thr Arg Asp Cys Ser Leu Gln Arg Arg
 225 230 235 240
 Phe Gln Lys Leu Val Glu Glu Ala Pro Ala Pro Phe Leu Thr Asp Asp
 245 250 255
 Gln Arg Glu Arg Leu His Ser Ser Ala Lys Ala Ile Cys Lys Glu Ala
 260 265 270
 Gly Tyr Tyr Gly Ala Gly Thr Val Glu Tyr Leu Val Gly Ser Asp Gly
 275 280 285
 Leu Ile Ser Phe Leu Glu Val Asn Thr Arg Leu Gln Val Glu His Pro
 290 295 300
 Val Thr Glu Glu Thr Thr Gly Ile Asp Leu Val Arg Glu Met Phe Arg
 305 310 315 320
 Ile Ala Glu Gly His Glu Leu Ser Ile Lys Glu Asp Pro Ala Pro Arg
 325 330 335
 Gly His Ala Phe Glu Phe Arg Ile Asn Gly Glu Asp Ala Gly Ser Asn
 340 345 350
 Phe Met Pro Ala Pro Gly Lys Ile Thr Ser Tyr Arg Glu Pro Gln Gly
 355 360 365
 Pro Gly Val Arg Met Asp Ser Gly Val Val Glu Gly Ser Glu Ile Ser
 370 375 380
 Gly Gln Phe Asp Ser Met Leu Ala Lys Leu Ile Val Trp Gly Asp Thr
 385 390 395 400
 Arg Glu Gln Ala Leu Gln Arg Ser Arg Arg Ala Leu Ala Glu Tyr Val
 405 410 415
 Val Glu Gly Met Pro Thr Val Ile Pro Phe His Gln His Ile Val Glu
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 Asn Pro Ala Phe Val Gly Asn Asp Glu Gly Phe Glu Ile Tyr Thr Lys
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 Trp Ile Glu Glu Val Trp Asp Asn Pro Ile Ala Pro Tyr Val Asp Ala
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 Ser Glu Leu Asp Glu Asp Glu Asp Lys Thr Pro Ala Gln Lys Val Val
 465 470 475 480
 Val Glu Ile Asn Gly Arg Arg Val Glu Val Ala Leu Pro Gly Asp Leu
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 Ala Leu Gly Gly Thr Ala Gly Pro Lys Lys Lys Ala Lys Lys Arg Arg
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Ala Gly Gly Ala Lys Ala Gly Val Ser Gly Asp Ala Val Ala Ala Pro
 515 520 525

Met Gln Gly Thr Val Ile Lys Val Asn Val Glu Glu Gly Ala Glu Val
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Asn Glu Gly Asp Thr Val Val Val Leu Glu Ala Met Lys Met Glu Asn
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 <223> RXA02173

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gaa cac act tca gca ttg acg ctc ata gac tcg gtt ttg gac cct gac 163
 Glu His Thr Ser Ala Leu Thr Leu Ile Asp Ser Val Leu Asp Pro Asp
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agc ttc att tct tgg aat gaa act ccc caa tat gac aac ctc aat caa 211
 Ser Phe Ile Ser Trp Asn Glu Thr Pro Gln Tyr Asp Asn Leu Asn Gln
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ggc tat gca gag acc ttg gag cgg gct cga agc aag gcc aaa tgc gat 259
 Gly Tyr Ala Glu Thr Leu Glu Arg Ala Arg Ser Lys Ala Lys Cys Asp
 40 45 50

gaa tcg gta att act gga gaa ggc acc gtg gag ggc att ccg gta gcc 307
 Glu Ser Val Ile Thr Gly Glu Gly Thr Val Glu Gly Ile Pro Val Ala
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gtt att ttg tcc gat ttt tcc ttc ctc ggc ggt tct ttg ggc acg gtc 355
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 70 75 80 85

gcg tcg gtg cgc atc atg aag gcg att cac cgc gcc aca gag ctg aaa 403
 Ala Ser Val Arg Ile Met Lys Ala Ile His Arg Ala Thr Glu Leu Lys
 90 95 100

ctc cca ctg ctg gtc tcc cct gct tcc ggt ggt gcg cgc atg cag gaa 451
 Leu Pro Leu Leu Val Ser Pro Ala Ser Gly Gly Ala Arg Met Gln Glu
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gac aat cga gct ttt gtc atg atg gtg tcc ata acc gcg gct gtg cag	499
Asp Asn Arg Ala Phe Val Met Met Val Ser Ile Thr Ala Ala Val Gln	
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Arg His Arg Glu Ala His Leu Pro Phe Leu Val Tyr Leu Arg Asn Pro	
135 140 145	
acg atg ggt ggc gcc atg gcc tcg tgg ggt tca tct ggg cat ctc act	595
Thr Met Gly Gly Ala Met Ala Ser Trp Gly Ser Ser Gly His Leu Thr	
150 155 160 165	
ttt gcg gaa ccc ggc gcg cag ata ggt ttc ctg ggt cct cgc gtg gtg	643
Phe Ala Glu Pro Gly Ala Gln Ile Gly Phe Leu Gly Pro Arg Val Val	
170 175 180	
gag tta acc act ggg cat gcg ctt cca gac ggt gtg cag cag gcg gag	691
Glu Leu Thr Thr Gly His Ala Leu Pro Asp Gly Val Gln Gln Ala Glu	
185 190 195	
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Asn Leu Val Lys Thr Gly Val Ile Asp Gly Ile Val Ser Pro Leu Gln	
200 205 210	
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Leu Arg Ala Ala Val Ala Lys Thr Leu Lys Val Ile Gln Pro Val Glu	
215 220 225	
gca acg gat cgt ttt tct cca aca act cct ggc gtg gca ctt ccg gtg	835
Ala Thr Asp Arg Phe Ser Pro Thr Thr Pro Gly Val Ala Leu Pro Val	
230 235 240 245	
atg gag gcg att gcg cgt tct cgt gac ccg cag agg cct gga atc ggg	883
Met Glu Ala Ile Ala Arg Ser Arg Asp Pro Gln Arg Pro Gly Ile Gly	
250 255 260	
gag att atg gaa acg ttg ggg gca gac gtc gtc aag ctt tct ggt gcg	931
Glu Ile Met Glu Thr Leu Gly Ala Asp Val Val Lys Leu Ser Gly Ala	
265 270 275	
cgt gct ggc gca ttg agc ccg gct gtg cgc gtt gcc ctg gcg cgc atc	979
Arg Ala Gly Ala Leu Ser Pro Ala Val Arg Val Ala Leu Ala Arg Ile	
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ggg ggc cgg ccc gtg gtg ctg att ggg cag gat cgc cgc ttc acg ctt	1027
Gly Gly Arg Pro Val Val Leu Ile Gly Gln Asp Arg Arg Phe Thr Leu	
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Gly Pro Gln Glu Leu Arg Phe Ala Arg Arg Gly Ile Ser Leu Ala Arg	
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Glu Leu Asn Leu Pro Ile Val Ser Ile Ile Asp Thr Ser Gly Ala Glu	
330 335 340	
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Leu Ser Gln Ala Ala Glu Glu Leu Gly Ile Ala Ser Ser Ile Ala Arg	
345 350 355	
acc ttg tcc aag ctt atc gac gct ccc ctc ccc acc gtt tcg gtc att	1219

Thr Leu Ser Lys Leu Ile Asp Ala Pro Leu Pro Thr Val Ser Val Ile
 360 365 370

att ggt cag ggc gtt ggc ggt ggc gcg ctg gcc atg ctg ccc gcc gat 1267
 Ile Gly Gln Gly Val Gly Gly Gly Ala Leu Ala Met Leu Pro Ala Asp
 375 380 385

ctg gtc tac gcg gcc gaa aac gcg tgg ctg tcc gca ttg cca cca gag 1315
 Leu Val Tyr Ala Ala Glu Asn Ala Trp Leu Ser Ala Leu Pro Pro Glu
 390 395 400 405

ggc gcc tcg gcc atc ctc ttc cgc gac acc aac cac gcc gcg gaa atc 1363
 Gly Ala Ser Ala Ile Leu Phe Arg Asp Thr Asn His Ala Ala Glu Ile
 410 415 420

ata gag cga caa ggc gtg cag gcg cac gca ctt tta agc caa ggg ctt 1411
 Ile Glu Arg Gln Gly Val Gln Ala His Ala Leu Leu Ser Gln Gly Leu
 425 430 435

atc gac ggg atc gtc gcc gaa acc gag cac ttt gtt gaa gaa att ctc 1459
 Ile Asp Gly Ile Val Ala Glu Thr Glu His Phe Val Glu Glu Ile Leu
 440 445 450

ggc aca atc agc aac gcc ctc tcc gaa ttg gat aac aat ccg gag agg 1507
 Gly Thr Ile Ser Asn Ala Leu Ser Glu Leu Asp Asn Asn Pro Glu Arg
 455 460 465

gcg gga cgc gac agt cgc ttc aca cga ttt gag cgt tta gcg cag 1552
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Lys Ala Lys Cys Asp Glu Ser Val Ile Thr Gly Glu Gly Thr Val Glu
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Gly Ile Pro Val Ala Val Ile Leu Ser Asp Phe Ser Phe Leu Gly Gly
 65 70 75 80

Ser Leu Gly Thr Val Ala Ser Val Arg Ile Met Lys Ala Ile His Arg
 85 90 95

Ala Thr Glu Leu Lys Leu Pro Leu Leu Val Ser Pro Ala Ser Gly Gly
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Ala Arg Met Gln Glu Asp Asn Arg Ala Phe Val Met Met Val Ser Ile
 115 120 125
 Thr Ala Ala Val Gln Arg His Arg Glu Ala His Leu Pro Phe Leu Val
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 Tyr Leu Arg Asn Pro Thr Met Gly Gly Ala Met Ala Ser Trp Gly Ser
 145 150 155 160
 Ser Gly His Leu Thr Phe Ala Glu Pro Gly Ala Gln Ile Gly Phe Leu
 165 170 175
 Gly Pro Arg Val Val Glu Leu Thr Thr Gly His Ala Leu Pro Asp Gly
 180 185 190
 Val Gln Gln Ala Glu Asn Leu Val Lys Thr Gly Val Ile Asp Gly Ile
 195 200 205
 Val Ser Pro Leu Gln Leu Arg Ala Ala Val Ala Lys Thr Leu Lys Val
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 Ile Gln Pro Val Glu Ala Thr Asp Arg Phe Ser Pro Thr Thr Pro Gly
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 Val Ala Leu Pro Val Met Glu Ala Ile Ala Arg Ser Arg Asp Pro Gln
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 Arg Pro Gly Ile Gly Glu Ile Met Glu Thr Leu Gly Ala Asp Val Val
 260 265 270
 Lys Leu Ser Gly Ala Arg Ala Gly Ala Leu Ser Pro Ala Val Arg Val
 275 280 285
 Ala Leu Ala Arg Ile Gly Gly Arg Pro Val Val Leu Ile Gly Gln Asp
 290 295 300
 Arg Arg Phe Thr Leu Gly Pro Gln Glu Leu Arg Phe Ala Arg Arg Gly
 305 310 315 320
 Ile Ser Leu Ala Arg Glu Leu Asn Leu Pro Ile Val Ser Ile Ile Asp
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 Thr Ser Gly Ala Glu Leu Ser Gln Ala Ala Glu Glu Leu Gly Ile Ala
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 Ser Ser Ile Ala Arg Thr Leu Ser Lys Leu Ile Asp Ala Pro Leu Pro
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 Thr Val Ser Val Ile Ile Gly Gln Gly Val Gly Gly Gly Ala Leu Ala
 370 375 380
 Met Leu Pro Ala Asp Leu Val Tyr Ala Ala Glu Asn Ala Trp Leu Ser
 385 390 395 400
 Ala Leu Pro Pro Glu Gly Ala Ser Ala Ile Leu Phe Arg Asp Thr Asn
 405 410 415
 His Ala Ala Glu Ile Ile Glu Arg Gln Gly Val Gln Ala His Ala Leu
 420 425 430
 Leu Ser Gln Gly Leu Ile Asp Gly Ile Val Ala Glu Thr Glu His Phe

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Asn	Asn	Pro	Glu	Arg	Ala	Gly	Arg	Asp	Ser	Arg	Phe	Thr	Arg	Phe	Glu		
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825						830						835					
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<223> RXA01764
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				Met	Ser	Leu	Asn	Gly									
				1				5									
aaa	gtc	gcc	atc	gtt	acc	gga	tct	ggt	gca	gga	ctt	ggt	cgt	tcc	ttc		163
Lys	Val	Ala	Ile	Val	Thr	Gly	Ser	Gly	Ala	Gly	Leu	Gly	Arg	Ser	Phe		
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gct	cag	gag	ctt	gcc	cgt	cag	ggt	gca	tct	gtc	atc	gtc	aat	gac	gta		211
Ala	Gln	Glu	Leu	Ala	Arg	Gln	Gly	Ala	Ser	Val	Ile	Val	Asn	Asp	Val		
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Asn	Gln	Ala	Ala	Ala	Asp	Glu	Thr	Val	Ala	Ala	Ile	Thr	Glu	Ala	Gly		
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ggc	aaa	gcc	gcc	gcc	gtt	atc	gcc	ccc	gtt	gga	ccc	tct	gaa	agc	gcc		307
Gly	Lys	Ala	Ala	Ala	Val	Ile	Ala	Pro	Val	Gly	Pro	Ser	Glu	Ser	Ala		
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Ala	Leu	Leu	Val	Arg	Glu	Ala	Val	Asp	Lys	Phe	Gly	Ser	Leu	Asp	Ile		
70				75						80					85		
ctt	gtc	aca	aac	gcg	ggc	atc	ctt	cgt	gat	agg	tcc	ctg	ctg	aag	atg		403
Leu	Val	Thr	Asn	Ala	Gly	Ile	Leu	Arg	Asp	Arg	Ser	Leu	Leu	Lys	Met		
				90					95					100			
acg	gac	gat	gat	ttc	gat	gca	gtc	att	aac	gtg	cac	ctc	aag	ggc	act		451
Thr	Asp	Asp	Asp	Phe	Asp	Ala	Val	Ile	Asn	Val	His	Leu	Lys	Gly	Thr		
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Phe	Thr	Cys	Val	Arg	Glu	Ala	Phe	Gly	Tyr	Phe	Lys	Glu	Asn	Gly	Ile		
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 Ala Gly Arg Ile Val Thr Ile Gly Ser Pro Thr Gly Gln Arg Gly Asn
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gtt cgc acg tgg gcg ctg gag atg aag cgc gca ggt gtc acc att aac 643
 Val Arg Thr Trp Ala Leu Glu Met Lys Arg Ala Gly Val Thr Ile Asn
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gcg atc att ccg gaa gca gcc acc gat atg acc aag acg gtg cca tat 691
 Ala Ile Ile Pro Glu Ala Ala Thr Asp Met Thr Lys Thr Val Pro Tyr
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ttc cag aag gct gta gag gcc gat gag cgt ggc gag gcc atg cca gca 739
 Phe Gln Lys Ala Val Glu Ala Asp Glu Arg Gly Glu Ala Met Pro Ala
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 Ala Ile Gly Ala Gly Gly Asp Arg Met Gln Val Trp Lys His Pro Glu
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 Pro Ala Val Thr Glu Phe Asn Pro Gly Gly Trp Thr Tyr Glu Ala Leu
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cag gaa cgt ggc aag aac att att gag ggc aac ctg cag tcc gtc ggt 979
 Gln Glu Arg Gly Lys Asn Ile Ile Glu Gly Asn Leu Gln Ser Val Gly
 280 285 290

gtc gtt ttc cct gaa ctg ccg gca gag ctt cag cca caa atc cca gtc 1027
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 Lys Ala
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<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 28

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 Ile Thr Glu Ala Gly Gly Lys Ala Ala Ala Val Ile Ala Pro Val Gly
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 Pro Ser Glu Ser Ala Ala Leu Leu Val Arg Glu Ala Val Asp Lys Phe
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 Ser Leu Leu Lys Met Thr Asp Asp Asp Phe Asp Ala Val Ile Asn Val
 100 105 110
 His Leu Lys Gly Thr Phe Thr Cys Val Arg Glu Ala Phe Gly Tyr Phe
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 Lys Glu Asn Gly Ile Ala Gly Arg Ile Val Thr Ile Gly Ser Pro Thr
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 Gly Gln Arg Gly Asn Phe Gly Gln Ser Asn Tyr Ala Ala Ala Lys Ala
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 Gly Ile Val Gly Met Val Arg Thr Trp Ala Leu Glu Met Lys Arg Ala
 165 170 175
 Gly Val Thr Ile Asn Ala Ile Ile Pro Glu Ala Ala Thr Asp Met Thr
 180 185 190
 Lys Thr Val Pro Tyr Phe Gln Lys Ala Val Glu Ala Asp Glu Arg Gly
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 Glu Ala Met Pro Ala Phe Phe Arg Glu Thr Leu Gly Phe Gly Thr Pro
 210 215 220
 Gln Asp Val Ala Gly Leu Val Ala Phe Leu Ser Ser Asp Glu Ala Ala
 225 230 235 240
 Asn Ile Ser Gly Gln Ala Ile Gly Ala Gly Gly Asp Arg Met Gln Val
 245 250 255
 Trp Lys His Pro Glu Pro Ala Val Thr Glu Phe Asn Pro Gly Gly Trp
 260 265 270
 Thr Tyr Glu Ala Leu Gln Glu Arg Gly Lys Asn Ile Ile Glu Gly Asn
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 Pro Gln Ile Pro Val Lys Ala
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<222> (101)..(1804)

<223> RXN02487

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                                   Met Ser Ala Tyr Glu
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Thr Lys Glu Trp Leu Gln His Tyr Pro Glu Trp Thr Pro His Ser Leu
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Glu Tyr Gly Asp Thr Thr Leu Leu Asp Val Tyr Asp Asn Asn Leu Ala
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Tyr Gly Glu Leu Asp Lys Glu Val Arg Lys Thr Ala Ala Gly Leu Arg
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Ala Leu Gly Val Arg Pro Gly Asp His Val Ala Ile Ile Leu Pro Asn
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Cys Pro Gln His Ile Ala Ala Phe Tyr Ala Val Leu Lys Leu Gly Ala
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Pro Phe Lys Asp His Gly Ala Arg Val Ala Ile Val Trp Asp Lys Ala
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gca gcc cta cca atg ttc cac Ala Ala Leu Pro Met Phe His 265	gca tac ggt ctg acc atg gtc Ala Tyr Gly Leu Thr Met Val 270	ggc aca Gly Thr 275	931
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acc atg ccc gac ggc agc gaa Thr Met Pro Asp Gly Ser Glu 410	ggc gaa gtc cta gtc aag ggc Gly Glu Val Leu Val Lys Gly 415	cca cag Pro Gln 420	1363
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cac ggc gag tgg tac cgc acc His Gly Glu Trp Tyr Arg Thr 440	ggc gac gtc gga gtg atg gaa Gly Asp Val Gly Val Met Glu 445	gaa gaa gac Glu Glu Asp 450	1459

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 Gly Phe Asn Val Tyr Pro Ala Glu Val Glu Glu Val Leu Ala Glu His
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 cca gac att gaa gat tcc gca gtc gtt ggt atc ccg cgt gaa gac ggc 1603
 Pro Asp Ile Glu Asp Ser Ala Val Val Gly Ile Pro Arg Glu Asp Gly
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 Asp Pro Asp Gly Leu Lys Glu Phe Ala Arg Lys Asn Leu Thr Arg Tyr
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 aag gtt ccg cgc act ttc tac cac ttt gag gag atg ccg cgg gat cag 1747
 Lys Val Pro Arg Thr Phe Tyr His Phe Glu Glu Met Pro Arg Asp Gln
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 Gly Arg Ser Gln Thr Tyr Gly Glu Leu Asp Lys Glu Val Arg Lys Thr
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 Leu Lys Leu Gly Ala Val Val Ile Glu His Asn Pro Leu Tyr Thr Ala
 100 105 110

His Glu Leu Leu Glu Pro Phe Lys Asp His Gly Ala Arg Val Ala Ile
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 Val Trp Asp Lys Ala Ser Pro Thr Val Glu Gln Leu Arg Gly Gln Thr
 130 135 140
 Gln Leu Glu Thr Ile Val Ser Val Asn Met Ile Asn Ala Met Pro Pro
 145 150 155 160
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 Arg Glu Ser Leu Ser Gly Ala Ala Pro Asn Thr Val Pro Phe Glu Thr
 180 185 190
 Leu Thr Ser Ala Ala Met Gly Gly Asp Gly Asp Asp Val Val Ser Glu
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 Pro Thr Val Thr Lys Glu Ser Val Ala Leu Ile Leu Tyr Thr Ser Gly
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 Thr Thr Gly Arg Pro Lys Gly Ala Gln Leu Thr His Gly Asn Leu Phe
 225 230 235 240
 Phe Asn Leu Leu Gln Gly Lys His Trp Val Pro Gly Leu Gly Asp Lys
 245 250 255
 Pro Glu Arg Met Leu Ala Ala Leu Pro Met Phe His Ala Tyr Gly Leu
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 Thr Met Val Gly Thr Leu Ser Val Phe Ile Gly Gly Glu Met Val Leu
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 Thr Pro Thr Trp Leu Pro Gly Val Pro Thr Leu Tyr Glu Lys Ile Val
 305 310 315 320
 Asp Ala Ser Glu Lys Glu Gly Ile Pro Ile Lys Gly Val Arg Asn Ala
 325 330 335
 Phe Ser Gly Ala Ser Thr Leu Ser Gln Arg Thr Val Glu Arg Trp Glu
 340 345 350
 Lys His Thr Gly Gly Arg Leu Val Glu Gly Tyr Gly Leu Thr Glu Thr
 355 360 365
 Ser Pro Ile Ile Val Gly Asn Pro Met Ser Asp His Arg Arg Gln Gly
 370 375 380
 Tyr Val Gly Ile Pro Phe Pro Asp Thr Ile Val Arg Ile Ala Asn Pro
 385 390 395 400
 Glu Asn Leu Asp Glu Thr Met Pro Asp Gly Ser Glu Gly Glu Val Leu
 405 410 415
 Val Lys Gly Pro Gln Val Phe Lys Gly Tyr Leu Asn Gln Glu Glu Ala
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 Thr Lys Asn Ser Phe His Gly Glu Trp Tyr Arg Thr Gly Asp Val Gly

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Val Ile Ile Thr Gly Gly Phe Asn Val Tyr Pro Ala Glu Val Glu Glu		
465	470	475
Val Leu Ala Glu His Pro Asp Ile Glu Asp Ser Ala Val Val Gly Ile		
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Pro Arg Glu Asp Gly Ser Glu Asn Val Val Ala Ala Ile Thr Leu Val		
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Glu Gly Ala Ala Leu Asp Pro Asp Gly Leu Lys Glu Phe Ala Arg Lys		
515	520	525
Asn Leu Thr Arg Tyr Lys Val Pro Arg Thr Phe Tyr His Phe Glu Glu		
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 Val Tyr Pro Ala Glu
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 gtt gaa gaa gtc ctc gca gag cac cca gac att gaa gat tcc gca gtc 163
 Val Glu Glu Val Leu Ala Glu His Pro Asp Ile Glu Asp Ser Ala Val
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 Val Gly Ile Pro Arg Glu Asp Gly Ser Glu Asn Val Val Ala Ala Ile
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 Thr Leu Val Glu Gly Ala Ala Leu Asp Pro Asp Gly Leu Lys Glu Phe
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 gcc cgc aag aac ctc acc cgc tac aag gtt ccg cgc act ttc tac cac 307
 Ala Arg Lys Asn Leu Thr Arg Tyr Lys Val Pro Arg Thr Phe Tyr His
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Phe Glu Glu Met Pro Arg Asp Gln Met Gly Lys Ile Arg Arg Arg Glu
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cga 411

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 Gly Leu Lys Glu Phe Ala Arg Lys Asn Leu Thr Arg Tyr Lys Val Pro
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 Thr Lys Glu Trp Leu Gln His Tyr Pro Glu Trp Thr Pro His Ser Leu
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Cys Pro Gln His Ile Ala Ala Phe Tyr Ala Val Leu Lys Leu Gly Ala																														
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<400> 34

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Gly Arg Ser Gln Thr Tyr Gly Glu Leu Asp Lys Glu Val Arg Lys Thr
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Ala Ala Gly Leu Arg Ala Leu Gly Val Arg Pro Gly Asp His Val Ala
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Ile Ile Leu Pro Asn Cys Pro Gln His Ile Ala Ala Phe Tyr Ala Val
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Leu Lys Leu Gly Ala Val Val Ile Glu His Asn Pro Leu Tyr Thr Ala
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His Glu Leu Leu Glu Pro Phe Lys Asp His Gly Ala Arg Val Ala Ile
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Val Trp Asp Lys Ala Ser Pro Thr Val Glu Gln Leu Arg Gly Gln Thr
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Gln Leu Glu Thr Ile Val Ser Val Asn Met Ile Asn Ala Met Pro Pro
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Leu Gln Arg Leu Ala Leu Arg Leu Pro Ile Pro Ala Leu Arg Lys Ser
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Arg Glu Ser Leu Ser Gly Ala Ala Pro Asn Thr Val Pro Phe Glu Thr
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Leu Thr Ser Ala Ala Met Gly Gly Asp Gly Asp Asp Val Val Ser Glu
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Pro Thr Val Thr Lys Glu Ser Val Ala Leu Ile Leu Tyr Thr Ser Gly
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Thr Thr Gly Arg Pro Lys Gly Ala Gln Leu Thr His Gly Asn Leu Phe
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Ser Asn Leu Leu Gln Gly Lys His Trp Val Pro Gly Leu Gly Asp Lys
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Ala Glu Gly Pro Asn Val Phe Ala Ser Val Ala Lys Ile Leu Gln Asp
      20          25          30

Val Gly Gly Ile Ser Ala Glu Asp Val Thr Pro Glu Ser Arg Phe Thr
      35          40          45

Glu Asp Leu Ala Val Ser Ser Leu Asn Tyr Ile Glu Leu Ile Val Asn
  50          55          60

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 Leu Thr Thr Val Gln Asp Leu Ile Asp Phe Ile Asn Thr Asn Lys Ala
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 <223> RXA00796

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 Met Ser Lys Ile Ala
 1 5
 atc atc acc ggt tcc acc cgt cca ggc cgc gtc aac att gac gta gcc 163
 Ile Ile Thr Gly Ser Thr Arg Pro Gly Arg Val Asn Ile Asp Val Ala
 10 15 20
 aac tgg gtt ctc gag cgc gca caa gag cgc aac gat gca cag tac gag 211
 Asn Trp Val Leu Glu Arg Ala Gln Glu Arg Asn Asp Ala Gln Tyr Glu
 25 30 35
 ctc gtt gat atc gcc gat ttc aac ttc ccc gtc ctc gac gaa gca atg 259
 Leu Val Asp Ile Ala Asp Phe Asn Phe Pro Val Leu Asp Glu Ala Met
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 35 40 45
 Leu Asp Glu Ala Met Pro Ala Gly Tyr Gly Gln Tyr Ala Asn Glu His
 50 55 60

Thr Lys
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<223> RXA01897

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Met Lys Ile Gly Val
1 5
atc ctg ggc agt atc cgc gaa ggc cgc ttc ggc caa ggc gtt gcc gat 163
Ile Leu Gly Ser Ile Arg Glu Gly Arg Phe Gly Gln Gly Val Ala Asp
10 15 20
tgg gtc atg gaa caa atc ggg gct tat gac gca ccc gat gtg gaa ttt 211
Trp Val Met Glu Gln Ile Gly Ala Tyr Asp Ala Pro Asp Val Glu Phe
25 30 35
gaa ctc atc gac ctc aaa gct ttc aac gtg ccc ctg ttg gaa tcc gcg 259
Glu Leu Ile Asp Leu Lys Ala Phe Asn Val Pro Leu Leu Glu Ser Ala
40 45 50
aca gtt cca ggt tcc gcg gat aaa cag tac gac gac ccg cgc gta act 307
Thr Val Pro Gly Ser Ala Asp Lys Gln Tyr Asp Asp Pro Arg Val Thr
55 60 65
gcc tgg tca cag gcc att gat gcc tgc gat gcc ttc ctt ttc atc acc 355
Ala Trp Ser Gln Ala Ile Asp Ala Cys Asp Ala Phe Leu Phe Ile Thr
70 75 80 85
ccg gaa tac aac cac ggt gtg ccc ggc gcg ttc aaa aat gcg tat gac 403
Pro Glu Tyr Asn His Gly Val Pro Gly Ala Phe Lys Asn Ala Tyr Asp
90 95 100
atc ctg ggc aat gaa tgg ctg aac aaa acc gtc ggt ttc att tcc tac 451
Ile Leu Gly Asn Glu Trp Leu Asn Lys Thr Val Gly Phe Ile Ser Tyr
105 110 115
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Gly Ala Val Glu Gly Ile Arg Val Val Glu Gln Trp Arg Gln Ile Val
120 125 130
gcc acc ttc aac atg tac gat atc cgc agc cag cta tcc ttt tcc acc 547
Ala Thr Phe Asn Met Tyr Asp Ile Arg Ser Gln Leu Ser Phe Ser Thr
135 140 145
ttc acc gag aac aac aac ggc act ttt gcg ccc aat gat cga cgc ccc 595
Phe Thr Glu Asn Asn Asn Gly Thr Phe Ala Pro Asn Asp Arg Arg Pro
150 155 160 165

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 35 40 45
 Leu Leu Glu Ser Ala Thr Val Pro Gly Ser Ala Asp Lys Gln Tyr Asp
 50 55 60
 Asp Pro Arg Val Thr Ala Trp Ser Gln Ala Ile Asp Ala Cys Asp Ala
 65 70 75 80
 Phe Leu Phe Ile Thr Pro Glu Tyr Asn His Gly Val Pro Gly Ala Phe
 85 90 95
 Lys Asn Ala Tyr Asp Ile Leu Gly Asn Glu Trp Leu Asn Lys Thr Val
 100 105 110
 Gly Phe Ile Ser Tyr Gly Ala Val Glu Gly Ile Arg Val Val Glu Gln
 115 120 125
 Trp Arg Gln Ile Val Ala Thr Phe Asn Met Tyr Asp Ile Arg Ser Gln
 130 135 140
 Leu Ser Phe Ser Thr Phe Thr Glu Asn Asn Asn Gly Thr Phe Ala Pro
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 Ala Glu Trp Asn Asn Lys Ala Ala Gly Ile Val Ser Tyr Gly Ser Ala
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 Met Gly Val Arg Ala Ala Glu His Leu Arg Gly Ile Leu Ser Glu Leu
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cag atc gca cac gtt caa aag acc ggc ctg ctg agc atc ttc acc gac 192
 Gln Ile Ala His Val Gln Lys Thr Gly Leu Leu Ser Ile Phe Thr Asp
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ttc gaa tac cct aac ttc aag cct tcc gag cag ggc atc tcc tct gtg 240
 Phe Glu Tyr Pro Asn Phe Lys Pro Ser Glu Gln Gly Ile Ser Ser Val
 65 70 75 80

gac gct atg ctt gag cag ctt gtt gtc tgg acc aag gca atg tcc acc 288
 Asp Ala Met Leu Glu Gln Leu Val Val Trp Thr Lys Ala Met Ser Thr
 85 90 95

att cgc gag tct gcg aac gtc tat cac tta aga acc cct cac aaa agt 336
 Ile Arg Glu Ser Ala Asn Val Tyr His Leu Arg Thr Pro His Lys Ser
 100 105 110

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 Gly Glu Leu Pro Asp Trp Asp Ser Pro Leu Phe Val Phe
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<210> 42

<211> 125

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 42

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 35 40 45

Gln Ile Ala His Val Gln Lys Thr Gly Leu Leu Ser Ile Phe Thr Asp
 50 55 60

Phe Glu Tyr Pro Asn Phe Lys Pro Ser Glu Gln Gly Ile Ser Ser Val
 65 70 75 80

Asp Ala Met Leu Glu Gln Leu Val Val Trp Thr Lys Ala Met Ser Thr
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Ile Arg Glu Ser Ala Asn Val Tyr His Leu Arg Thr Pro His Lys Ser
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Gly Glu Leu Pro Asp Trp Asp Ser Pro Leu Phe Val Phe
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 <223> FRXA02809

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 Lys Ala Ala Gly Ile Val Ser Tyr Gly Ser Ala Met Gly Val Arg Ala
 20 25 30
 gct gag cac ctc cgc ggc atc ctt tcc gag ctt cag atc gca cac gtt 144
 Ala Glu His Leu Arg Gly Ile Leu Ser Glu Leu Gln Ile Ala His Val
 35 40 45
 caa aag acc ggc ctg ctg agc atc ttc acc gac ttc gaa tac cct aac 192
 Gln Lys Thr Gly Leu Leu Ser Ile Phe Thr Asp Phe Glu Tyr Pro Asn
 50 55 60
 ttc aag cct tcc gag cag ggc atc tcc tct gtg gac gct atg ctt gag 240
 Phe Lys Pro Ser Glu Gln Gly Ile Ser Ser Val Asp Ala Met Leu Glu
 65 70 75 80
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 44
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 35 40 45
 Gln Lys Thr Gly Leu Leu Ser Ile Phe Thr Asp Phe Glu Tyr Pro Asn
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Val Arg Ile Val Leu
1 5
acc acc gaa ggc gaa gta gca gcc aag ctg gtt acc cgc ttc gca att 163
Thr Thr Glu Gly Glu Val Ala Ala Lys Leu Val Thr Arg Phe Ala Ile
10 15 20
cgt gga cgc atc acc acc aac gaa atg gct gca cca gca gat tcc tac 211
Arg Gly Arg Ile Thr Thr Asn Glu Met Ala Ala Pro Ala Asp Ser Tyr
25 30 35
ggc gca cgc gac gaa gtt gtc gag gca acc cct cgt tcc ttc atc cgc 259
Gly Ala Arg Asp Glu Val Val Glu Ala Thr Pro Arg Ser Phe Ile Arg
40 45 50
cag gca act gtt tct gca cct gca gac atg acc cca ttc gcc atg gtt 307
Gln Ala Thr Val Ser Ala Pro Ala Asp Met Thr Pro Phe Ala Met Val
55 60 65
tct ggt gac tac aac cca att cac acc tct gac aac gct gca aag ctt 355
Ser Gly Asp Tyr Asn Pro Ile His Thr Ser Asp Asn Ala Ala Lys Leu
70 75 80 85
gtt ggc ctg gac gca gct ctt gtc cac ggc atg tgg ctg tcc gct acc 403
Val Gly Leu Asp Ala Ala Leu Val His Gly Met Trp Leu Ser Ala Thr
90 95 100
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Ala Gln His Leu Ala Gly Leu Gly Ser Glu Val Ile Gly Trp Thr Tyr
105 110 115
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Ser Met Tyr Gly Met Val Gln Leu Asn Asp Val Val Asp Ile Thr Val
120 125 130
gag cgt gtt ggc cgc gca ggt ctg aag cct gca tac gag gtc acc tgc 547
Glu Arg Val Gly Arg Ala Gly Leu Lys Pro Ala Tyr Glu Val Thr Cys
135 140 145
cgc att gat ggc aac gtt gtc tcc cgc gga cag gca ctg ctc aag gct 595
Arg Ile Asp Gly Asn Val Val Ser Arg Gly Gln Ala Leu Leu Lys Ala
150 155 160 165

cct tcc acc gct tat gtt tac cca agc cag ggc atc cag gct aag ggc	643
Pro Ser Thr Ala Tyr Val Tyr Pro Ser Gln Gly Ile Gln Ala Lys Gly	
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Glu Arg Ala Asp Ala His Thr Arg Ala Asn Leu Gly Phe Ser Ile Gln	
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Gln Val Ile Asp Glu Asn Pro Thr Glu Leu Lys Val Gly Asp Thr Thr	
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Phe Val His Pro Ala Gly Val Leu Asn Leu Thr Gln Phe Thr Gln Val	
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Ala Leu Ala Val Val Ala Tyr Ala Gln Thr Glu Arg Leu Lys Ala Ala	
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Asn Ala Ile Val Asp Gly Ser Leu Tyr Ala Gly His Ser Leu Gly Glu	
265 270 275	
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Tyr Thr Ala Leu Ala Ser Leu Gly Asn Ile Phe Glu Leu Glu Gly Val	
280 285 290	
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Ile Asp Val Val Phe Ser Arg Gly Ser Ala Met His Ser Leu Val Pro	
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Arg Asp Glu Lys Gly Arg Ser Asn Tyr Gly Leu Ala Ala Phe Arg Pro	
310 315 320 325	
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Asn Met Ile Asn Val Ala Ala Thr Glu Val Glu Asn Trp Val Asp Arg	
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Leu Lys Ala Ser Ala Ser Ala Asn Pro Arg Ala Tyr Val Asn Ile Pro	
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Gly Ile Asp Val Pro Phe His Ser Ser Val Leu Arg Pro Gly Val Pro	
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Ala Phe Ala Glu Lys Leu Asp Glu Leu Leu Pro Glu Thr Ile Asp Ile	
410 415 420	
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Glu Leu Thr Gln Ser Phe Val Asp Ala Ile Leu Ala Val Val Pro Ser	
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Glu Arg Leu Lys Gly Ile Lys Val Glu Asp Thr Asp Glu Asn Thr Leu	
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Ala Arg Leu Leu Leu Ile Glu Leu Leu Ser Trp Gln Phe Ala Ser Pro	
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Thr	Gly	Glu	Thr	Val	Val	Lys	Gln	Ala	Ala	Trp	Trp	Ala	Glu	His	Val														
890										895						900													

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Ser Gln Gly Ala Thr Val Ile Leu Thr Ala Ser Asn Val Ser Gln Ala	
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Arg Lys Glu Tyr Ala Arg Lys Leu Tyr Ala Ala Asn Ala Thr Pro Asn	
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Ser Thr Val Thr Val Thr Lys Pro Ala Leu Thr Pro Thr Leu Ala Tyr	
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cca ttc gca gct cca tcc gta tcc ggt acc ttg gcg gat gca ggc cca	3235
Pro Phe Ala Ala Pro Ser Val Ser Gly Thr Leu Ala Asp Ala Gly Pro	
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cag gct gaa aac cag gca cgc ctg ctc ctc tgg tcc gtg gag cgc acc	3283
Gln Ala Glu Asn Gln Ala Arg Leu Leu Leu Trp Ser Val Glu Arg Thr	
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Ile Ala Gly Leu Ala Asp Leu Ala Ser Arg Gly Val Asp Gly Arg Val	
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cac gtt gta ctc cca ggt tcc ccg aac cgc gga atg ttc ggt ggc gac	3379
His Val Val Leu Pro Gly Ser Pro Asn Arg Gly Met Phe Gly Gly Asp	
1080 1085 1090	
ggc gct tac ggc gaa gtc aag gct gct ttc gac gcc atc ctt gcc aag	3427
Gly Ala Tyr Gly Glu Val Lys Ala Ala Phe Asp Ala Ile Leu Ala Lys	
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Trp Gly Ser Glu Thr Gly Trp Pro Gln Phe Val Ser Leu Ala Gln Ala	
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cgc atc ggc tgg gtc gca ggc acc ggc ctc atg ggt cgc aac gac gtg	3523
Arg Ile Gly Trp Val Ala Gly Thr Gly Leu Met Gly Arg Asn Asp Val	
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ctc atc cct gcc gct gaa aag ctg ggc atc cac gtc tac acc cct gaa	3571
Leu Ile Pro Ala Ala Glu Lys Leu Gly Ile His Val Tyr Thr Pro Glu	
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Glu Ile Ser Ser Glu Leu Leu Gly Leu Ala Ser Ala Glu Ser Arg Glu	
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Lys Ala Leu Glu Ala Pro Ile Asp Tyr Asp Leu Thr Gly Gly Leu Ser	
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Gly Gly Val Ser Ile Ala Ala Leu Ala Ala Ser Leu Glu Ser Asp Ala	
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gta gag acc acc tct gca gca gaa gac acc atc aag gcg ctt cca tca	3763
Val Glu Thr Thr Ser Ala Ala Glu Asp Thr Ile Lys Ala Leu Pro Ser	
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Pro Lys His Pro Glu Gln Pro Val Gly Thr Pro Val Gly Glu Val Lys	
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Thr Asp Leu Glu Asp Met Val Val Met Val Gly Val Gly Glu Val Ser	
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Ser Trp Gly Ser Gly Arg Thr Arg Phe Glu Ala Glu Tyr Gly Ile Gln	
1255 1260 1265	
cgc gac ggc tcc gtt gac ctc acc gca gca ggc gtc ctt gag ctt gca	3955
Arg Asp Gly Ser Val Asp Leu Thr Ala Ala Gly Val Leu Glu Leu Ala	
1270 1275 1280 1285	
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Trp Met Met Gly Leu Ile Ser Trp Ser Glu Asp Pro Lys Pro Ala Trp	
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Tyr Asp Ala Asp Gly Thr Glu Val Pro Glu Glu Glu Ile Tyr Glu Arg	
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Phe Arg Asp Glu Val Ile Ala Arg Cys Gly Val Arg Glu Leu Val Asp	
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Asp Ala Phe Leu Val Asp Gly Gly Ser Leu Asp Ala Ala Glu Val Phe	
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ctc gac cgc gac atc tcc ttc tcc gta acc tct gct gaa gaa gca cag	4195
Leu Asp Arg Asp Ile Ser Phe Ser Val Thr Ser Ala Glu Glu Ala Gln	
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gcc tac gtc gat gca gat gct tcc gtg acc gtt gaa gaa gca gac ggc	4243
Ala Tyr Val Asp Ala Asp Ala Ser Val Thr Val Glu Glu Ala Asp Gly	
1370 1375 1380	
gaa tgg atc gtg acc aag aag aag ggc tcc acc tcc ttc gtg cca cgc	4291

Glu Trp Ile Val Thr Lys Lys Lys Gly Ser Thr Ser Phe Val Pro Arg	
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aag gca acc ctg acc cgc tcc gta gca ggc cag ctg cca acc gac ttc	4339
Lys Ala Thr Leu Thr Arg Ser Val Ala Gly Gln Leu Pro Thr Asp Phe	
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gac cct gcc aag tgg ggt atc cca gcc tcc atg atc gat gca ctc gac	4387
Asp Pro Ala Lys Trp Gly Ile Pro Ala Ser Met Ile Asp Ala Leu Asp	
1415	1420 1425
aac atc gca gcg tgg aac ctg gtc act gca gtc gac gcc ttc ctg tcc	4435
Asn Ile Ala Ala Trp Asn Leu Val Thr Ala Val Asp Ala Phe Leu Ser	
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tcc ggc ttc agc cca gca gaa ctc ctg cag tcc atc cac cca gct gac	4483
Ser Gly Phe Ser Pro Ala Glu Leu Leu Gln Ser Ile His Pro Ala Asp	
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gtg tcc tcc acc cag ggc acc ggt atc ggt ggc atg cag tcc cta cgc	4531
Val Ser Ser Thr Gln Gly Thr Gly Ile Gly Gly Met Gln Ser Leu Arg	
1465	1470 1475
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Lys Leu Phe Val Asn Arg Phe Leu Gly Gln Asp Arg Pro Ser Asp Ile	
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ctc cag gag acc ctg cca aac gtt gtg gct gca cac acc atg cag tcc	4627
Leu Gln Glu Thr Leu Pro Asn Val Val Ala Ala His Thr Met Gln Ser	
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Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys Ala	
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Thr Ala Ala Val Ser Val Glu Glu Gly Val Asp Lys Ile Arg Leu Asn	
1530	1535 1540
aag gca gat ttc gtt gtc gcc ggt ggt atc gat gac atc cag gtt gaa	4771
Lys Ala Asp Phe Val Val Ala Gly Gly Ile Asp Asp Ile Gln Val Glu	
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Ser Leu Thr Gly Phe Gly Asp Met Asn Ala Thr Ala Asp Thr Gln Ala	
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Met Leu Asp Lys Gly Ile Asp Pro Arg Phe Ile Ser Arg Ala Asn Asp	
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Arg Arg Arg Ala Gly Phe Leu Glu Ala Ala Gly Gly Gly Thr Val Leu	
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Leu Ala Arg Ala Ser Val Ala Ala Glu Leu Gly Leu Pro Val Leu Ala	
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Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Gly Gly Lys Lys			
1640	1645	1650	
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Ser Val Leu Ala Arg Glu Leu Asn Lys Leu Gly Leu Thr Pro Asp Asp			
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Val Arg Val Val Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp Pro			
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Asn Glu Ser Glu Leu His Asn Leu Leu Trp Lys Thr Ile Gly Arg Glu			
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Ala Asp Asn Pro Met Phe Val Val Ser Gln Lys Ser Leu Thr Gly His			
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Ser Lys Gly Gly Ala Ala Leu Phe Gln Ile Gly Gly Leu Val Ser Ile			
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Leu Glu Thr Gly Lys Leu Pro Gln Asn Ala Ser Leu Asp Cys Val Asp			
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Pro Glu Met Glu Ala Lys Gly Glu Asn Phe Val Trp Leu Arg Lys Pro			
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ctg gat ctc ggc gca ggc tcc att aag gcc ggc gta ctt acc tca ctg			5443
Leu Asp Leu Gly Ala Gly Ser Ile Lys Ala Gly Val Leu Thr Ser Leu			
1770	1775	1780	
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Phe Glu Gln Ala Met Arg Asn Ala Gly Leu Asp Val Glu Ala Trp Arg			
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Ala Arg Ala Thr Gln Arg Leu Arg Thr Gly Ala Asn Arg Leu Glu Ala			
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Gly Met Val Gly Arg Ala Pro Leu Phe Glu Gln Val Asp Gly Arg Arg			
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Leu Pro Glu His Gly Ala His Gln Ala Glu Ile Asn Leu Leu Ile Asp			
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5745

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 35 40 45

Arg Ser Phe Ile Arg Gln Ala Thr Val Ser Ala Pro Ala Asp Met Thr
 50 55 60

Pro Phe Ala Met Val Ser Gly Asp Tyr Asn Pro Ile His Thr Ser Asp
 65 70 75 80

Asn Ala Ala Lys Leu Val Gly Leu Asp Ala Ala Leu Val His Gly Met
 85 90 95

Trp Leu Ser Ala Thr Ala Gln His Leu Ala Gly Leu Gly Ser Glu Val
 100 105 110

Ile Gly Trp Thr Tyr Ser Met Tyr Gly Met Val Gln Leu Asn Asp Val
 115 120 125

Val Asp Ile Thr Val Glu Arg Val Gly Arg Ala Gly Leu Lys Pro Ala
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Tyr Glu Val Thr Cys Arg Ile Asp Gly Asn Val Val Ser Arg Gly Gln
 145 150 155 160

Ala Leu Leu Lys Ala Pro Ser Thr Ala Tyr Val Tyr Pro Ser Gln Gly
 165 170 175

Ile Gln Ala Lys Gly Met Gly Gln Gly Asp Arg Thr Ala Ser Ala Glu
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Ala Arg Ala Val Trp Glu Arg Ala Asp Ala His Thr Arg Ala Asn Leu
 195 200 205

Gly Phe Ser Ile Gln Gln Val Ile Asp Glu Asn Pro Thr Glu Leu Lys
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Val Gly Asp Thr Thr Phe Val His Pro Ala Gly Val Leu Asn Leu Thr
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Gln Phe Thr Gln Val Ala Leu Ala Val Val Ala Tyr Ala Gln Thr Glu
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Arg Leu Lys Ala Ala Asn Ala Ile Val Asp Gly Ser Leu Tyr Ala Gly
 260 265 270

His Ser Leu Gly Glu Tyr Thr Ala Leu Ala Ser Leu Gly Asn Ile Phe
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 290 295 300
 His Ser Leu Val Pro Arg Asp Glu Lys Gly Arg Ser Asn Tyr Gly Leu
 305 310 315 320
 Ala Ala Phe Arg Pro Asn Met Ile Asn Val Ala Ala Thr Glu Val Glu
 325 330 335
 Asn Trp Val Asp Arg Val Ala Glu Glu Ser Gly Glu Phe Leu Gln Ile
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 Val Asn Tyr Asn Val Asp Gly Gln Gln Tyr Ala Val Ala Gly Thr Leu
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 Ala Gly Leu Lys Ala Leu Lys Ala Ser Ala Ser Ala Asn Pro Arg Ala
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 Tyr Val Asn Ile Pro Gly Ile Asp Val Pro Phe His Ser Ser Val Leu
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 Glu Thr Ile Asp Ile Asp Ala Leu Arg Gly Arg Tyr Ile Pro Asn Leu
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 Val Ala Arg Pro Phe Glu Leu Thr Gln Ser Phe Val Asp Ala Ile Leu
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 Ala Val Val Pro Ser Glu Arg Leu Lys Gly Ile Lys Val Glu Asp Thr
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 Asp Glu Asn Thr Leu Ala Arg Leu Leu Leu Ile Glu Leu Leu Ser Trp
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 Gln Phe Ala Ser Pro Val Arg Trp Ile Glu Thr Gln Ala Leu Ile Ile
 485 490 495
 Asp Thr Val Asp Gln Ile Ile Glu Val Gly Leu Ala Ala Ser Pro Thr
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 Val Arg Gln Ala Pro Val Ala Glu Val Glu Glu Glu Ala Val Glu Glu
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 Ala Pro Ala Ala Ala Ala Ala Pro Ala Ala Glu Ala Pro Val Ala Ala
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 Ala Pro Val Ala Ala Ala Ala Pro Ala Pro Val Gly Asn Ala Pro Glu
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 Leu Lys Phe Asn Ala Ala Asn Ala Ile Met Val Leu Phe Ala Val Gln

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Ser	Thr	Glu	Leu	Ser	Val	Pro	Thr	Ile	Asp	Gly	Ala	Ala	Asp	Ala	Asp
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Pro	Phe	Gly	Pro	Val	Leu	Ser	Glu	Thr	Val	Arg	Ala	Arg	Leu	Arg	Ala
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Leu	Thr	Gly	Ala	Ala	Gly	Leu	Lys	Thr	Ser	Tyr	Ile	Gly	Asp	Arg	Val
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Val	Ser	Glu	Val	Ala	Ala	Lys	Pro	Ala	Asn	Glu	Pro	His	Ile	Asp	Asp
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Leu Thr Pro Asp Asp Val Arg Val Val Ser Lys His Asp Thr Ser Thr		
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Asn Ala Asn Asp Pro Asn Glu Ser Glu Leu His Asn Leu Leu Trp Lys		
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Thr Ile Gly Arg Glu Ala Asp Asn Pro Met Phe Val Val Ser Gln Lys		
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Trp Leu Arg Lys Pro Leu Asp Leu Gly Ala Gly Ser Ile Lys Ala Gly		
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Ala Leu Ala Ala Thr Leu Lys Gln Val Ser Glu Val Ala Ala Lys Pro	
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gcc aac gag cca cac atc gac gat gtt gcg ctg gtt acc ggt gcg gct	480
Ala Asn Glu Pro His Ile Asp Asp Val Ala Leu Val Thr Gly Ala Ala	
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Pro Glu Ser Ile Ala Gly Ala Val Ala Ala Arg Leu Leu Ser Gln Gly	
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gcg acc gtc att ctc acc gca tcg aac gtc tcc cag gcg cgt aag gaa	576
Ala Thr Val Ile Leu Thr Ala Ser Asn Val Ser Gln Ala Arg Lys Glu	
180 185 190	
tac gca cgc aag ctc tac gct gcg aac gca acc cct aac gca aag ctg	624
Tyr Ala Arg Lys Leu Tyr Ala Ala Asn Ala Thr Pro Asn Ala Lys Leu	
195 200 205	

tgg att gtt cct gcg aac atg tcc tcc tac cgc gat gtt gat gca gtc	672
Trp Ile Val Pro Ala Asn Met Ser Ser Tyr Arg Asp Val Asp Ala Val	
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Ile Asp Trp Ile Gly Asn Glu Gln Arg Val Thr Val Gly Ser Thr Val	
225 230 235 240	
acc gtg acc aag cca gct ctg acc cca acc ctt gcg tac cca ttc gca	768
Thr Val Thr Lys Pro Ala Leu Thr Pro Thr Leu Ala Tyr Pro Phe Ala	
245 250 255	
gct cca tcc gta tcc ggt acc ttg gcg gat gca ggc cca cag gct gaa	816
Ala Pro Ser Val Ser Gly Thr Leu Ala Asp Ala Gly Pro Gln Ala Glu	
260 265 270	
aac cag gca cgc ctg ctc ctc tgg tcc gtg gag cgc acc atc gca gga	864
Asn Gln Ala Arg Leu Leu Leu Trp Ser Val Glu Arg Thr Ile Ala Gly	
275 280 285	
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Leu Ala Asp Leu Ala Ser Arg Gly Val Asp Gly Arg Val His Val Val	
290 295 300	
ctc cca ggt tcc ccg aac cgc gga atg ttc ggt ggc gac ggc gct tac	960
Leu Pro Gly Ser Pro Asn Arg Gly Met Phe Gly Gly Asp Gly Ala Tyr	
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Gly Glu Val Lys Ala Ala Phe Asp Ala Ile Leu Ala Lys Trp Gly Ser	
325 330 335	
gag acc ggc tgg cca cag ttt gtc tcc ctc gca cag gca cgc atc ggc	1056
Glu Thr Gly Trp Pro Gln Phe Val Ser Leu Ala Gln Ala Arg Ile Gly	
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Trp Val Ala Gly Thr Gly Leu Met Gly Arg Asn Asp Val Leu Ile Pro	
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gcc gct gaa aag ctg ggc atc cac gtc tac acc cct gaa gag atc tct	1152
Ala Ala Glu Lys Leu Gly Ile His Val Tyr Thr Pro Glu Glu Ile Ser	
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Ser Glu Leu Leu Gly Leu Ala Ser Ala Glu Ser Arg Glu Lys Ala Leu	
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Glu Ala Pro Ile Asp Tyr Asp Leu Thr Gly Gly Leu Ser Gly Gly Val	
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Ser Ile Ala Ala Leu Ala Ala Ser Leu Glu Ser Asp Ala Val Glu Thr	
420 425 430	
acc tct gca gca gaa gac acc atc aag gcg ctt cca tca cct aag cac	1344
Thr Ser Ala Ala Glu Asp Thr Ile Lys Ala Leu Pro Ser Pro Lys His	
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Pro Glu Gln Pro Val Gly Thr Pro Val Gly Glu Val Lys Thr Asp Leu	
450 455 460	
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Glu Asp Met Val Val Met Val Gly Val Gly Glu Val Ser Ser Trp Gly	
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Ser Gly Arg Thr Arg Phe Glu Ala Glu Tyr Gly Ile Gln Arg Asp Gly	
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Ser Val Asp Leu Thr Ala Ala Gly Val Leu Glu Leu Ala Trp Met Met	
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Gly Leu Ile Ser Trp Ser Glu Asp Pro Lys Pro Ala Trp Tyr Asp Ala	
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Asp Gly Thr Glu Val Pro Glu Glu Glu Ile Tyr Glu Arg Phe Arg Asp	
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gaa gtc atc gca cga tgc ggt gtt cgt gag ctt gtc gac gac gca ttc	1680
Glu Val Ile Ala Arg Cys Gly Val Arg Glu Leu Val Asp Asp Ala Phe	
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Leu Val Asp Gly Gly Ser Leu Asp Ala Ala Glu Val Phe Leu Asp Arg	
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Asp Ile Ser Phe Ser Val Thr Ser Ala Glu Glu Ala Gln Ala Tyr Val	
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Asp Ala Asp Ala Ser Val Thr Val Glu Glu Ala Asp Gly Glu Trp Ile	
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Val Thr Lys Lys Lys Gly Ser Thr Ser Phe Val Pro Arg Lys Ala Thr	
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Leu Thr Arg Ser Val Ala Gly Gln Leu Pro Thr Asp Phe Asp Pro Ala	
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Lys Trp Gly Ile Pro Ala Ser Met Ile Asp Ala Leu Asp Asn Ile Ala	
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Val	Asn	Arg	Phe	Leu	Gly	Gln	Asp	Arg	Pro	Ser	Asp	Ile	Leu	Gln	Glu		
705					710					715					720		
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Thr	Leu	Pro	Asn	Val	Val	Ala	Ala	His	Thr	Met	Gln	Ser	Tyr	Val	Gly		
				725					730					735			
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Gly	Tyr	Gly	Gln	Met	Ile	His	Pro	Val	Ala	Ala	Cys	Ala	Thr	Ala	Ala		
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gtc	tcc	gtg	gaa	gaa	ggc	gtg	gac	aag	atc	cgc	ctc	aac	aag	gca	gat	2304	
Val	Ser	Val	Glu	Glu	Gly	Val	Asp	Lys	Ile	Arg	Leu	Asn	Lys	Ala	Asp		
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ttc	gtt	gtc	gcc	ggt	ggt	atc	gat	gac	atc	cag	gtt	gaa	tcc	ctg	acc	2352	
Phe	Val	Val	Ala	Gly	Gly	Ile	Asp	Asp	Ile	Gln	Val	Glu	Ser	Leu	Thr		
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ggc	ttc	ggt	gac	atg	aac	gcc	acc	gca	gac	acc	cag	gca	atg	ctg	gac	2400	
Gly	Phe	Gly	Asp	Met	Asn	Ala	Thr	Ala	Asp	Thr	Gln	Ala	Met	Leu	Asp		
785					790					795					800		
aag	ggc	atc	gac	cca	cgc	ttc	atc	tcc	cgc	gca	aac	gat	cga	cgt	cgc	2448	
Lys	Gly	Ile	Asp	Pro	Arg	Phe	Ile	Ser	Arg	Ala	Asn	Asp	Arg	Arg	Arg		
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gca	ggc	ttc	ctc	gaa	gca	gca	ggt	ggc	ggt	acc	gtc	ctc	ctg	gca	cgt	2496	
Ala	Gly	Phe	Leu	Glu	Ala	Ala	Gly	Gly	Gly	Thr	Val	Leu	Leu	Ala	Arg		
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gca	tcc	gtt	gct	gct	gaa	ctg	gga	ctg	cca	gtt	ctc	gca	gtt	gtt	gca	2544	
Ala	Ser	Val	Ala	Ala	Glu	Leu	Gly	Leu	Pro	Val	Leu	Ala	Val	Val	Ala		
			835				840					845					
cac	gca	cag	tcc	tac	gcc	gat	ggt	gct	cac	acc	tcc	atc	cca	gca	ccg	2592	
His	Ala	Gln	Ser	Tyr	Ala	Asp	Gly	Ala	His	Thr	Ser	Ile	Pro	Ala	Pro		
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Gly	Leu	Gly	Ala	Leu	Gly	Ala	Ala	Arg	Gly	Gly	Lys	Lys	Ser	Val	Leu		
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gct	cgc	gaa	ctg	aac	aaa	ttg	ggt	ctg	acc	cca	gat	gac	gtt	cgc	gtg	2688	
Ala	Arg	Glu	Leu	Asn	Lys	Leu	Gly	Leu	Thr	Pro	Asp	Asp	Val	Arg	Val		
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gtc	tcg	aag	cac	gac	acc	tcc	acc	aac	gcc	aac	gat	cca	aac	gag	tcc	2736	
Val	Ser	Lys	His	Asp	Thr	Ser	Thr	Asn	Ala	Asn	Asp	Pro	Asn	Glu	Ser		
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gag	ctg	cac	aac	ctg	ctg	tgg	aag	acc	att	gga	cgc	gaa	gcc	gac	aac	2784	
Glu	Leu	His	Asn	Leu	Leu	Trp	Lys	Thr	Ile	Gly	Arg	Glu	Ala	Asp	Asn		
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ccg	atg	ttc	gtc	gtc	tcc	cag	aag	tcc	ctt	acc	gga	cac	tca	aag	ggc	2832	
Pro	Met	Phe	Val	Val	Ser	Gln	Lys	Ser	Leu	Thr	Gly	His	Ser	Lys	Gly		

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Gly Ala Ala Leu Phe Gln Ile Gly Gly Leu Val Ser Ile Leu Glu Thr			
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ggc aag ctg cca cag aac gca tcc ctt gac tgc gtt gac cca gag atg			2928
Gly Lys Leu Pro Gln Asn Ala Ser Leu Asp Cys Val Asp Pro Glu Met			
	965	970	975
gaa gca aag ggc gag aac ttc gtc tgg ctg cgc aag cca ctg gat ctc			2976
Glu Ala Lys Gly Glu Asn Phe Val Trp Leu Arg Lys Pro Leu Asp Leu			
	980	985	990
ggc gca ggc tcc att aag gcc ggc gta ctt acc tca ctg ggc ttc ggc			3024
Gly Ala Gly Ser Ile Lys Ala Gly Val Leu Thr Ser Leu Gly Phe Gly			
	995	1000	1005
cac gtg gct gca gtc gtc gtg ctg gca acc agc ggc atc ttc gag cag			3072
His Val Ala Ala Val Val Val Leu Ala Thr Ser Gly Ile Phe Glu Gln			
	1010	1015	1020
gca atg cgc aac gca ggc ctc gac gtc gaa gca tgg cgt gca cgc gca			3120
Ala Met Arg Asn Ala Gly Leu Asp Val Glu Ala Trp Arg Ala Arg Ala			
	1025	1030	1035
acc cag cgc ctg cgc acc ggt gca aac cgc cta gaa gct ggc atg gtt			3168
Thr Gln Arg Leu Arg Thr Gly Ala Asn Arg Leu Glu Ala Gly Met Val			
	1045	1050	1055
ggc cga gca cca ttg ttc gag cag gtc gac gga cgt cgc ctg cca gag			3216
Gly Arg Ala Pro Leu Phe Glu Gln Val Asp Gly Arg Arg Leu Pro Glu			
	1060	1065	1070
cat ggc gct cac caa gca gag atc aac ttg ctt atc gac gct gac gct			3264
His Gly Ala His Gln Ala Glu Ile Asn Leu Leu Ile Asp Ala Asp Ala			
	1075	1080	1085
cgc ctc ggt gct gac ggc atc tac cag ggc taaacgtttag atagctaaga			3314
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Ile	Leu	Ser	Gln	Leu	Gly	Leu	Asp	Thr	Lys	Asp	Glu	Val	Glu	Gly	Ala
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Glu	Ile	Asp	Thr	Glu	Leu	Tyr	Asp	Ala	Val	Glu	Ala	Glu	Leu	Gly	Thr
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Gly 65	Trp	Leu	Lys	Leu	Val 70	Thr	Pro	Val	Phe	Ser 75	Ala	Asp	Arg	Ala	Ile 80
Leu	Phe	Asp	Asp	Arg 85	Trp	Ala	Ser	Ala	Arg 90	Glu	Asp	Leu	Ala	Arg 95	Leu
Ala	Asn	Gly	Glu	Asp 100	Ile	Ala	Val	Glu 105	Arg	Phe	Ala	Gly	Thr 110	Gly	Glu
Thr	Val 115	Val	Lys	Gln	Ala	Ala	Trp 120	Trp	Ala	Glu	His	Val 125	Glu	Asp	Thr
Ala	Leu 130	Ala	Ala	Thr	Leu	Lys 135	Gln	Val	Ser	Glu	Val 140	Ala	Ala	Lys	Pro
Ala 145	Asn	Glu	Pro	His 150	Ile	Asp	Asp	Val	Ala	Leu 155	Val	Thr	Gly	Ala	Ala 160
Pro	Glu	Ser	Ile	Ala 165	Gly	Ala	Val	Ala	Ala 170	Arg	Leu	Leu	Ser	Gln 175	Gly
Ala	Thr	Val 180	Ile	Leu	Thr	Ala	Ser	Asn 185	Val	Ser	Gln	Ala	Arg 190	Lys	Glu
Tyr	Ala	Arg 195	Lys	Leu	Tyr	Ala	Ala 200	Asn	Ala	Thr	Pro	Asn 205	Ala	Lys	Leu
Trp	Ile 210	Val	Pro	Ala	Asn 215	Met	Ser	Ser	Tyr	Arg	Asp 220	Val	Asp	Ala	Val
Ile 225	Asp	Trp	Ile	Gly	Asn 230	Glu	Gln	Arg	Val	Thr 235	Val	Gly	Ser	Thr	Val 240
Thr	Val	Thr	Lys	Pro 245	Ala	Leu	Thr	Pro	Thr 250	Leu	Ala	Tyr	Pro	Phe 255	Ala
Ala	Pro	Ser 260	Val	Ser	Gly	Thr	Leu	Ala 265	Asp	Ala	Gly	Pro	Gln 270	Ala	Glu
Asn	Gln 275	Ala	Arg	Leu	Leu	Leu	Trp 280	Ser	Val	Glu	Arg	Thr 285	Ile	Ala	Gly
Leu 290	Ala	Asp	Leu	Ala	Ser	Arg	Gly 295	Val	Asp	Gly	Arg	Val	His	Val	Val
Leu 305	Pro	Gly	Ser	Pro	Asn 310	Arg	Gly	Met	Phe	Gly 315	Gly	Asp	Gly	Ala	Tyr 320
Gly	Glu	Val	Lys	Ala 325	Ala	Phe	Asp	Ala	Ile 330	Leu	Ala	Lys	Trp	Gly 335	Ser
Glu	Thr	Gly 340	Trp	Pro	Gln	Phe	Val	Ser 345	Leu	Ala	Gln	Ala	Arg 350	Ile	Gly
Trp	Val 355	Ala	Gly	Thr	Gly	Leu	Met 360	Gly	Arg	Asn	Asp	Val 365	Leu	Ile	Pro
Ala 370	Ala	Glu	Lys	Leu	Gly	Ile 375	His	Val	Tyr	Thr	Pro 380	Glu	Glu	Ile	Ser

Ser Glu Leu Leu Gly Leu Ala Ser Ala Glu Ser Arg Glu Lys Ala Leu
 385 390 395 400
 Glu Ala Pro Ile Asp Tyr Asp Leu Thr Gly Gly Leu Ser Gly Gly Val
 405 410 415
 Ser Ile Ala Ala Leu Ala Ala Ser Leu Glu Ser Asp Ala Val Glu Thr
 420 425 430
 Thr Ser Ala Ala Glu Asp Thr Ile Lys Ala Leu Pro Ser Pro Lys His
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 Pro Glu Gln Pro Val Gly Thr Pro Val Gly Glu Val Lys Thr Asp Leu
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 Glu Asp Met Val Val Met Val Gly Val Gly Glu Val Ser Ser Trp Gly
 465 470 475 480
 Ser Gly Arg Thr Arg Phe Glu Ala Glu Tyr Gly Ile Gln Arg Asp Gly
 485 490 495
 Ser Val Asp Leu Thr Ala Ala Gly Val Leu Glu Leu Ala Trp Met Met
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 Gly Leu Ile Ser Trp Ser Glu Asp Pro Lys Pro Ala Trp Tyr Asp Ala
 515 520 525
 Asp Gly Thr Glu Val Pro Glu Glu Glu Ile Tyr Glu Arg Phe Arg Asp
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 Glu Val Ile Ala Arg Cys Gly Val Arg Glu Leu Val Asp Asp Ala Phe
 545 550 555 560
 Leu Val Asp Gly Gly Ser Leu Asp Ala Ala Glu Val Phe Leu Asp Arg
 565 570 575
 Asp Ile Ser Phe Ser Val Thr Ser Ala Glu Glu Ala Gln Ala Tyr Val
 580 585 590
 Asp Ala Asp Ala Ser Val Thr Val Glu Glu Ala Asp Gly Glu Trp Ile
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 Val Thr Lys Lys Lys Gly Ser Thr Ser Phe Val Pro Arg Lys Ala Thr
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 Leu Thr Arg Ser Val Ala Gly Gln Leu Pro Thr Asp Phe Asp Pro Ala
 625 630 635 640
 Lys Trp Gly Ile Pro Ala Ser Met Ile Asp Ala Leu Asp Asn Ile Ala
 645 650 655
 Ala Trp Asn Leu Val Thr Ala Val Asp Ala Phe Leu Ser Ser Gly Phe
 660 665 670
 Ser Pro Ala Glu Leu Leu Gln Ser Ile His Pro Ala Asp Val Ser Ser
 675 680 685
 Thr Gln Gly Thr Gly Ile Gly Gly Met Gln Ser Leu Arg Lys Leu Phe
 690 695 700

Val Asn Arg Phe Leu Gly Gln Asp Arg Pro Ser Asp Ile Leu Gln Glu
 705 710 715 720
 Thr Leu Pro Asn Val Val Ala Ala His Thr Met Gln Ser Tyr Val Gly
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 Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys Ala Thr Ala Ala
 740 745 750
 Val Ser Val Glu Glu Gly Val Asp Lys Ile Arg Leu Asn Lys Ala Asp
 755 760 765
 Phe Val Val Ala Gly Gly Ile Asp Asp Ile Gln Val Glu Ser Leu Thr
 770 775 780
 Gly Phe Gly Asp Met Asn Ala Thr Ala Asp Thr Gln Ala Met Leu Asp
 785 790 795 800
 Lys Gly Ile Asp Pro Arg Phe Ile Ser Arg Ala Asn Asp Arg Arg Arg
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 Ala Gly Phe Leu Glu Ala Ala Gly Gly Gly Thr Val Leu Leu Ala Arg
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 Ala Ser Val Ala Ala Glu Leu Gly Leu Pro Val Leu Ala Val Val Ala
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 His Ala Gln Ser Tyr Ala Asp Gly Ala His Thr Ser Ile Pro Ala Pro
 850 855 860
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 Ala Arg Glu Leu Asn Lys Leu Gly Leu Thr Pro Asp Asp Val Arg Val
 885 890 895
 Val Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp Pro Asn Glu Ser
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 Pro Met Phe Val Val Ser Gln Lys Ser Leu Thr Gly His Ser Lys Gly
 930 935 940
 Gly Ala Ala Leu Phe Gln Ile Gly Gly Leu Val Ser Ile Leu Glu Thr
 945 950 955 960
 Gly Lys Leu Pro Gln Asn Ala Ser Leu Asp Cys Val Asp Pro Glu Met
 965 970 975
 Glu Ala Lys Gly Glu Asn Phe Val Trp Leu Arg Lys Pro Leu Asp Leu
 980 985 990
 Gly Ala Gly Ser Ile Lys Ala Gly Val Leu Thr Ser Leu Gly Phe Gly
 995 1000 1005
 His Val Ala Ala Val Val Val Leu Ala Thr Ser Gly Ile Phe Glu Gln
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 Ala Met Arg Asn Ala Gly Leu Asp Val Glu Ala Trp Arg Ala Arg Ala

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 Leu Lys Thr Leu Arg
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cgc gca aat gcg ctg ctt gca cta gtt gca gat gat ctc att ggc acc 211
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ctt cca ttt ggt ttc gat cca gtg gct tgg gct aac aac tcc gaa gat 259
 Leu Pro Phe Gly Phe Asp Pro Val Ala Trp Ala Asn Asn Ser Glu Asp
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 Pro Ala Phe Asp Thr Ala Gln Ser Ala Val Ser Val Pro Gly Ile Phe
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 Val Ser Gln Ile Ala Thr Leu Asp Ser Leu Glu Ala Gln Arg Leu Asp
 70 75 80 85

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 Val Asp Gln Ala Val Ser Ser Ile Gly His Ser Gln Gly Val Leu Gly
 90 95 100

gtg cac ctg ctc aat gat gcg act cgt gct gat gaa ctc gtt gcc att 451
 Val His Leu Leu Asn Asp Ala Thr Arg Ala Asp Glu Leu Val Ala Ile
 105 110 115

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Leu Ile Ala Gln Gly Asp Asn Met Pro Met Leu Ser Ile Ala Gly Ile	
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Ser Arg Glu Gln Leu Gln Gln Ala Ile Asp Ala Ala Cys Ala Glu Val	
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Pro Ala Glu Ile Arg Pro Val Ile Gly Leu Arg Asn Ser Arg Asp Ser	
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Tyr Val Leu Val Gly Arg Pro Asp Asp Asn Ala Arg Val Val Lys Val	
185 190 195	
att gag gca atg gct gcc aag gat aag aag gcc att gaa gat aag ctg	739
Ile Glu Ala Met Ala Ala Lys Asp Lys Lys Ala Ile Glu Asp Lys Leu	
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Ala Ala Asp Val Leu Val Asn Pro Val Asp Trp Val Ala Arg Val Asn	
265 270 275	
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Glu Ala Tyr Glu Ala Gly Ala Arg Trp Phe Leu Asp Val Gly Pro Asp	
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ggt ggc atc gtt aag ctg act gcc aac atc ctt gag ggc cgc ggc gcg	1027
Gly Gly Ile Val Lys Leu Thr Ala Asn Ile Leu Glu Gly Arg Gly Ala	
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gat tcc ttc tat gtt ggt gac gcc gca ggc cag gcc aag ata ttt gat	1075
Asp Ser Phe Tyr Val Gly Asp Ala Ala Gly Gln Ala Lys Ile Phe Asp	
310 315 320 325	
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Ala Gly Met Ala Pro Glu Leu Pro Val Asp Tyr Gln Glu Phe Ala Pro	
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cgc gtt gag cac gtt gat gga acc cca cgc ctg gtt acc aag ttc act	1171
Arg Val Glu His Val Asp Gly Thr Pro Arg Leu Val Thr Lys Phe Thr	
345 350 355	
gag ctg acc ggc cgc acc cca atg atg ctg gct ggc atg acc cca acc	1219
Glu Leu Thr Gly Arg Thr Pro Met Met Leu Ala Gly Met Thr Pro Thr	

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Thr Val Asp Pro Ala Ile Val Ala Ala Ala Ala Asn Gly Gly His Trp															
375 380 385															
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Ala Glu Leu Ala Gly Gly Gly Gln Val Thr Pro Glu Leu Leu Glu Thr															
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cac atc gca cag ctc acc gac atg ctt gag cca ggt atc aac gcc cag	1363														
His Ile Ala Gln Leu Thr Asp Met Leu Glu Pro Gly Ile Asn Ala Gln															
410 415 420															
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Phe Asn Ser Met Phe Leu Asp Pro Tyr Leu Trp Lys Met Gln Ile Gly															
425 430 435															
ggc aag cgc ctt gtt cct aag gcc cgc gct aat ggt gca tcc atc gac	1459														
Gly Lys Arg Leu Val Pro Lys Ala Arg Ala Asn Gly Ala Ser Ile Asp															
440 445 450															
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Gly Ile Val Ile Thr Ala Gly Ile Pro Glu Lys Asp Glu Ala Val Ala															
455 460 465															
ttg gtc aag gaa ctg atg cgt gat ggt ttc cct tgg atc gca ttc aag	1555														
Leu Val Lys Glu Leu Met Arg Asp Gly Phe Pro Trp Ile Ala Phe Lys															
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cca ggt gcc atc aag cag gtt aac tct gtg ttg gct atc gct aag gaa	1603														
Pro Gly Ala Ile Lys Gln Val Asn Ser Val Leu Ala Ile Ala Lys Glu															
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Val Pro Glu Leu Pro Ile Ile Ile Gln Ile Glu Gly Gly Val Ala Gly															
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Gly His His Ser Trp Glu Asp Leu Asp Glu Leu Leu Ile Ala Thr Tyr															
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gag gtt gca ggc gat gag acg gct gtg cag gcg cgc cgg gat gag atc Glu Val Ala Gly Asp Glu Thr Ala Val Gln Ala Arg Arg Asp Glu Ile 650 655 660	2083
att gaa gcg att ggc aag acc gcc aag gtg tac ttc ggt gac atc gga Ile Glu Ala Ile Gly Lys Thr Ala Lys Val Tyr Phe Gly Asp Ile Gly 665 670 675	2131
tcc atg act tac gag cag tgg ctc aac cgc tac ctc gag ctg tct ggc Ser Met Thr Tyr Glu Gln Trp Leu Asn Arg Tyr Leu Glu Leu Ser Gly 680 685 690	2179
cct gtt gat ggt cag tgg att gat gct tcc tgg gct gca cgt ttt gcc Pro Val Asp Gly Gln Trp Ile Asp Ala Ser Trp Ala Ala Arg Phe Ala 695 700 705	2227
cag atg ctg gag cgt gcc gag gcg cgt ttg atc gag cag gat cat ggc Gln Met Leu Glu Arg Ala Glu Ala Arg Leu Ile Glu Gln Asp His Gly 710 715 720 725	2275
caa ttt gag cca agc ctg acg gtg gag gat ggc gtc gac aag ctt gtt Gln Phe Glu Pro Ser Leu Thr Val Glu Asp Gly Val Asp Lys Leu Val 730 735 740	2323
gct gct tac ccg cat gcc gca acc gac ctg ctc acc ccg gct gat gtc Ala Ala Tyr Pro His Ala Ala Thr Asp Leu Leu Thr Pro Ala Asp Val 745 750 755	2371
gcc tgg ttc ttg ggc ctg tgc cgc acg ccg ggc aag cct gtg aac ttt Ala Trp Phe Leu Gly Leu Cys Arg Thr Pro Gly Lys Pro Val Asn Phe 760 765 770	2419
gtg ccc gtc att gat aag gac gtg cgt cgc tgg tgg cgc tcg gac tcc Val Pro Val Ile Asp Lys Asp Val Arg Arg Trp Trp Arg Ser Asp Ser 775 780 785	2467
ctg tgg cag tcc cac gat gat cgc tac acc gct gat cag gtg gct att Leu Trp Gln Ser His Asp Asp Arg Tyr Thr Ala Asp Gln Val Ala Ile 790 795 800 805	2515
atc cct ggt gtc gtc gcc gtt gct ggc atc acc aag gcc aac gaa cct Ile Pro Gly Val Val Ala Val Ala Gly Ile Thr Lys Ala Asn Glu Pro 810 815 820	2563
gtc gct gac ctg ctt gat cgc ttt gtc gac gcc acc atc gag cgc atc Val Ala Asp Leu Leu Asp Arg Phe Val Asp Ala Thr Ile Glu Arg Ile 825 830 835	2611
gat gag cac gat tcc cgc tcc cgc gac atc atg ggc aaa gtg ctt tcc Asp Glu His Asp Ser Arg Ser Arg Asp Ile Met Gly Lys Val Leu Ser 840 845 850	2659

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Ser Pro Gly Thr Phe Trp Ala Gly Arg Asn Ile Pro Ser Val Ile His	
855 860 865	
agc ctt ggg cat gct gac aag tgg tcc cgc tcc gaa ttc gaa gca ttc	2755
Ser Leu Gly His Ala Asp Lys Trp Ser Arg Ser Glu Phe Glu Ala Phe	
870 875 880 885	
cat agc cca acc ggc gcc aac ttg gtg tac gaa gac gcc gag cac gcg	2803
His Ser Pro Thr Gly Ala Asn Leu Val Tyr Glu Asp Ala Glu His Ala	
890 895 900	
atg ctg act gtg cct ttg gcg ggt tcc acc gca ttc ggc acc acc gct	2851
Met Leu Thr Val Pro Leu Ala Gly Ser Thr Ala Phe Gly Thr Thr Ala	
905 910 915	
gag ctg aaa atc cgt ttc acc agc ccc atc gac gct ctg cca agc gct	2899
Glu Leu Lys Ile Arg Phe Thr Ser Pro Ile Asp Ala Leu Pro Ser Ala	
920 925 930	
gtc cca ctg gtc acc cag gaa gac gct gaa gcc gcg atg ggt gaa ctg	2947
Val Pro Leu Val Thr Gln Glu Asp Ala Glu Ala Met Gly Glu Leu	
935 940 945	
acc cgc atc gca gct ggc ggc acc ctg gca act gtg aac aat ggc acc	2995
Thr Arg Ile Ala Ala Gly Gly Thr Leu Ala Thr Val Asn Asn Gly Thr	
950 955 960 965	
gct acc tgg gaa acc tcc gtc gat gcc ggc gtc atc gct gac tac aac	3043
Ala Thr Trp Glu Thr Ser Val Asp Ala Gly Val Ile Ala Asp Tyr Asn	
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Asn Val Thr Ala Gly Tyr Leu Pro Ala Ser Val Val Pro Ala His Thr	
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Ala Pro Asp Val Leu Val Gly Arg Ala Trp Pro Ala Val Phe Ala Ala	
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Val Lys Ser Ala Val Ile Pro Gly Thr Asp Ser Ala Ser Val Val Glu	
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Gly Met Leu Ser Leu Val His Leu Glu His His Ile Val Leu Lys Ser	
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gat gtc cca acc gac ggc gcg ctg aag gtt tcc gcg act gcc gat gag	3283
Asp Val Pro Thr Asp Gly Ala Leu Lys Val Ser Ala Thr Ala Asp Glu	
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Val Val Asp Thr Asp Leu Gly Arg Leu Val Ile Val Arg Ala Glu Ile	
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gcc gac gca gaa ggc aac ctg att gct acg ttg gct gag cgt ttc gcg	3379
Ala Asp Ala Glu Gly Asn Leu Ile Ala Thr Leu Ala Glu Arg Phe Ala	
1080 1085 1090	
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Ile Arg Gly Arg Lys Gly Asn Ala Val Ala Arg Thr Asn Thr Ser Ala	
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Leu Pro Thr Thr Val Asp Thr Pro Arg Ser Ala Arg Ala Val Ala Thr	
1110	1115 1120 1125
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Val Val Ala Pro Glu Ser Met Arg Pro Phe Ala Val Ile Ser Gly Asp	
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Lys Val Val Glu Tyr Thr Ala Thr Met Leu Ala Pro Val Leu Pro Gly	
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Gly Met Gly Glu Val Arg Thr Val Thr Ala Thr Val Asn Gly Asn Leu	
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Val Leu Thr Ala Thr Ala Val Val Ala Ala Pro Ser Thr Phe Tyr Ala	
	1240 1245 1250
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Phe Pro Gly Gln Gly Ile Gln Ser Gln Gly Met Gly Met Glu Ala Arg	
	1255 1260 1265
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	1270 1275 1280 1285
acc cgc aat aag ctg ggc ttc tcc atc gtg gaa atc gtg gaa aac aac	4003
Thr Arg Asn Lys Leu Gly Phe Ser Ile Val Glu Ile Val Glu Asn Asn	
	1290 1295 1300
cca cgc gaa gta acc gtg gca ggg gag aag ttc ttc cac cca gac ggc	4051
Pro Arg Glu Val Thr Val Ala Gly Glu Lys Phe Phe His Pro Asp Gly	
	1305 1310 1315
gtt ttg tac ctg acc cag ttc acc cag gtg ggc atg gca act ctg ggc	4099*
Val Leu Tyr Leu Thr Gln Phe Thr Gln Val Gly Met Ala Thr Leu Gly	
	1320 1325 1330
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Val Ala Gln Ile Ala Glu Met Arg Glu Ala His Ala Leu Asn Gln Arg	

1335	1340	1345	
gca tac ttt gct gga cac tcc gtt ggt gag tac aac gcg ctt gct gca			4195
Ala Tyr Phe Ala Gly His Ser Val Gly Glu Tyr Asn Ala Leu Ala Ala			
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tat gct ggt gtg ctg tcc ctg gaa tcc gtt ctg gag atc gtt tac cgt			4243
Tyr Ala Gly Val Leu Ser Leu Glu Ser Val Leu Glu Ile Val Tyr Arg			
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Arg Gly Leu Thr Met His Arg Leu Val Asp Arg Asp Glu Asn Gly Leu			
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Ser Asn Tyr Ala Leu Ala Ala Leu Arg Pro Asn Lys Met Gly Leu Thr			
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Ala Asp Asn Val Phe Asp Tyr Val Ala Ser Val Ser Glu Ala Ser Gly			
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Glu Phe Leu Glu Ile Val Asn Tyr Asn Leu Ala Gly Leu Gln Tyr Ala			
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Asn Arg Ala Pro Gly Gln Arg Ala Phe Ile Leu Ile Pro Gly Ile Asp			
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Val Pro Phe His Ser Ser Lys Leu Arg Asp Gly Val Gly Ala Phe Arg			
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gag cac ctt gat tcc ctg atc cca gct gag ctg gat ctg gat gtg ctg			4627
Glu His Leu Asp Ser Leu Ile Pro Ala Glu Leu Asp Leu Asp Val Leu			
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gtt ggc cgc tac att cca aac ttg gtg gct cgc cca ttc gaa ctc act			4675
Val Gly Arg Tyr Ile Pro Asn Leu Val Ala Arg Pro Phe Glu Leu Thr			
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Glu Glu Phe Val Ala Ser Met Ala Glu Val Val Glu Ser Thr Tyr Val			
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aat gag atc ttg gct gat ttc aag gct gct tcc gcc gat aag cag aag			4771
Asn Glu Ile Leu Ala Asp Phe Lys Ala Ala Ser Ala Asp Lys Gln Lys			
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Leu Ala Arg Thr Leu Leu Ile Glu Leu Leu Ala Trp Gln Phe Ala Ser			
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Pro Val Arg Trp Ile Glu Thr Gln Asp Leu Leu Ile Lys Gly Leu Gln			
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Ala Glu Arg Phe Val Glu Val Gly Val Gly Ser Ala Pro Thr Leu Ala	
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Asp Glu Val Val Arg Glu Val Ala Val Glu Glu Thr Pro Ala Ala Pro	
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Ala Glu Thr Thr Glu Thr Pro Ala Thr Pro Ala Thr Pro Ala Pro Val	
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Ala Ala Ala Ala Pro Ala Thr Gly Gly Pro Arg Pro Asp Asp Ile Ser	
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Phe Thr Pro Ser Asp Ala Thr Glu Met Leu Ile Ala Ile Trp Thr Lys	
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Ile Asp Ala Ala Val Gln Ala Val Ala Ser Arg Arg Gly Val Ala Val	
1850	1855 1860
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Ser Leu Pro Ser Ala Gly Gly Ala Ala Gly Gly Val Val Asp Ser Ala	
1865	1870 1875
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Ala Leu Gly Glu Phe Ala Glu Gln Val Thr Gly His Asp Gly Val Leu	
1880	1885 1890
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Ala Gln Ala Ala Arg Thr Ile Leu Thr Gln Leu Gly Leu Asp Lys Pro	
1895	1900 1905
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Ala Thr Val Ser Val Glu Asp Thr Ala Glu Glu Asp Leu Tyr Glu Leu	
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Val Ser Lys Glu Leu Gly Ser Asp Trp Pro Arg Gln Val Ala Pro Ser	
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Phe Asp Glu Glu Lys Val Val Leu Leu Asp Asp Arg Trp Ala Ser Ala	
1945	1950 1955
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Arg Glu Asp Leu Ser Ala Leu Leu Ala Asn Ser Gln Gln Leu Ile	
1960	1965 1970
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Ser Met Ser Gln Ala Gln Ala Lys Leu Leu Gln His Lys Leu Asn Ser	
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Leu Asp Leu Met Ile Ser Gln Leu Gly Ser Arg Thr Lys Leu Leu Gly	
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2010	

<210> 50

<211> 2012

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

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 35 40 45
 Asn Asn Ser Glu Asp Pro Ala Phe Asp Thr Ala Gln Ser Ala Val Ser
 50 55 60
 Val Pro Gly Ile Phe Val Ser Gln Ile Ala Thr Leu Asp Ser Leu Glu
 65 70 75 80
 Ala Gln Arg Leu Asp Val Asp Gln Ala Val Ser Ser Ile Gly His Ser
 85 90 95
 Gln Gly Val Leu Gly Val His Leu Leu Asn Asp Ala Thr Arg Ala Asp
 100 105 110
 Glu Leu Val Ala Ile Ala Gln Leu Ile Gly Ala Ala Ile Thr Arg Thr
 115 120 125
 Ala Arg Met Thr Gly Leu Ile Ala Gln Gly Asp Asn Met Pro Met Leu
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 Ser Ile Ala Gly Ile Ser Arg Glu Gln Leu Gln Gln Ala Ile Asp Ala
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 Ala Cys Ala Glu Val Pro Ala Glu Ile Arg Pro Val Ile Gly Leu Arg
 165 170 175
 Asn Ser Arg Asp Ser Tyr Val Leu Val Gly Arg Pro Asp Asp Asn Ala
 180 185 190
 Arg Val Val Lys Val Ile Glu Ala Met Ala Ala Lys Asp Lys Lys Ala
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 Ile Glu Asp Lys Leu Arg Gly Gly Ser Ala Phe Ser Pro Arg Ile Thr
 210 215 220
 Pro Leu Lys Val Gln Ala Ala Phe His His Pro Ala Met Asn Met Ala
 225 230 235 240
 Val Glu Gln Thr Val Ala Trp Ala Thr Thr Ala Gly Leu Asp Val Glu
 245 250 255
 Leu Thr Arg Glu Ile Ala Ala Asp Val Leu Val Asn Pro Val Asp Trp
 260 265 270
 Val Ala Arg Val Asn Glu Ala Tyr Glu Ala Gly Ala Arg Trp Phe Leu
 275 280 285
 Asp Val Gly Pro Asp Gly Gly Ile Val Lys Leu Thr Ala Asn Ile Leu
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 Glu Gly Arg Gly Ala Asp Ser Phe Tyr Val Gly Asp Ala Ala Gly Gln
 305 310 315 320
 Ala Lys Ile Phe Asp Ala Gly Met Ala Pro Glu Leu Pro Val Asp Tyr
 325 330 335
 Gln Glu Phe Ala Pro Arg Val Glu His Val Asp Gly Thr Pro Arg Leu
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 Val Thr Lys Phe Thr Glu Leu Thr Gly Arg Thr Pro Met Met Leu Ala

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Gly Met Thr Pro Thr Thr	Val Asp Pro Ala Ile Val	Ala Ala Ala Ala
370	375	380
Asn Gly Gly His Trp	Ala Glu Leu Ala Gly Gly Gly	Gln Val Thr Pro
385	390	395
Glu Leu Leu Glu Thr His	Ile Ala Gln Leu Thr Asp Met	Leu Glu Pro
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Gly Ile Asn Ala Gln Phe	Asn Ser Met Phe Leu Asp Pro	Tyr Leu Trp
420	425	430
Lys Met Gln Ile Gly Gly	Lys Arg Leu Val Pro Lys	Ala Arg Ala Asn
435	440	445
Gly Ala Ser Ile Asp Gly	Ile Val Ile Thr Ala Gly	Ile Pro Glu Lys
450	455	460
Asp Glu Ala Val Ala Leu	Val Lys Glu Leu Met Arg	Asp Gly Phe Pro
465	470	475
Trp Ile Ala Phe Lys Pro	Gly Ala Ile Lys Gln Val	Asn Ser Val Leu
485	490	495
Ala Ile Ala Lys Glu Val	Pro Glu Leu Pro Ile Ile	Ile Gln Ile Glu
500	505	510
Gly Gly Val Ala Gly Gly	His His Ser Trp Glu Asp	Leu Asp Glu Leu
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Leu Ile Ala Thr Tyr Gly	Lys Val Arg Ala Leu Asp	Asn Val Val Leu
530	535	540
Cys Val Gly Gly Gly Ile	Gly Ser Pro Glu Arg Ala	Ala Asp Tyr Val
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Thr Gly Ser Trp Ser Thr	Ser Tyr Gly Leu Pro Ala	Met Pro Val Asp
565	570	575
Gly Ile Leu Val Gly Thr	Ala Ala Met Ala Thr Lys	Glu Ala Thr Thr
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Ser Gln Ala Val Lys Glu	Leu Leu Val Ser Thr Gln	Gly Ser Asp Glu
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Trp Val Pro Ala Gly Gly	Ala Lys Asn Gly Met Ala	Ser Gly Arg Ser
610	615	620
Gln Leu Gly Ala Asp Ile	His Glu Ile Asp Asn Ser	Phe Ala Lys Ala
625	630	635
Gly Arg Leu Leu Asp Glu	Val Ala Gly Asp Glu Thr	Ala Val Gln Ala
645	650	655
Arg Arg Asp Glu Ile Ile	Glu Ala Ile Gly Lys Thr	Ala Lys Val Tyr
660	665	670
Phe Gly Asp Ile Gly Ser	Met Thr Tyr Glu Gln Trp	Leu Asn Arg Tyr
675	680	685

Leu Glu Leu Ser Gly Pro Val Asp Gly Gln Trp Ile Asp Ala Ser Trp
 690 695 700
 Ala Ala Arg Phe Ala Gln Met Leu Glu Arg Ala Glu Ala Arg Leu Ile
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 Glu Gln Asp His Gly Gln Phe Glu Pro Ser Leu Thr Val Glu Asp Gly
 725 730 735
 Val Asp Lys Leu Val Ala Ala Tyr Pro His Ala Ala Thr Asp Leu Leu
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 Thr Pro Ala Asp Val Ala Trp Phe Leu Gly Leu Cys Arg Thr Pro Gly
 755 760 765
 Lys Pro Val Asn Phe Val Pro Val Ile Asp Lys Asp Val Arg Arg Trp
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 Trp Arg Ser Asp Ser Leu Trp Gln Ser His Asp Asp Arg Tyr Thr Ala
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 Asp Gln Val Ala Ile Ile Pro Gly Val Val Ala Val Ala Gly Ile Thr
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 Lys Ala Asn Glu Pro Val Ala Asp Leu Leu Asp Arg Phe Val Asp Ala
 820 825 830
 Thr Ile Glu Arg Ile Asp Glu His Asp Ser Arg Ser Arg Asp Ile Met
 835 840 845
 Gly Lys Val Leu Ser Ser Pro Gly Thr Phe Trp Ala Gly Arg Asn Ile
 850 855 860
 Pro Ser Val Ile His Ser Leu Gly His Ala Asp Lys Trp Ser Arg Ser
 865 870 875 880
 Glu Phe Glu Ala Phe His Ser Pro Thr Gly Ala Asn Leu Val Tyr Glu
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 Asp Ala Glu His Ala Met Leu Thr Val Pro Leu Ala Gly Ser Thr Ala
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 Phe Gly Thr Thr Ala Glu Leu Lys Ile Arg Phe Thr Ser Pro Ile Asp
 915 920 925
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 930 935 940
 Ala Met Gly Glu Leu Thr Arg Ile Ala Ala Gly Gly Thr Leu Ala Thr
 945 950 955 960
 Val Asn Asn Gly Thr Ala Thr Trp Glu Thr Ser Val Asp Ala Gly Val
 965 970 975
 Ile Ala Asp Tyr Asn Asn Val Thr Ala Gly Tyr Leu Pro Ala Ser Val
 980 985 990
 Val Pro Ala His Thr Ala Pro Asp Val Leu Val Gly Arg Ala Trp Pro
 995 1000 1005

Ala Val Phe Ala Ala Val Lys Ser Ala Val Ile Pro Gly Thr Asp Ser
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Ala Ser Val Val Glu Gly Met Leu Ser Leu Val His Leu Glu His His
1025 1030 1035 1040

Ile Val Leu Lys Ser Asp Val Pro Thr Asp Gly Ala Leu Lys Val Ser
1045 1050 1055

Ala Thr Ala Asp Glu Val Val Asp Thr Asp Leu Gly Arg Leu Val Ile
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Val Arg Ala Glu Ile Ala Asp Ala Glu Gly Asn Leu Ile Ala Thr Leu
1075 1080 1085

Ala Glu Arg Phe Ala Ile Arg Gly Arg Lys Gly Asn Ala Val Ala Arg
1090 1095 1100

Thr Asn Thr Ser Ala Leu Pro Thr Thr Val Asp Thr Pro Arg Ser Ala
1105 1110 1115 1120

Arg Ala Val Ala Thr Val Val Ala Pro Glu Ser Met Arg Pro Phe Ala
1125 1130 1135

Val Ile Ser Gly Asp Arg Asn Pro Ile His Val Ser Asp Val Ala Ala
1140 1145 1150

Ser Leu Ala Gly Leu Pro Gly Val Ile Val His Gly Met Trp Thr Ser
1155 1160 1165

Ala Ile Gly Glu Leu Ile Ala Gly Ala Ala Phe Asn Asp Glu Gln Ile
1170 1175 1180

Gln Thr Pro Ala Ala Lys Val Val Glu Tyr Thr Ala Thr Met Leu Ala
1185 1190 1195 1200

Pro Val Leu Pro Gly Glu Glu Ile Glu Phe Ser Val Glu Arg Ser Ala
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Val Asp Asn Arg Pro Gly Met Gly Glu Val Arg Thr Val Thr Ala Thr
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Val Asn Gly Asn Leu Val Leu Thr Ala Thr Ala Val Val Ala Ala Pro
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Ser Thr Phe Tyr Ala Phe Pro Gly Gln Gly Ile Gln Ser Gln Gly Met
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Gly Met Glu Ala Arg Arg Asn Ser Gln Ala Ala Arg Ala Ile Trp Asp
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Arg Ala Asp Ala His Thr Arg Asn Lys Leu Gly Phe Ser Ile Val Glu
1285 1290 1295

Ile Val Glu Asn Asn Pro Arg Glu Val Thr Val Ala Gly Glu Lys Phe
1300 1305 1310

Phe His Pro Asp Gly Val Leu Tyr Leu Thr Gln Phe Thr Gln Val Gly
1315 1320 1325

Met Ala Thr Leu Gly Val Ala Gln Ile Ala Glu Met Arg Glu Ala His

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Ala Leu Asn Gln Arg Ala Tyr Phe Ala Gly His Ser Val Gly Glu Tyr			
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Asn Ala Leu Ala Ala Tyr Ala Gly Val Leu Ser Leu Glu Ser Val Leu			
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Glu Ile Val Tyr Arg Arg Gly Leu Thr Met His Arg Leu Val Asp Arg			
	1380	1385	1390
Asp Glu Asn Gly Leu Ser Asn Tyr Ala Leu Ala Ala Leu Arg Pro Asn			
	1395	1400	1405
Lys Met Gly Leu Thr Ala Asp Asn Val Phe Asp Tyr Val Ala Ser Val			
	1410	1415	1420
Ser Glu Ala Ser Gly Glu Phe Leu Glu Ile Val Asn Tyr Asn Leu Ala			
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			1440
Gly Leu Gln Tyr Ala Val Ala Gly Thr Gln Ala Gly Leu Ala Ala Leu			
	1445	1450	1455
Arg Ala Asp Val Glu Asn Arg Ala Pro Gly Gln Arg Ala Phe Ile Leu			
	1460	1465	1470
Ile Pro Gly Ile Asp Val Pro Phe His Ser Ser Lys Leu Arg Asp Gly			
	1475	1480	1485
Val Gly Ala Phe Arg Glu His Leu Asp Ser Leu Ile Pro Ala Glu Leu			
	1490	1495	1500
Asp Leu Asp Val Leu Val Gly Arg Tyr Ile Pro Asn Leu Val Ala Arg			
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			1520
Pro Phe Glu Leu Thr Glu Glu Phe Val Ala Ser Met Ala Glu Val Val			
	1525	1530	1535
Glu Ser Thr Tyr Val Asn Glu Ile Leu Ala Asp Phe Lys Ala Ala Ser			
	1540	1545	1550
Ala Asp Lys Gln Lys Leu Ala Arg Thr Leu Leu Ile Glu Leu Leu Ala			
	1555	1560	1565
Trp Gln Phe Ala Ser Pro Val Arg Trp Ile Glu Thr Gln Asp Leu Leu			
	1570	1575	1580
Ile Lys Gly Leu Gln Ala Glu Arg Phe Val Glu Val Gly Val Gly Ser			
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			1600
Ala Pro Thr Leu Ala Asn Met Met Gly Gln Thr Leu Arg Leu Pro Gln			
	1605	1610	1615
Tyr Ala Asp Ala Thr Ile Glu Val Leu Asn Ile Glu Arg Asp Arg Pro			
	1620	1625	1630
Val Val Phe Ala Thr Asp Glu Val Val Arg Glu Val Ala Val Glu Glu			
	1635	1640	1645
Thr Pro Ala Ala Pro Ala Glu Thr Thr Glu Thr Pro Ala Thr Pro Ala			
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Thr Pro Ala Pro Val Ala Ala Ala Pro Ala Thr Gly Gly Pro Arg
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 Pro Asp Asp Ile Ser Phe Thr Pro Ser Asp Ala Thr Glu Met Leu Ile
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 Ala Ile Trp Thr Lys Val Arg Pro Asp Gln Met Gly Ala Thr Asp Ser
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 Ile Glu Thr Leu Val Glu Gly Val Ser Ser Arg Arg Asn Gln Leu Leu
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 Leu Asp Leu Gly Val Glu Phe Gly Leu Gly Ala Ile Asp Gly Ala Ala
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 Asp Ala Glu Leu Gly Asp Leu Lys Val Thr Val Ser Lys Met Ala Lys
 1745 1750 1755 1760
 Gly Tyr Lys Ala Phe Gly Pro Val Leu Ser Asp Ala Ala Ala Asp Ala
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 Leu Arg Arg Leu Thr Gly Pro Thr Gly Lys Arg Pro Gly Tyr Ile Ala
 1780 1785 1790
 Glu Arg Val Thr Gly Thr Trp Glu Leu Gly Gln Gly Trp Ala Asp His
 1795 1800 1805
 Val Val Ala Glu Val Val Ile Gly Ala Arg Glu Gly Ala Ser Leu Arg
 1810 1815 1820
 Gly Gly Asp Leu Ala Ser Leu Ser Pro Ala Ser Pro Ala Ser Ala Ser
 1825 1830 1835 1840
 Asp Leu Asp Ser Leu Ile Asp Ala Ala Val Gln Ala Val Ala Ser Arg
 1845 1850 1855
 Arg Gly Val Ala Val Ser Leu Pro Ser Ala Gly Gly Ala Ala Gly Gly
 1860 1865 1870
 Val Val Asp Ser Ala Ala Leu Gly Glu Phe Ala Glu Gln Val Thr Gly
 1875 1880 1885
 His Asp Gly Val Leu Ala Gln Ala Ala Arg Thr Ile Leu Thr Gln Leu
 1890 1895 1900
 Gly Leu Asp Lys Pro Ala Thr Val Ser Val Glu Asp Thr Ala Glu Glu
 1905 1910 1915 1920
 Asp Leu Tyr Glu Leu Val Ser Lys Glu Leu Gly Ser Asp Trp Pro Arg
 1925 1930 1935
 Gln Val Ala Pro Ser Phe Asp Glu Glu Lys Val Val Leu Leu Asp Asp
 1940 1945 1950
 Arg Trp Ala Ser Ala Arg Glu Asp Leu Ser Ala Leu Leu Leu Ala Asn
 1955 1960 1965
 Ser Gln Gln Leu Ile Ser Met Ser Gln Ala Gln Ala Lys Leu Leu Gln
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 Val Thr Glu Leu Ser
 1 5
 agg aac ttc ggg gcc agc cga ctg att aac cgc ttt ggc cag gag cct 163
 Arg Asn Phe Gly Ala Ser Arg Leu Ile Asn Arg Phe Gly Gln Glu Pro
 10 15 20
 ttt gcc ttc gct ttc gcc ggc caa gga tat gac tgg ttg aag acc ctt 211
 Phe Ala Phe Ala Phe Ala Gly Gln Gly Tyr Asp Trp Leu Lys Thr Leu
 25 30 35
 cgt gcc gcg gtt gcc gca ggt gca ggc acc aat gtt agt gac atc gtc 259
 Arg Ala Ala Val Ala Ala Gly Ala Gly Thr Asn Val Ser Asp Ile Val
 40 45 50
 gag cgc gca aat gcg ctg ctt gca cta gtt gca gat gat ctc att ggc 307
 Glu Arg Ala Asn Ala Leu Leu Ala Leu Val Ala Asp Asp Leu Ile Gly
 55 60 65
 acc ctt cca ttt ggt ttc gat cca gtg gct tgg gct aac aac tcc gaa 355
 Thr Leu Pro Phe Gly Phe Asp Pro Val Ala Trp Ala Asn Asn Ser Glu
 70 75 80 85
 gat cca gct ttc gat act gca caa tct gca gtg agc gtg ccg ggt atc 403
 Asp Pro Ala Phe Asp Thr Ala Gln Ser Ala Val Ser Val Pro Gly Ile
 90 95 100
 ttt gtc tcc cag atc gca acc ctg gat tcc ctt gag gcg cag cgc ctt 451
 Phe Val Ser Gln Ile Ala Thr Leu Asp Ser Leu Glu Ala Gln Arg Leu
 105 110 115
 gat gtg gat cag gct gtg tcc agc att ggt cat tcc cag ggc gta ttg 499
 Asp Val Asp Gln Ala Val Ser Ser Ile Gly His Ser Gln Gly Val Leu
 120 125 130
 ggc gtg cac ctg ctc aat gat gcg act cgt gct gat gaa ctc gtt gcc 547
 Gly Val His Leu Leu Asn Asp Ala Thr Arg Ala Asp Glu Leu Val Ala
 135 140 145
 att gcg cag ttg atc ggt gca gcg atc acc cgc acc gca cgc atg acg 595

Ile	Ala	Gln	Leu	Ile	Gly	Ala	Ala	Ile	Thr	Arg	Thr	Ala	Arg	Met	Thr		
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ggc	ctg	atc	gcg	cag	ggc	gac	aac	atg	ccg	atg	ctg	tcg	atc	gcc	gga	643	
Gly	Leu	Ile	Ala	Gln	Gly	Asp	Asn	Met	Pro	Met	Leu	Ser	Ile	Ala	Gly		
				170					175					180			
att	tcc	cgc	gaa	cag	ctt	cag	caa	gct	atc	gac	gcg	gcc	tgc	gcc	gaa	691	
Ile	Ser	Arg	Glu	Gln	Leu	Gln	Gln	Ala	Ile	Asp	Ala	Ala	Cys	Ala	Glu		
			185					190					195				
gtc	cct	gcg	gag	atc	cgc	ccg	gtt	atc	ggg	ctg	cgc	aac	tca	cgc	gat	739	
Val	Pro	Ala	Glu	Ile	Arg	Pro	Val	Ile	Gly	Leu	Arg	Asn	Ser	Arg	Asp		
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tct	tat	gtt	ttg	gtt	ggc	cgc	cca	gac	gac	aac	gct	cgc	gtt	gtt	aag	787	
Ser	Tyr	Val	Leu	Val	Gly	Arg	Pro	Asp	Asp	Asn	Ala	Arg	Val	Val	Lys		
	215					220					225						
gtc	att	gag	gca	atg	gct	gcc	aag	gat	aag	aag	gcc	att	gaa	gat	aag	835	
Val	Ile	Glu	Ala	Met	Ala	Ala	Lys	Asp	Lys	Lys	Ala	Ile	Glu	Asp	Lys		
230					235						240				245		
ctg	cgc	ggc	ggg	tcc	gcg	ttc	agc	ccc	cgt	att	act	ccg	ctg	aag	gtg	883	
Leu	Arg	Gly	Gly	Ser	Ala	Phe	Ser	Pro	Arg	Ile	Thr	Pro	Leu	Lys	Val		
				250					255					260			
cag	gct	gct	ttc	cat	cac	cca	gct	atg	aac	atg	gct	gtg	gag	cag	acc	931	
Gln	Ala	Ala	Phe	His	His	Pro	Ala	Met	Asn	Met	Ala	Val	Glu	Gln	Thr		
			265					270					275				
gtg	gcg	tgg	gca	acc	act	gct	ggg	ttg	gat	gtg	gaa	ctc	acc	cgc	gag	979	
Val	Ala	Trp	Ala	Thr	Thr	Ala	Gly	Leu	Asp	Val	Glu	Leu	Thr	Arg	Glu		
		280					285					290					
atc	gcc	gct	gat	gtt	ttg	gtt	aac	cct	gtc	gat	tgg	gta	gca	cgc	gtc	1027	
Ile	Ala	Ala	Asp	Val	Leu	Val	Asn	Pro	Val	Asp	Trp	Val	Ala	Arg	Val		
	295					300					305						
aac	gaa	gcg	tat	gag	gct	ggc	gct	cgc	tgg	ttc	ctc	gac	gtt	gga	cca	1075	
Asn	Glu	Ala	Tyr	Glu	Ala	Gly	Ala	Arg	Trp	Phe	Leu	Asp	Val	Gly	Pro		
310					315					320				325			
gat	ggg	ggc	atc	gtt	aag	ctg	act	gcc	aac	atc	ctt	gag	ggc	cgc	ggc	1123	
Asp	Gly	Gly	Ile	Val	Lys	Leu	Thr	Ala	Asn	Ile	Leu	Glu	Gly	Arg	Gly		
				330					335					340			
gcg	gat	tcc	ttc	tat	gtt	ggg	gac	gcc	gca	ggc	cag	gcc	aag	ata	ttt	1171	
Ala	Asp	Ser	Phe	Tyr	Val	Gly	Asp	Ala	Ala	Gly	Gln	Ala	Lys	Ile	Phe		
			345					350					355				
gat	gct	ggc	atg	gca	cct	gaa	ctt	cca	gtg	gat	tac	cag	gag	ttc	gca	1219	
Asp	Ala	Gly	Met	Ala	Pro	Glu	Leu	Pro	Val	Asp	Tyr	Gln	Glu	Phe	Ala		
			360				365					370					
cca	cgc	gtt	gag	cac	gtt	gat	gga	acc	cca	cgc	ctg	gtt	acc	aag	ttc	1267	
Pro	Arg	Val	Glu	His	Val	Asp	Gly	Thr	Pro	Arg	Leu	Val	Thr	Lys	Phe		
			375			380					385						
act	gag	ctg	acc	ggc	cgc	acc	cca	atg	atg	ctg	gct	ggc	atg	acc	cca	1315	
Thr	Glu	Leu	Thr	Gly	Arg	Thr	Pro	Met	Met	Leu	Ala	Gly	Met	Thr	Pro		

390	395	400	405	
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Thr Thr Val Asp Pro Ala Ile Val Ala Ala Ala Asn Gly Gly His				
410 415 420				
tgg gct gag ctc gct ggt ggc gga cag gtt acc cca gag ctg ctg gaa	1411			
Trp Ala Glu Leu Ala Gly Gly Gly Gln Val Thr Pro Glu Leu Leu Glu				
425 430 435				
acc cac atc gca cag ctc acc gac atg ctt gag cca ggt atc aac gcc	1459			
Thr His Ile Ala Gln Leu Thr Asp Met Leu Glu Pro Gly Ile Asn Ala				
440 445 450				
cag ttc aac tcc atg ttc ttg gat cca tac ctg tgg aag atg cag att	1507			
Gln Phe Asn Ser Met Phe Leu Asp Pro Tyr Leu Trp Lys Met Gln Ile				
455 460 465				
ggt ggc aag cgc ctt gtt cct aag gcc cgc gct aat ggt gca tcc atc	1555			
Gly Gly Lys Arg Leu Val Pro Lys Ala Arg Ala Asn Gly Ala Ser Ile				
470 475 480 485				
gac ggc atc gtc atc acc gcc ggc att cct gaa aag gat gaa gct gtt	1603			
Asp Gly Ile Val Ile Thr Ala Gly Ile Pro Glu Lys Asp Glu Ala Val				
490 495 500				
gca ttg gtc aag gaa ctg atg cgt gat ggt ttc cct tgg atc gca ttc	1651			
Ala Leu Val Lys Glu Leu Met Arg Asp Gly Phe Pro Trp Ile Ala Phe				
505 510 515				
aag cca ggt gcc atc aag cag gtt aac tct gtg ttg gct atc gct aag	1699			
Lys Pro Gly Ala Ile Lys Gln Val Asn Ser Val Leu Ala Ile Ala Lys				
520 525 530				
gaa gtt cca gaa ctc ccc atc atc att cag att gag ggt ggc gtt gca	1747			
Glu Val Pro Glu Leu Pro Ile Ile Ile Gln Ile Glu Gly Gly Val Ala				
535 540 545				
ggt gga cac cac tct tgg gaa gac ctc gat gag ctg ctg atc gcc acc	1795			
Gly Gly His His Ser Trp Glu Asp Leu Asp Glu Leu Leu Ile Ala Thr				
550 555 560 565				
tac ggc aag gtc cgc gca ctg gat aac gtg gtg ctg tgt gtc ggc ggt	1843			
Tyr Gly Lys Val Arg Ala Leu Asp Asn Val Val Leu Cys Val Gly Gly				
570 575 580				
ggc att ggc tca cct gag cgc gct gct gat tac gtc acc ggt tcc tgg	1891			
Gly Ile Gly Ser Pro Glu Arg Ala Ala Asp Tyr Val Thr Gly Ser Trp				
585 590 595				
tcc act tcc tac ggc ctg cca gct atg cct gtt gat ggc atc ttg gtg	1939			
Ser Thr Ser Tyr Gly Leu Pro Ala Met Pro Val Asp Gly Ile Leu Val				
600 605 610				
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Gly Thr Ala Ala Met Ala Thr Lys Glu Ala Thr Thr Ser Gln Ala Val				
615 620 625				
aag gaa ctt ctt gtt tcc acc cag ggc tct gat gaa tgg gtt cct gct	2035			
Lys Glu Leu Leu Val Ser Thr Gln Gly Ser Asp Glu Trp Val Pro Ala				
630 635 640 645				

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 gac atc cac gag atc gac aac tcc ttt gct aag gct gga cgc ctt ctt 2131
 Asp Ile His Glu Ile Asp Asn Ser Phe Ala Lys Ala Gly Arg Leu Leu
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 gat gag gtt gca ggc cat gaa acg gat ttg caa gcg cgc ccg gat gag 2179
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 35 40 45
 Val Ser Asp Ile Val Glu Arg Ala Asn Ala Leu Leu Ala Leu Val Ala
 50 55 60
 Asp Asp Leu Ile Gly Thr Leu Pro Phe Gly Phe Asp Pro Val Ala Trp
 65 70 75 80
 Ala Asn Asn Ser Glu Asp Pro Ala Phe Asp Thr Ala Gln Ser Ala Val
 85 90 95
 Ser Val Pro Gly Ile Phe Val Ser Gln Ile Ala Thr Leu Asp Ser Leu
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 Glu Ala Gln Arg Leu Asp Val Asp Gln Ala Val Ser Ser Ile Gly His
 115 120 125
 Ser Gln Gly Val Leu Gly Val His Leu Leu Asn Asp Ala Thr Arg Ala
 130 135 140
 Asp Glu Leu Val Ala Ile Ala Gln Leu Ile Gly Ala Ala Ile Thr Arg
 145 150 155 160
 Thr Ala Arg Met Thr Gly Leu Ile Ala Gln Gly Asp Asn Met Pro Met
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 Leu Ser Ile Ala Gly Ile Ser Arg Glu Gln Leu Gln Gln Ala Ile Asp
 180 185 190
 Ala Ala Cys Ala Glu Val Pro Ala Glu Ile Arg Pro Val Ile Gly Leu

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225				230						235					240
Ala	Ile	Glu	Asp	Lys	Leu	Arg	Gly	Gly	Ser	Ala	Phe	Ser	Pro	Arg	Ile
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Thr	Pro	Leu	Lys	Val	Gln	Ala	Ala	Phe	His	His	Pro	Ala	Met	Asn	Met
			260					265					270		
Ala	Val	Glu	Gln	Thr	Val	Ala	Trp	Ala	Thr	Thr	Ala	Gly	Leu	Asp	Val
			275				280					285			
Glu	Leu	Thr	Arg	Glu	Ile	Ala	Ala	Asp	Val	Leu	Val	Asn	Pro	Val	Asp
	290					295					300				
Trp	Val	Ala	Arg	Val	Asn	Glu	Ala	Tyr	Glu	Ala	Gly	Ala	Arg	Trp	Phe
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Leu	Asp	Val	Gly	Pro	Asp	Gly	Gly	Ile	Val	Lys	Leu	Thr	Ala	Asn	Ile
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Leu	Glu	Gly	Arg	Gly	Ala	Asp	Ser	Phe	Tyr	Val	Gly	Asp	Ala	Ala	Gly
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Gln	Ala	Lys	Ile	Phe	Asp	Ala	Gly	Met	Ala	Pro	Glu	Leu	Pro	Val	Asp
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Tyr	Gln	Glu	Phe	Ala	Pro	Arg	Val	Glu	His	Val	Asp	Gly	Thr	Pro	Arg
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Leu	Val	Thr	Lys	Phe	Thr	Glu	Leu	Thr	Gly	Arg	Thr	Pro	Met	Met	Leu
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Ala	Gly	Met	Thr	Pro	Thr	Thr	Val	Asp	Pro	Ala	Ile	Val	Ala	Ala	Ala
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Ala	Asn	Gly	Gly	His	Trp	Ala	Glu	Leu	Ala	Gly	Gly	Gly	Gln	Val	Thr
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Pro	Glu	Leu	Leu	Glu	Thr	His	Ile	Ala	Gln	Leu	Thr	Asp	Met	Leu	Glu
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Pro	Gly	Ile	Asn	Ala	Gln	Phe	Asn	Ser	Met	Phe	Leu	Asp	Pro	Tyr	Leu
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Trp	Lys	Met	Gln	Ile	Gly	Gly	Lys	Arg	Leu	Val	Pro	Lys	Ala	Arg	Ala
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Asn	Gly	Ala	Ser	Ile	Asp	Gly	Ile	Val	Ile	Thr	Ala	Gly	Ile	Pro	Glu
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Lys	Asp	Glu	Ala	Val	Ala	Leu	Val	Lys	Glu	Leu	Met	Arg	Asp	Gly	Phe
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Pro	Trp	Ile	Ala	Phe	Lys	Pro	Gly	Ala	Ile	Lys	Gln	Val	Asn	Ser	Val
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 565 570 575
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 Val Thr Gly Ser Trp Ser Thr Ser Tyr Gly Leu Pro Ala Met Pro Val
 595 600 605
 Asp Gly Ile Leu Val Gly Thr Ala Ala Met Ala Thr Lys Glu Ala Thr
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 Thr Ser Gln Ala Val Lys Glu Leu Leu Val Ser Thr Gln Gly Ser Asp
 625 630 635 640
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 645 650 655
 Ser Gln Leu Gly Ala Asp Ile His Glu Ile Asp Asn Ser Phe Ala Lys
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 Trp Ile Asp Ala Ser Trp Ala Ala Arg Phe Ala Gln Met Leu Glu Arg
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 gcc gag gcg cgt ttg atc gag cag gat cat ggc caa ttt gag cca agc 144
 Ala Glu Ala Arg Leu Ile Glu Gln Asp His Gly Gln Phe Glu Pro Ser
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 Leu Thr Val Glu Asp Gly Val Asp Lys Leu Val Ala Ala Tyr Pro His
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gcc gca acc gac ctg ctc acc ccg gct gat gtc gcc tgg ttc ttg ggc	240
Ala Ala Thr Asp Leu Leu Thr Pro Ala Asp Val Ala Trp Phe Leu Gly	
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Leu Cys Arg Thr Pro Gly Lys Pro Val Asn Phe Val Pro Val Ile Asp	
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Lys Asp Val Arg Arg Trp Trp Arg Ser Asp Ser Leu Trp Gln Ser His	
100 105 110	
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Asp Asp Arg Tyr Thr Ala Asp Gln Val Ala Ile Ile Pro Gly Val Val	
115 120 125	
gcc gtt gct ggc atc acc aag gcc aac gaa cct gtc gct gac ctg ctt	432
Ala Val Ala Gly Ile Thr Lys Ala Asn Glu Pro Val Ala Asp Leu Leu	
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Asp Arg Phe Val Asp Ala Thr Ile Glu Arg Ile Asp Glu His Asp Ser	
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Arg Ser Arg Asp Ile Met Gly Lys Val Leu Ser Ser Pro Gly Thr Phe	
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Trp Ala Gly Arg Asn Ile Pro Ser Val Ile His Ser Leu Gly His Ala	
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Asp Lys Trp Ser Arg Ser Glu Phe Glu Ala Phe His Ser Pro Thr Gly	
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Ala Asn Leu Val Tyr Glu Asp Ala Glu His Ala Met Leu Thr Val Pro	
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Phe Thr Ser Pro Ile Asp Ala Leu Pro Ser Ala Val Pro Leu Val Thr	
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Gln Glu Asp Ala Glu Ala Ala Met Gly Glu Leu Thr Arg Ile Ala Ala	
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Gly Gly Thr Leu Ala Thr Val Asn Asn Gly Thr Ala Thr Trp Glu Thr	
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tcc gtc gat gcc ggc gtc atc gct gac tac aac aac gtc acc gca ggc	912
Ser Val Asp Ala Gly Val Ile Ala Asp Tyr Asn Asn Val Thr Ala Gly	
290 295 300	

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Tyr Leu Pro Ala Ser Val Val Pro Ala His Thr Ala Pro Asp Val Leu	
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Val Gly Arg Ala Trp Pro Ala Val Phe Ala Ala Val Lys Ser Ala Val	
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Ile Pro Gly Thr Asp Ser Ala Ser Val Val Glu Gly Met Leu Ser Leu	
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Val His Leu Glu His His Ile Val Leu Lys Ser Asp Val Pro Thr Asp	
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Gly Ala Leu Lys Val Ser Ala Thr Ala Asp Glu Val Val Asp Thr Asp	
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Leu Gly Arg Leu Val Ile Val Arg Ala Glu Ile Ala Asp Ala Glu Gly	
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Asn Leu Ile Ala Thr Leu Ala Glu Arg Phe Ala Ile Arg Gly Arg Lys	
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Gly Asn Ala Val Ala Arg Thr Asn Thr Ser Ala Leu Pro Thr Thr Val	
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Asp Thr Pro Arg Ser Ala Arg Ala Val Ala Thr Val Val Ala Pro Glu	
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tcc atg cgc cca ttc gct gtg atc tcc ggt gac cgc aac cca att cac	1392
Ser Met Arg Pro Phe Ala Val Ile Ser Gly Asp Arg Asn Pro Ile His	
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Val Ser Asp Val Ala Ala Ser Leu Ala Gly Leu Pro Gly Val Ile Val	
465 470 475 480	
cac ggc atg tgg acc tct gcc atc ggt gaa ctg atc gcc ggt gca gca	1488
His Gly Met Trp Thr Ser Ala Ile Gly Glu Leu Ile Ala Gly Ala Ala	
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Phe Asn Asp Glu Gln Ile Gln Thr Pro Ala Ala Lys Val Val Glu Tyr	
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Thr Ala Thr Met Leu Ala Pro Val Leu Pro Gly Glu Glu Ile Glu Phe	
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Ser Val Glu Arg Ser Ala Val Asp Asn Arg Pro Gly Met Gly Glu Val	
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Ala Val Val Ala Ala Pro Ser Thr Phe Tyr Ala Phe Pro Gly Gln Gly	
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Ile Gln Ser Gln Gly Met Gly Met Glu Ala Arg Arg Asn Ser Gln Ala	
580 585 590	
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Ala Arg Ala Ile Trp Asp Arg Ala Asp Ala His Thr Arg Asn Lys Leu	
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Gly Phe Ser Ile Val Glu Ile Val Glu Asn Asn Pro Arg Glu Val Thr	
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Val Ala Gly Glu Lys Phe Phe His Pro Asp Gly Val Leu Tyr Leu Thr	
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Gln Phe Thr Gln Val Gly Met Ala Thr Leu Gly Val Ala Gln Ile Ala	
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Glu Met Arg Glu Ala His Ala Leu Asn Gln Arg Ala Tyr Phe Ala Gly	
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cac tcc gtt ggt gag tac aac gcg ctt gct gca tat gct ggt gtg ctg	2064
His Ser Val Gly Glu Tyr Asn Ala Leu Ala Ala Tyr Ala Gly Val Leu	
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tcc ctg gaa tcc gtt ctg gag atc gtt tac cgt cgt ggc ttg acc atg	2112
Ser Leu Glu Ser Val Leu Glu Ile Val Tyr Arg Arg Gly Leu Thr Met	
690 695 700	
cac cgc ttg gtg gat cgc gat gaa aac ggt ctg tcc aac tac gcg ctc	2160
His Arg Leu Val Asp Arg Asp Glu Asn Gly Leu Ser Asn Tyr Ala Leu	
705 710 715 720	
gca gct ctt cgc ccc aac aag atg ggt ctg acc gca gac aac gtt ttc	2208
Ala Ala Leu Arg Pro Asn Lys Met Gly Leu Thr Ala Asp Asn Val Phe	
725 730 735	
gat tac gtt gcg tct gtt tcc gaa gct tcc ggt gaa ttc ctg gag atc	2256
Asp Tyr Val Ala Ser Val Ser Glu Ala Ser Gly Glu Phe Leu Glu Ile	
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Val Asn Tyr Asn Leu Ala Gly Leu Gln Tyr Ala Val Ala Gly Thr Gln	
755 760 765	
gct ggt ctt gcc gcc ctt cgt gcc gat gtt gag aac cgt gca cca ggt	2352
Ala Gly Leu Ala Ala Leu Arg Ala Asp Val Glu Asn Arg Ala Pro Gly	
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Gln Arg Ala Phe Ile Leu Ile Pro Gly Ile Asp Val Pro Phe His Ser	

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805	810	815		
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Leu Ile Pro Ala Glu Leu Asp Leu Asp Val Leu Val Gly Arg Tyr Ile				
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cca aac ttg gtg gct cgc cca ttc gaa ctc act gaa gag ttc gtg gca	2544			
Pro Asn Leu Val Ala Arg Pro Phe Glu Leu Thr Glu Glu Phe Val Ala				
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tcc atg gca gaa gtg gtg gag tcc acc tat gtc aat gag atc ttg gct	2592			
Ser Met Ala Glu Val Val Glu Ser Thr Tyr Val Asn Glu Ile Leu Ala				
850	855	860		
gat ttc aag gct gct tcc gcc gat aag cag aag ctt gcc cgc acg ttg	2640			
Asp Phe Lys Ala Ala Ser Ala Asp Lys Gln Lys Leu Ala Arg Thr Leu				
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ctt att gag ctg ctt gca tgg cag ttc gca tca cct gtg cgc tgg atc	2688			
Leu Ile Glu Leu Ala Trp Gln Phe Ala Ser Pro Val Arg Trp Ile				
885	890	895		
gag act cag gat ctg ttg atc aag ggc ctt caa gct gag cgt ttc gtg	2736			
Glu Thr Gln Asp Leu Leu Ile Lys Gly Leu Gln Ala Glu Arg Phe Val				
900	905	910		
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Glu Val Gly Val Gly Ser Ala Pro Thr Leu Ala Asn Met Met Gly Gln				
915	920	925		
acc ctg cgc ctt cct cag tac gcg gac gcc acc att gag gtg tta aac	2832			
Thr Leu Arg Leu Pro Gln Tyr Ala Asp Ala Thr Ile Glu Val Leu Asn				
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Ile Glu Arg Asp Arg Pro Val Val Phe Ala Thr Asp Glu Val Val Arg				
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Glu Val Ala Val Glu Glu Thr Pro Ala Ala Pro Ala Glu Thr Thr Glu				
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Thr Pro Ala Thr Pro Ala Thr Pro Ala Pro Val Ala Ala Ala Ala Pro				
980	985	990		
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Ala Thr Gly Gly Pro Arg Pro Asp Asp Ile Ser Phe Thr Pro Ser Asp				
995	1000	1005		
gcc act gaa atg ctc atc gct atc tgg acc aag gtt cgc cca gat cag	3072			
Ala Thr Glu Met Leu Ile Ala Ile Trp Thr Lys Val Arg Pro Asp Gln				
1010	1015	1020		
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Met Gly Ala Thr Asp Ser Ile Glu Thr Leu Val Glu Gly Val Ser Ser				
1025	1030	1035	1040	

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Val Ser Lys Met Ala Lys Gly Tyr Lys Ala Phe Gly Pro Val Leu Ser	
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Asp Ala Ala Ala Asp Ala Leu Arg Arg Leu Thr Gly Pro Thr Gly Lys	
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Arg Pro Gly Tyr Ile Ala Glu Arg Val Thr Gly Thr Trp Glu Leu Gly	
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Glu Gly Ala Ser Leu Arg Gly Gly Asp Leu Ala Ser Leu Ser Pro Ala	
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Ser Pro Ala Ser Ala Ser Asp Leu Asp Ser Leu Ile Asp Ala Ala Val	
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Gly Gly Ala Ala Gly Gly Val Val Asp Ser Ala Ala Leu Gly Glu Phe	
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Thr Ile Leu Thr Gln Leu Gly Leu Asp Lys Pro Ala Thr Val Ser Val	
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gaa gac acc gca gag gaa gac ctc tac gag ttg gtc tcc aag gaa ctc	3744
Glu Asp Thr Ala Glu Glu Asp Leu Tyr Glu Leu Val Ser Lys Glu Leu	
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Gly Ser Asp Trp Pro Arg Gln Val Ala Pro Ser Phe Asp Glu Glu Lys	
1250 1255 1260	
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1265 1270 1275	

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 <211> 1277
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 54

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Trp	Ile	Asp	Ala	Ser	Trp	Ala	Ala	Arg	Phe	Ala	Gln	Met	Leu	Glu	Arg	20	25	30	
Ala	Glu	Ala	Arg	Leu	Ile	Glu	Gln	Asp	His	Gly	Gln	Phe	Glu	Pro	Ser	35	40	45	
Leu	Thr	Val	Glu	Asp	Gly	Val	Asp	Lys	Leu	Val	Ala	Ala	Tyr	Pro	His	50	55	60	
Ala	Ala	Thr	Asp	Leu	Leu	Thr	Pro	Ala	Asp	Val	Ala	Trp	Phe	Leu	Gly	65	70	75	80
Leu	Cys	Arg	Thr	Pro	Gly	Lys	Pro	Val	Asn	Phe	Val	Pro	Val	Ile	Asp	85	90	95	
Lys	Asp	Val	Arg	Arg	Trp	Trp	Arg	Ser	Asp	Ser	Leu	Trp	Gln	Ser	His	100	105	110	
Asp	Asp	Arg	Tyr	Thr	Ala	Asp	Gln	Val	Ala	Ile	Ile	Pro	Gly	Val	Val	115	120	125	
Ala	Val	Ala	Gly	Ile	Thr	Lys	Ala	Asn	Glu	Pro	Val	Ala	Asp	Leu	Leu	130	135	140	
Asp	Arg	Phe	Val	Asp	Ala	Thr	Ile	Glu	Arg	Ile	Asp	Glu	His	Asp	Ser	145	150	155	160
Arg	Ser	Arg	Asp	Ile	Met	Gly	Lys	Val	Leu	Ser	Ser	Pro	Gly	Thr	Phe	165	170	175	
Trp	Ala	Gly	Arg	Asn	Ile	Pro	Ser	Val	Ile	His	Ser	Leu	Gly	His	Ala	180	185	190	
Asp	Lys	Trp	Ser	Arg	Ser	Glu	Phe	Glu	Ala	Phe	His	Ser	Pro	Thr	Gly	195	200	205	
Ala	Asn	Leu	Val	Tyr	Glu	Asp	Ala	Glu	His	Ala	Met	Leu	Thr	Val	Pro	210	215	220	
Leu	Ala	Gly	Ser	Thr	Ala	Phe	Gly	Thr	Thr	Ala	Glu	Leu	Lys	Ile	Arg	225	230	235	240
Phe	Thr	Ser	Pro	Ile	Asp	Ala	Leu	Pro	Ser	Ala	Val	Pro	Leu	Val	Thr	245	250	255	
Gln	Glu	Asp	Ala	Glu	Ala	Ala	Met	Gly	Glu	Leu	Thr	Arg	Ile	Ala	Ala	260	265	270	
Gly	Gly	Thr	Leu	Ala	Thr	Val	Asn	Asn	Gly	Thr	Ala	Thr	Trp	Glu	Thr	275	280	285	

Ser Val Asp Ala Gly Val Ile Ala Asp Tyr Asn Asn Val Thr Ala Gly
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 Tyr Leu Pro Ala Ser Val Val Pro Ala His Thr Ala Pro Asp Val Leu
 305 310 315 320
 Val Gly Arg Ala Trp Pro Ala Val Phe Ala Ala Val Lys Ser Ala Val
 325 330 335
 Ile Pro Gly Thr Asp Ser Ala Ser Val Val Glu Gly Met Leu Ser Leu
 340 345 350
 Val His Leu Glu His His Ile Val Leu Lys Ser Asp Val Pro Thr Asp
 355 360 365
 Gly Ala Leu Lys Val Ser Ala Thr Ala Asp Glu Val Val Asp Thr Asp
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 385 390 395 400
 Asn Leu Ile Ala Thr Leu Ala Glu Arg Phe Ala Ile Arg Gly Arg Lys
 405 410 415
 Gly Asn Ala Val Ala Arg Thr Asn Thr Ser Ala Leu Pro Thr Thr Val
 420 425 430
 Asp Thr Pro Arg Ser Ala Arg Ala Val Ala Thr Val Val Ala Pro Glu
 435 440 445
 Ser Met Arg Pro Phe Ala Val Ile Ser Gly Asp Arg Asn Pro Ile His
 450 455 460
 Val Ser Asp Val Ala Ala Ser Leu Ala Gly Leu Pro Gly Val Ile Val
 465 470 475 480
 His Gly Met Trp Thr Ser Ala Ile Gly Glu Leu Ile Ala Gly Ala Ala
 485 490 495
 Phe Asn Asp Glu Gln Ile Gln Thr Pro Ala Ala Lys Val Val Glu Tyr
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 Thr Ala Thr Met Leu Ala Pro Val Leu Pro Gly Glu Glu Ile Glu Phe
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 Arg Thr Val Thr Ala Thr Val Asn Gly Asn Leu Val Leu Thr Ala Thr
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 Ala Val Val Ala Ala Pro Ser Thr Phe Tyr Ala Phe Pro Gly Gln Gly
 565 570 575
 Ile Gln Ser Gln Gly Met Gly Met Glu Ala Arg Arg Asn Ser Gln Ala
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 Ala Arg Ala Ile Trp Asp Arg Ala Asp Ala His Thr Arg Asn Lys Leu
 595 600 605
 Gly Phe Ser Ile Val Glu Ile Val Glu Asn Asn Pro Arg Glu Val Thr

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Gln	Phe	Thr	Gln	Val	Gly	Met	Ala	Thr	Leu	Gly	Val	Ala	Gln	Ile	Ala
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Glu	Met	Arg	Glu	Ala	His	Ala	Leu	Asn	Gln	Arg	Ala	Tyr	Phe	Ala	Gly
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His	Ser	Val	Gly	Glu	Tyr	Asn	Ala	Leu	Ala	Ala	Tyr	Ala	Gly	Val	Leu
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Ser	Leu	Glu	Ser	Val	Leu	Glu	Ile	Val	Tyr	Arg	Arg	Gly	Leu	Thr	Met
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His	Arg	Leu	Val	Asp	Arg	Asp	Glu	Asn	Gly	Leu	Ser	Asn	Tyr	Ala	Leu
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Val	Asn	Tyr	Asn	Leu	Ala	Gly	Leu	Gln	Tyr	Ala	Val	Ala	Gly	Thr	Gln
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785				790							795				800
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Pro	Asn	Leu	Val	Ala	Arg	Pro	Phe	Glu	Leu	Thr	Glu	Glu	Phe	Val	Ala
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Ser	Met	Ala	Glu	Val	Val	Glu	Ser	Thr	Tyr	Val	Asn	Glu	Ile	Leu	Ala
		850					855					860			
Asp	Phe	Lys	Ala	Ala	Ser	Ala	Asp	Lys	Gln	Lys	Leu	Ala	Arg	Thr	Leu
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Leu	Ile	Glu	Leu	Leu	Ala	Trp	Gln	Phe	Ala	Ser	Pro	Val	Arg	Trp	Ile
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Glu	Val	Gly	Val	Gly	Ser	Ala	Pro	Thr	Leu	Ala	Asn	Met	Met	Gly	Gln
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Thr	Leu	Arg	Leu	Pro	Gln	Tyr	Ala	Asp	Ala	Thr	Ile	Glu	Val	Leu	Asn
		930					935					940			

Ile Glu Arg Asp Arg Pro Val Val Phe Ala Thr Asp Glu Val Val Arg
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 Glu Val Ala Val Glu Glu Thr Pro Ala Ala Pro Ala Glu Thr Thr Glu
 965 970 975
 Thr Pro Ala Thr Pro Ala Thr Pro Ala Pro Val Ala Ala Ala Pro
 980 985 990
 Ala Thr Gly Gly Pro Arg Pro Asp Asp Ile Ser Phe Thr Pro Ser Asp
 995 1000 1005
 Ala Thr Glu Met Leu Ile Ala Ile Trp Thr Lys Val Arg Pro Asp Gln
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 Val Ser Lys Met Ala Lys Gly Tyr Lys Ala Phe Gly Pro Val Leu Ser
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 Arg Pro Gly Tyr Ile Ala Glu Arg Val Thr Gly Thr Trp Glu Leu Gly
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 Gln Gly Trp Ala Asp His Val Val Ala Glu Val Val Ile Gly Ala Arg
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 Gln Ala Val Ala Ser Arg Arg Gly Val Ala Val Ser Leu Pro Ser Ala
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      145             150             155             160

Lys Met Glu Glu Phe Ser Thr Ile Gly Gly Tyr Leu Ser Asp Ile Ser
      165             170             175

Ser Phe Asp Ala Glu Phe Phe Gly Leu Ser Pro Leu Glu Ala Ala Asn
      180             185             190

Met Asp Pro Gln Gln Arg Ile Leu Leu Glu Leu Thr Trp Glu Ala Leu
      195             200             205

Glu Tyr Ala Arg Ile Ala Pro Asn Thr Leu Arg Gly Glu Ala Val Gly
      210             215             220

Val Phe Ile Gly Ser Ser Asn Asn Asp Tyr Gly Met Met Ile Ala Ala
      225             230             235             240

Asp Pro Ala Glu Ala His Pro Tyr Ala Leu Thr Gly Thr Ser Ser Ala
      245             250             255

Ile Val Ala Asn Arg Ile Asn Tyr Ala Phe Asp Phe Arg Gly Pro Ser
      260             265             270

Val Asn Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Val His Gln
      275             280             285

Ala Val Arg Ala Leu Arg Asn Gly Glu Ala Asp His Ala Ile Ala Gly
      290             295             300

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Gly Val Asn Ile Leu Ala Ser Pro Phe Val Thr Thr Ala Phe Ala Glu
 305 310 315 320
 Leu Gly Val Ile Ser Pro Thr Gly Lys Ile His Ala Phe Ser Asp Asp
 325 330 335
 Ala Asp Gly Phe Val Arg Ser Asp Gly Ala Gly Val Val Val Leu Lys
 340 345 350
 Arg Val Asp Asp Ala Ile Arg Asp Gly Asp Lys Ile Ile Gly Val Ile
 355 360 365
 Lys Gly Ser Ala Val Asn Ser Asp Gly His Ser Asn Gly Leu Thr Ala
 370 375 380
 Pro Asn Pro Asp Ala Gln Val Asp Val Leu Gln Arg Ala Tyr Val Asp
 385 390 395 400
 Ala Gln Val Asp Pro Thr Thr Val Asp Tyr Val Glu Ala His Gly Thr
 405 410 415
 Gly Thr Ile Leu Gly Asp Pro Ile Glu Ala Thr Ala Leu Gly Ala Val
 420 425 430
 Leu Gly Tyr Gly Arg Asp Ala Ser Thr Pro Thr Leu Leu Gly Ser Ala
 435 440 445
 Lys Ser Asn Phe Gly His Thr Glu Ser Ala Ala Gly Ile Ala Gly Val
 450 455 460
 Ile Lys Val Leu Leu Ala Leu Gln Asn Lys Thr Leu Pro Pro Thr Val
 465 470 475 480
 Asn Phe Ala Gly Pro Asn Arg Tyr Ile Asp Phe Asp Ala Glu Arg Leu
 485 490 495
 Glu Val Val Glu Asp Pro Arg Glu Trp Pro Glu Tyr Asn Gly His Ala
 500 505 510
 Val Ala Gly Val Ser Ala Phe Gly Phe Gly Gly Thr Asn Ala His Val
 515 520 525
 Val Ile Ser Glu Tyr Asn Ala Glu Asp Tyr Glu Thr Arg Ala Pro Lys
 530 535 540
 Glu Ala Leu Leu Pro Asp Gln Gln Val Ala Leu Pro Val Ser Gly His
 545 550 555 560
 Leu Pro Ser Arg Arg Arg Gln Ala Ala Ala Asp Leu Ala Asp Phe Leu
 565 570 575
 Glu Gly Arg Lys Asp Cys Asp Leu Thr Pro Val Ala Arg Ala Leu Ala
 580 585 590
 Gly Arg Asn His Gly Arg Ser Arg Ala Val Val Leu Ala Ser Thr Ile
 595 600 605
 Glu Glu Ala Val Lys Arg Leu Arg Gln Val Ala Glu Gly Lys Val Ser
 610 615 620

Val Gly Ile Ser Ala Ala Asp Ser Pro Ala Ala Asn Gly Pro Val Phe
 625 630 635 640
 Val Tyr Ser Gly Phe Gly Ser Gln His Arg Leu Met Ile Lys Glu Leu
 645 650 655
 Cys Ser Ile Ser Pro Gln Phe Arg Glu Arg Ile Glu Glu Leu Asp Glu
 660 665 670
 Met Val Lys Phe Glu Ser Gly Trp Ser Ile Met Lys Leu Val Leu Asp
 675 680 685
 Asp Glu Gln Thr Tyr Asp Thr Glu Thr Ala Gln Val Val Ile Thr Ala
 690 695 700
 Ile Gln Ile Ala Leu Thr Asp Leu Leu Ala Ser Phe Gly Val Lys Pro
 705 710 715 720
 Ala Ala Val Met Gly Met Ser Met Gly Glu Ile Ala Ala Ala Tyr Ala
 725 730 735
 Ala Gly Gly Leu Ser Asp Arg Asp Thr Met Leu Ile Ala Ser His Arg
 740 745 750
 Ser Arg Leu Met Gly Glu Gly Glu Lys Ser Leu Ala Glu Asp Gln Leu
 755 760 765
 Gly Ala Met Ala Val Val Glu Phe Ala Ala Ala Asp Leu Asp Lys Phe
 770 775 780
 Ile Glu Glu Asn Pro Glu Tyr Lys Gly Ile Glu Pro Ala Val Tyr Ala
 785 790 795 800
 Gly Pro Gly Met Thr Thr Val Gly Gly Pro Arg Asp Ala Val Val Gln
 805 810 815
 Phe Val Glu Lys Leu Glu Ser Glu Asp Lys Phe Ala Arg Leu Leu Asn
 820 825 830
 Val Lys Gly Ala Gly His Thr Ser Ala Val Glu Pro Leu Leu Gly Glu
 835 840 845
 Leu Ala Gly Glu Ile Ala Gly Ile Glu Pro Leu Pro Leu Gln Ile Pro
 850 855 860
 Leu Phe Ser Ser Val Asp Gln Gly Val Thr Tyr Pro Val Gly Ala Val
 865 870 875 880
 Val His Asp Ala Asp Tyr Met Leu Arg Cys Thr Arg Gln Ser Val Tyr
 885 890 895
 Phe Gln Asp Ser Thr Glu Ala Ala Phe Ala Ala Gly His Asn Thr Leu
 900 905 910
 Val Glu Ile Ser Pro Asn Pro Val Ala Leu Met Gly Met Met Asn Thr
 915 920 925
 Ala Phe Thr Val Gly Lys Pro Asp Ala Gln Leu Leu Phe Ser Leu Lys
 930 935 940
 Arg Lys Val Pro Glu Ala Glu Ser Leu Arg Asp Leu Leu Ala Lys Leu

945	950	955	960
Tyr Val Asn Gly Ala	Asn Val Asp Phe Ser	Ala Leu Tyr Gly Glu Gly	
965	970	975	
Glu Thr Ile Asp Pro Pro His Ile Thr Trp Lys His Gln Arg Phe Trp			
980	985	990	
Thr Ser Ala Arg Pro Ser Ser Gly Ala Ser Leu Asp Leu Pro Gly Phe			
995	1000	1005	
Arg Val Asn Leu Pro Asn Asn Thr Val Ala Phe Ser Thr Ala Ala Glu			
1010	1015	1020	
Leu Ala Pro Ser Ala Val Ala Ile Met Glu Ala Ala Ala Met Ala Val			
1025	1030	1035	1040
Thr Pro Gly Ser Ser Val Asp Ala Val Asp Glu Arg Asp Met Leu Pro			
1045	1050	1055	
Pro Ser Gly Glu Ile Thr Thr Ile Val Thr Arg Ser Leu Gly Gly Leu			
1060	1065	1070	
Ser Leu Ser Val Tyr Lys Ile Glu Gly Thr Thr Ser Thr Leu Val Ala			
1075	1080	1085	
Glu Gly Phe Ala Ala Asn Pro Gly Phe Ala Ala Ala Ser Ser Phe Asp			
1090	1095	1100	
Gly Pro Gly Tyr Asp Gly Phe Asn Thr Asp Tyr Ser Asp Gln Pro Asp			
1105	1110	1115	1120
Pro Arg Ser Asp Leu Pro Leu Asp Ile Glu Ala Val Arg Trp Asp Pro			
1125	1130	1135	
Ala Thr Glu Thr Val Glu Glu Arg Met Arg Ala Ile Val Ser Glu Ala			
1140	1145	1150	
Met Gly Tyr Asp Val Asp Asp Leu Pro Arg Glu Leu Pro Leu Ile Asp			
1155	1160	1165	
Leu Gly Leu Asp Ser Leu Met Gly Met Arg Ile Lys Asn Arg Ile Glu			
1170	1175	1180	
Asn Asp Phe Gln Ile Pro Pro Leu Gln Val Gln Ala Leu Arg Asp Ala			
1185	1190	1195	1200
Ser Val Ala Asp Val Val Ile Met Val Glu Asn Met Val Ala Gly Arg			
1205	1210	1215	
Ser Ser Glu Thr Leu Val Asp Ala Thr Pro Gln Val Pro Ala Glu Ala			
1220	1225	1230	
Ala Gly Glu Ala Gln Ala Ala Glu Ser Ser Ala Ser Gly Glu Asp Val			
1235	1240	1245	
Gln Gly Val Gly Val Ala Pro Arg Asp Ala Ser Glu Arg Met Val Phe			
1250	1255	1260	
Gly Thr Trp Ala Gly Leu Thr Gly Ala Ala Ala Ala Gly Val Thr Ser			
1265	1270	1275	1280

Lys Leu Pro Gln Ile Asp Val Asp Thr Ala Thr Ala Ile Ala Glu Arg
 1285 1290 1295
 Leu Thr Glu Arg Ser Gly Ile Glu Ile Ser Thr Glu Gln Val Leu Ala
 1300 1305 1310
 Ala Glu Thr Leu Glu Pro Leu Ser Asp Leu Val Arg Glu Gly Leu Glu
 1315 1320 1325
 Thr Glu Val Gln Gly Asn Ile Arg Val Leu Arg Gly Arg Ala Glu Gly
 1330 1335 1340
 Ser Thr Lys Pro Ala Val Phe Met Phe His Pro Ala Gly Gly Ser Ser
 1345 1350 1355 1360
 Val Val Tyr Gln Pro Leu Met Arg Arg Leu Pro Glu Asp Val Pro Val
 1365 1370 1375
 Tyr Gly Val Glu Arg Leu Glu Gly Asp Leu Ala Asp Arg Ala Ala Ala
 1380 1385 1390
 Tyr Val Asp Asp Ile Lys Lys Tyr Ser Asp Gly Phe Pro Val Val Leu
 1395 1400 1405
 Gly Gly Trp Ser Phe Gly Gly Ala Val Ala Phe Glu Val Ala His Gln
 1410 1415 1420
 Leu Val Gly Ser Asp Val Glu Val Ala Thr Val Ala Leu Leu Asp Thr
 1425 1430 1435 1440
 Val Gln Pro Ser Asn Pro Ala Pro Asp Thr Ala Glu Glu Thr Arg Ala
 1445 1450 1455
 Arg Trp Thr Arg Tyr Ala Asp Phe Ala Lys Lys Thr Tyr Gly Leu Asp
 1460 1465 1470
 Phe Glu Val Pro Phe Glu Ile Leu Asp Thr Ile Gly Glu Asp Gly Met
 1475 1480 1485
 Leu Ser Met Met Thr Asp Phe Leu Ala Asn Thr Asp Ala Ser Glu His
 1490 1495 1500
 Gly Leu Ser Ala Gly Val Leu Glu His Gln Arg Ala Ser Phe Val Asp
 1505 1510 1515 1520
 Asn Arg Ile Leu Ala Lys Leu Asn Phe Ala Asp Trp Ala Asn Val Glu
 1525 1530 1535
 Ala Pro Val Ile Leu Phe Arg Ala Glu Arg Met His Asp Gly Ala Ile
 1540 1545 1550
 Glu Leu Glu Pro Asn Tyr Ala Lys Ile Asp Gln Asp Gly Gly Trp Ser
 1555 1560 1565
 Gly Ile Val Asn Asp Leu Glu Ile Val Gln Leu Asn Gly Asp His Leu
 1570 1575 1580
 Ala Val Val Asp Glu Pro Glu Ile Gly Thr Val Gly Ala His Leu Ser
 1585 1590 1595 1600

Arg Arg Ile Asp Glu Ile Ser Arg Lys Asn
1605 1610

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<222> (101)..(907)
<223> RXA02691

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Met Asn Thr Met Pro
1 5

gac caa ccg ctc aac cag gac gga ttc cct acc gca tcc aaa ggg gtg 163
Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr Ala Ser Lys Gly Val
10 15 20

gaa ccc gac aac ctc ccc gac cgc gtt ctc gtg gac ggc ctt aaa cca 211
Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val Asp Gly Leu Lys Pro
25 30 35

aag cat cag cag ctt cgt gaa att ttg gag gaa atc tgc acc acc cag 259
Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu Ile Cys Thr Thr Gln
40 45 50

ctt cag cct ggg gac atg ctg cct ggt gag cgc atc ctg gaa gaa aag 307
Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg Ile Leu Glu Glu Lys
55 60 65

tat ggc gtc agc cga att acg gtt cgt cgg gcg att ggt gat ctg gtc 355
Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala Ile Gly Asp Leu Val
70 75 80 85

gcg tcc ggc agg ttg aag cga gct cgc ggc aaa ggt acc ttc gtg gcc 403
Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys Gly Thr Phe Val Ala
90 95 100

cac tcg ccg ttg att tcc cgc ctg cat ttg gcc tcg ttt tcc gca gag 451
His Ser Pro Leu Ile Ser Arg Leu His Leu Ala Ser Phe Ser Ala Glu
105 110 115

atg gcc gcc cag aag cta tcg gct acc agc agg att ttg agt tct tcc 499
Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg Ile Leu Ser Ser Ser
120 125 130

cgc ggt ccc gcc cca gat gat att gct gat ttc ttt ggt acc gat cgc 547
Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe Phe Gly Thr Asp Arg
135 140 145

gcg gcc cag cac atc acg ttg cgc cgc ctg cgc ttt gga aat ggt cga 595
Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg Phe Gly Asn Gly Arg
150 155 160 165

ccc tat gcc att gac aac ggt tgg tac aac tcc gaa ttc gca cct gac 643
 Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser Glu Phe Ala Pro Asp
 170 175 180

ctg ctg gaa aat gat gtg tac aac tcc gtg tac tcc atc ctg gac cgc 691
 Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr Ser Ile Leu Asp Arg
 185 190 195

gtc tat ggc gtc ccc gtc acc cag gcc gag caa acg gtc acc gcc gta 739
 Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln Thr Val Thr Ala Val
 200 205 210

gca gcc gac gaa gac acc gca cgg ctt ctg gac gtc acc ccc ggc gcc 787
 Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp Val Thr Pro Gly Ala
 215 220 225

cca ctc ctt cgt atc ctt cga cag tca ctt tct ggc gat aag ccc gtg 835
 Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser Gly Asp Lys Pro Val
 230 235 240 245

gaa tgg tgc gtt tcc ttg tac cga acc gac cga tat tct tta aaa aca 883
 Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg Tyr Ser Leu Lys Thr
 250 255 260

ttg gtt aca cgc tcc gaa gat ctc tgacgtgaac ccattttggt ggc 930
 Leu Val Thr Arg Ser Glu Asp Leu
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<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

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Ala Ser Lys Gly Val Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val
 20 25 30

Asp Gly Leu Lys Pro Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu
 35 40 45

Ile Cys Thr Thr Gln Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg
 50 55 60

Ile Leu Glu Glu Lys Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala
 65 70 75 80

Ile Gly Asp Leu Val Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys
 85 90 95

Gly Thr Phe Val Ala His Ser Pro Leu Ile Ser Arg Leu His Leu Ala
 100 105 110

Ser Phe Ser Ala Glu Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg
 115 120 125

Ile Leu Ser Ser Ser Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe
 130 135 140

Phe Gly Thr Asp Arg Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg
145 150 155 160

Phe Gly Asn Gly Arg Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser
165 170 175

Glu Phe Ala Pro Asp Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr
180 185 190

Ser Ile Leu Asp Arg Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln
195 200 205

Thr Val Thr Ala Val Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp
210 215 220

Val Thr Pro Gly Ala Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser
225 230 235 240

Gly Asp Lys Pro Val Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg
245 250 255

Tyr Ser Leu Lys Thr Leu Val Thr Arg Ser Glu Asp Leu
260 265

<210> 59

<211> 1968

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1945)

<223> RXA00880

<400> 59

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Met Thr Ser Pro Asn
1 5

acc ctg cag gaa tac act gaa cct gcc aag tac acc atc gga gaa tct 163
Thr Leu Gln Glu Tyr Thr Glu Pro Ala Lys Tyr Thr Ile Gly Glu Ser
10 15 20

gaa acc tgc ctg acc gcc ctt cta gat cag att aag act cga cct tac 211
Glu Thr Cys Leu Thr Ala Leu Leu Asp Gln Ile Lys Thr Arg Pro Tyr
25 30 35

gga gtt ttg ttc agc aag cct gcc aac tat gag tgg gtg aat gta act 259
Gly Val Leu Phe Ser Lys Pro Ala Asn Tyr Glu Trp Val Asn Val Thr
40 45 50

gcc aaa gaa ttt cag gac gag gtt ttt gcg gtt gca aaa gga att att 307
Ala Lys Glu Phe Gln Asp Glu Val Phe Ala Val Ala Lys Gly Ile Ile
55 60 65

tca gtc ggc gta gag cag gga gac cgt gtc gcg ctg ctg tcc aat act 355
Ser Val Gly Val Glu Gln Gly Asp Arg Val Ala Leu Leu Ser Asn Thr

70	75	80	85	
cgc tat gag tgg gct gtg ctt gat ttc gct atc tgg gcc gct ggc gca				403
Arg Tyr Glu Trp Ala Val Leu Asp Phe Ala Ile Trp Ala Ala Gly Ala				
	90	95	100	
gtg agc gtg cct atc tac agc tcc tct tca ctg tcc caa att gag tgg				451
Val Ser Val Pro Ile Tyr Ser Ser Ser Ser Leu Ser Gln Ile Glu Trp				
	105	110	115	
atc att gag gat tcc ggc gct gtt ttg gcc att acc gaa acc cct gat				499
Ile Ile Glu Asp Ser Gly Ala Val Leu Ala Ile Thr Glu Thr Pro Asp				
	120	125	130	
cat acc gac ttg atg aag aac ctg gtc atc ggt gaa gac gga act cca				547
His Thr Asp Leu Met Lys Asn Leu Val Ile Gly Glu Asp Gly Thr Pro				
	135	140	145	
gcg att aag ggt tca cct tcc aag ctg cgc cgc att cta gag atc aac				595
Ala Ile Lys Gly Ser Pro Ser Lys Leu Arg Arg Ile Leu Glu Ile Asn				
	150	155	160	165
tct tcg gcg ttg gag acc ttg aag ttt gag ggc cgc gag ctt tct gat				643
Ser Ser Ala Leu Glu Thr Leu Lys Phe Glu Gly Arg Glu Leu Ser Asp				
	170	175	180	
gag ctg gtg tgg gaa cgc att cat gca acc aag gcc gct gac ctg gcg				691
Glu Leu Val Trp Glu Arg Ile His Ala Thr Lys Ala Ala Asp Leu Ala				
	185	190	195	
tct ttg gtg tac acc tct ggc aca act ggt agg ccg aag ggc tgc gag				739
Ser Leu Val Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys Gly Cys Glu				
	200	205	210	
ttg tcc cac tac cac tgg ttg gct gag gtc cga gcg ctg atc acc aat				787
Leu Ser His Tyr His Trp Leu Ala Glu Val Arg Ala Leu Ile Thr Asn				
	215	220	225	
gac atc gga gcg atc gcg atg cca ggt tca agg ttg ctc acc ttc ctt				835
Asp Ile Gly Ala Ile Ala Met Pro Gly Ser Arg Leu Leu Thr Phe Leu				
	230	235	240	245
cct ttg gcg cac gtt ctt gct cgc gca gtg cac ttg gcc ttc gct gtc				883
Pro Leu Ala His Val Leu Ala Arg Ala Val His Leu Ala Phe Ala Val				
	250	255	260	
acc ggt gca acc cag tcc cac tgg tct gat ttc agc acc ctt act ttg				931
Thr Gly Ala Thr Gln Ser His Trp Ser Asp Phe Ser Thr Leu Thr Leu				
	265	270	275	
gaa ctg cag cgt tcc cgc ccg aac ctg att ttg ggt gtt cca cgc gtg				979
Glu Leu Gln Arg Ser Arg Pro Asn Leu Ile Leu Gly Val Pro Arg Val				
	280	285	290	
ttt gaa aag gtc cgc aac gcc gct gct gct aat gct gct gac ggt ggc				1027
Phe Glu Lys Val Arg Asn Ala Ala Ala Asn Ala Ala Asp Gly Gly				
	295	300	305	
gca atc aag cgc atc atg ttt gag cgt gcc gaa aag gcg gcc att gaa				1075
Ala Ile Lys Arg Ile Met Phe Glu Arg Ala Glu Lys Ala Ala Ile Glu				
	310	315	320	325

tac tcc atg gct ctt gat act gca gaa ggc cca agc aag tcc cag gtt	1123
Tyr Ser Met Ala Leu Asp Thr Ala Glu Gly Pro Ser Lys Ser Gln Val	
330 335 340	
atg gca cat aaa gcg ttt gac aag ctg gtg tac tcc aag atc cgt gca	1171
Met Ala His Lys Ala Phe Asp Lys Leu Val Tyr Ser Lys Ile Arg Ala	
345 350 355	
gct gtc ggt ggc gat gtg cag tac gcc atc acc ggt ggt tca gcg atg	1219
Ala Val Gly Gly Asp Val Gln Tyr Ala Ile Thr Gly Gly Ser Ala Met	
360 365 370	
ggg cag gag ctg ctg cac ttc ttc cgc ggt gtg ggc atg acc atc tac	1267
Gly Gln Glu Leu Leu His Phe Phe Arg Gly Val Gly Met Thr Ile Tyr	
375 380 385	
gaa ggt tat ggt ctg acg gaa tct gcg gct gct gca gcg gtg gac ttc	1315
Glu Gly Tyr Gly Leu Thr Glu Ser Ala Ala Ala Ala Val Asp Phe	
390 395 400 405	
act gat caa aag atc ggc act gtg ggt aag ccg atg ggt ggc atg acc	1363
Thr Asp Gln Lys Ile Gly Thr Val Gly Lys Pro Met Gly Gly Met Thr	
410 415 420	
atc aag atc aat gaa gat ggc gaa atc atg cta aaa ggc gag atg ttg	1411
Ile Lys Ile Asn Glu Asp Gly Glu Ile Met Leu Lys Gly Glu Met Leu	
425 430 435	
ttc cag gga tat tgg aac aac cca gaa gcc aca gca gaa gcc ctc cac	1459
Phe Gln Gly Tyr Trp Asn Asn Pro Glu Ala Thr Ala Glu Ala Leu His	
440 445 450	
gac ggt tgg ttc aac acc ggc gat ctg ggt gag ctg ttg gag tct gga	1507
Asp Gly Trp Phe Asn Thr Gly Asp Leu Gly Glu Leu Leu Glu Ser Gly	
455 460 465	
cac ctg gtg atc acc gga cgt aag aaa gat ctg atc gtg acc gcg ggc	1555
His Leu Val Ile Thr Gly Arg Lys Lys Asp Leu Ile Val Thr Ala Gly	
470 475 480 485	
ggc aag aac gtt tcc cca gga ccc atg gaa gac atc atc cgc gca cac	1603
Gly Lys Asn Val Ser Pro Gly Pro Met Glu Asp Ile Ile Arg Ala His	
490 495 500	
cca ctg gtc agc cag gcc atg gtg gtg ggc gat ggt aaa cca ttc gtt	1651
Pro Leu Val Ser Gln Ala Met Val Val Gly Asp Gly Lys Pro Phe Val	
505 510 515	
ggc ctg ctg gtg acc ttg gat cca gat atg ttg aag cgg tgg aag ctg	1699
Gly Leu Leu Val Thr Leu Asp Pro Asp Met Leu Lys Arg Trp Lys Leu	
520 525 530	
aac cac aac att gcg gaa tcc cgc acg gtt tct gag att gct act gat	1747
Asn His Asn Ile Ala Glu Ser Arg Thr Val Ser Glu Ile Ala Thr Asp	
535 540 545	
cct gca ctg cgt gcg gaa atc cag gat gca gtc aac aac gct aat gcc	1795
Pro Ala Leu Arg Ala Glu Ile Gln Asp Ala Val Asn Asn Ala Asn Ala	
550 555 560 565	

acg gtg tct cat tca gag gcg atc aag cgg ttc tac atc ctt gat cgc 1843
 Thr Val Ser His Ser Glu Ala Ile Lys Arg Phe Tyr Ile Leu Asp Arg
 570 575 580

gac ctg acc gag gaa gcc gac gag ctg acc cca acg ctg aag gtc aag 1891
 Asp Leu Thr Glu Glu Ala Asp Glu Leu Thr Pro Thr Leu Lys Val Lys
 585 590 595

cgc aac gtt gtt gtt cgc cgt tac gca gac gcc atc gac cac atc tac 1939
 Arg Asn Val Val Val Arg Arg Tyr Ala Asp Ala Ile Asp His Ile Tyr
 600 605 610

aac cga tgagtaacac agagacccaa ttt 1968
 Asn Arg
 615

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<211> 615

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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 20 25 30

Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser Lys Pro Ala Asn Tyr Glu
 35 40 45

Trp Val Asn Val Thr Ala Lys Glu Phe Gln Asp Glu Val Phe Ala Val
 50 55 60

Ala Lys Gly Ile Ile Ser Val Gly Val Glu Gln Gly Asp Arg Val Ala
 65 70 75 80

Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala Val Leu Asp Phe Ala Ile
 85 90 95

Trp Ala Ala Gly Ala Val Ser Val Pro Ile Tyr Ser Ser Ser Ser Leu
 100 105 110

Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser Gly Ala Val Leu Ala Ile
 115 120 125

Thr Glu Thr Pro Asp His Thr Asp Leu Met Lys Asn Leu Val Ile Gly
 130 135 140

Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser Pro Ser Lys Leu Arg Arg
 145 150 155 160

Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu Thr Leu Lys Phe Glu Gly
 165 170 175

Arg Glu Leu Ser Asp Glu Leu Val Trp Glu Arg Ile His Ala Thr Lys
 180 185 190

Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr Ser Gly Thr Thr Gly Arg
 195 200 205

Pro Lys Gly Cys Glu Leu Ser His Tyr His Trp Leu Ala Glu Val Arg
 210 215 220
 Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile Ala Met Pro Gly Ser Arg
 225 230 235 240
 Leu Leu Thr Phe Leu Pro Leu Ala His Val Leu Ala Arg Ala Val His
 245 250 255
 Leu Ala Phe Ala Val Thr Gly Ala Thr Gln Ser His Trp Ser Asp Phe
 260 265 270
 Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser Arg Pro Asn Leu Ile Leu
 275 280 285
 Gly Val Pro Arg Val Phe Glu Lys Val Arg Asn Ala Ala Ala Ala Asn
 290 295 300
 Ala Ala Asp Gly Gly Ala Ile Lys Arg Ile Met Phe Glu Arg Ala Glu
 305 310 315 320
 Lys Ala Ala Ile Glu Tyr Ser Met Ala Leu Asp Thr Ala Glu Gly Pro
 325 330 335
 Ser Lys Ser Gln Val Met Ala His Lys Ala Phe Asp Lys Leu Val Tyr
 340 345 350
 Ser Lys Ile Arg Ala Ala Val Gly Gly Asp Val Gln Tyr Ala Ile Thr
 355 360 365
 Gly Gly Ser Ala Met Gly Gln Glu Leu Leu His Phe Phe Arg Gly Val
 370 375 380
 Gly Met Thr Ile Tyr Glu Gly Tyr Gly Leu Thr Glu Ser Ala Ala Ala
 385 390 395 400
 Ala Ala Val Asp Phe Thr Asp Gln Lys Ile Gly Thr Val Gly Lys Pro
 405 410 415
 Met Gly Gly Met Thr Ile Lys Ile Asn Glu Asp Gly Glu Ile Met Leu
 420 425 430
 Lys Gly Glu Met Leu Phe Gln Gly Tyr Trp Asn Asn Pro Glu Ala Thr
 435 440 445
 Ala Glu Ala Leu His Asp Gly Trp Phe Asn Thr Gly Asp Leu Gly Glu
 450 455 460
 Leu Leu Glu Ser Gly His Leu Val Ile Thr Gly Arg Lys Lys Asp Leu
 465 470 475 480
 Ile Val Thr Ala Gly Gly Lys Asn Val Ser Pro Gly Pro Met Glu Asp
 485 490 495
 Ile Ile Arg Ala His Pro Leu Val Ser Gln Ala Met Val Val Gly Asp
 500 505 510
 Gly Lys Pro Phe Val Gly Leu Leu Val Thr Leu Asp Pro Asp Met Leu
 515 520 525

Lys Arg Trp Lys Leu Asn His Asn Ile Ala Glu Ser Arg Thr Val Ser
 530 535 540
 Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala Glu Ile Gln Asp Ala Val
 545 550 555 560
 Asn Asn Ala Asn Ala Thr Val Ser His Ser Glu Ala Ile Lys Arg Phe
 565 570 575
 Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu Ala Asp Glu Leu Thr Pro
 580 585 590
 Thr Leu Lys Val Lys Arg Asn Val Val Val Arg Arg Tyr Ala Asp Ala
 595 600 605
 Ile Asp His Ile Tyr Asn Arg
 610 615

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 <222> (101)..(1024)
 <223> RXA01060

<400> 61
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 cttccataact ttacttgatt gataagaatg gacaaagaca atg aac cgc aca ctc 115
 Met Asn Arg Thr Leu
 1 5
 cga aca ctt ggc tgg ctt gct gcc gta att caa gaa gat ccg gag ccc 163
 Arg Thr Leu Gly Trp Leu Ala Ala Val Ile Gln Glu Asp Pro Glu Pro
 10 15 20
 tgg ttc acc act gat ccc gac acc gat tat gtc cct tat gta aat agt 211
 Trp Phe Thr Thr Asp Pro Asp Thr Asp Tyr Val Pro Tyr Val Asn Ser
 25 30 35
 ttc tca ttt gaa tcc ctt tcc ctc gtt cca gat gct ctg atg ctg ctc 259
 Phe Ser Phe Glu Ser Leu Ser Leu Val Pro Asp Ala Leu Met Leu Leu
 40 45 50
 aaa cgt tct ctt cac ctt gcg atg gag caa cag gac ctc cca gtg aag 307
 Lys Arg Ser Leu His Leu Ala Met Glu Gln Gln Asp Leu Pro Val Lys
 55 60 65
 gat cta caa gaa gca ctg agg cac gta cta gtt ttc aaa ttc cac ttc 355
 Asp Leu Gln Glu Ala Leu Arg His Val Leu Val Phe Lys Phe His Phe
 70 75 80 85
 agg gaa gaa tgg gag ctg gaa tta gca tgg gac tcc gag cgg acc aag 403
 Arg Glu Glu Trp Glu Leu Glu Leu Ala Trp Asp Ser Glu Arg Thr Lys
 90 95 100
 tct gcg gtg aga att att gag agc aca aaa gaa tct ctt gcc gat caa 451

Ser Ala Val Arg Ile Ile Glu Ser Thr Lys Glu Ser Leu Ala Asp Gln
 105 110 115
 tac aga gat tac aaa tac gca ttc ttg cct gag cta att ttc cag gaa 499
 Tyr Arg Asp Tyr Lys Tyr Ala Phe Leu Pro Glu Leu Ile Phe Gln Glu
 120 125 130
 tca cgc ggg atc ttt gac ttt gag ctg gag gga tac acc ctc aaa gta 547
 Ser Arg Gly Ile Phe Asp Phe Glu Leu Glu Gly Tyr Thr Leu Lys Val
 135 140 145
 gga caa agc acg ctt tcc att cct tgg gac atg atc gcc aat ggt tat 595
 Gly Gln Ser Thr Leu Ser Ile Pro Trp Asp Met Ile Ala Asn Gly Tyr
 150 155 160 165
 gtc cct gca agt ctt cgg aat ttt gga gaa tta atg gac cgt gac acc 643
 Val Pro Ala Ser Leu Arg Asn Phe Gly Glu Leu Met Asp Arg Asp Thr
 170 175 180
 gga gat ctt gat gca gat ccc att ctg aga cct cga gaa ctc aaa ttt 691
 Gly Asp Leu Asp Ala Asp Pro Ile Leu Arg Pro Arg Glu Leu Lys Phe
 185 190 195
 gag atc cat aat tgt cca gat ctt aat cct tgg ata atg cgg gaa act 739
 Glu Ile His Asn Cys Pro Asp Leu Asn Pro Trp Ile Met Arg Glu Thr
 200 205 210
 ttt gat ttc atg atg gaa atc gca act gaa aca gga tgg ttc cat gct 787
 Phe Asp Phe Met Met Glu Ile Ala Thr Glu Thr Gly Trp Phe His Ala
 215 220 225
 ctc aac ccc gca tat aat tcc gtc tac acc tac gat ctt att tct cgc 835
 Leu Asn Pro Ala Tyr Asn Ser Val Tyr Thr Tyr Asp Leu Ile Ser Arg
 230 235 240 245
 atg cca gat ttc ctt gtt gaa ggg agc ttt cgt ccg cat tca gtg aaa 883
 Met Pro Asp Phe Leu Val Glu Gly Ser Phe Arg Pro His Ser Val Lys
 250 255 260
 cga tct tgg gaa aaa att caa aag ata gct aaa gct gtt gag tct tat 931
 Arg Ser Trp Glu Lys Ile Gln Lys Ile Ala Lys Ala Val Glu Ser Tyr
 265 270 275
 gca tct cac gat tac tgc atg tca acg ctg aca cat gac tac agg gca 979
 Ala Ser His Asp Tyr Cys Met Ser Thr Leu Thr His Asp Tyr Arg Ala
 280 285 290
 atc gag tta tcc ctg acg cct aca aaa act gag gaa cca agc aca 1024
 Ile Glu Leu Ser Leu Thr Pro Thr Lys Thr Glu Glu Pro Ser Thr
 295 300 305
 taagaaaacc tcgcctgccc act 1047

<210> 62

<211> 308

<212> PRT

<213> Corynebacterium glutamicum

<400> 62

Met Asn Arg Thr Leu Arg Thr Leu Gly Trp Leu Ala Ala Val Ile Gln

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Glu Asp Pro Glu Pro Trp Phe Thr Thr Asp Pro Asp Thr Asp Tyr Val	20	25	30
Pro Tyr Val Asn Ser Phe Ser Phe Glu Ser Leu Ser Leu Val Pro Asp	35	40	45
Ala Leu Met Leu Leu Lys Arg Ser Leu His Leu Ala Met Glu Gln Gln	50	55	60
Asp Leu Pro Val Lys Asp Leu Gln Glu Ala Leu Arg His Val Leu Val	65	70	75
Phe Lys Phe His Phe Arg Glu Glu Trp Glu Leu Glu Leu Ala Trp Asp	85	90	95
Ser Glu Arg Thr Lys Ser Ala Val Arg Ile Ile Glu Ser Thr Lys Glu	100	105	110
Ser Leu Ala Asp Gln Tyr Arg Asp Tyr Lys Tyr Ala Phe Leu Pro Glu	115	120	125
Leu Ile Phe Gln Glu Ser Arg Gly Ile Phe Asp Phe Glu Leu Glu Gly	130	135	140
Tyr Thr Leu Lys Val Gly Gln Ser Thr Leu Ser Ile Pro Trp Asp Met	145	150	155
Ile Ala Asn Gly Tyr Val Pro Ala Ser Leu Arg Asn Phe Gly Glu Leu	165	170	175
Met Asp Arg Asp Thr Gly Asp Leu Asp Ala Asp Pro Ile Leu Arg Pro	180	185	190
Arg Glu Leu Lys Phe Glu Ile His Asn Cys Pro Asp Leu Asn Pro Trp	195	200	205
Ile Met Arg Glu Thr Phe Asp Phe Met Met Glu Ile Ala Thr Glu Thr	210	215	220
Gly Trp Phe His Ala Leu Asn Pro Ala Tyr Asn Ser Val Tyr Thr Tyr	225	230	235
Asp Leu Ile Ser Arg Met Pro Asp Phe Leu Val Glu Gly Ser Phe Arg	245	250	255
Pro His Ser Val Lys Arg Ser Trp Glu Lys Ile Gln Lys Ile Ala Lys	260	265	270
Ala Val Glu Ser Tyr Ala Ser His Asp Tyr Cys Met Ser Thr Leu Thr	275	280	285
His Asp Tyr Arg Ala Ile Glu Leu Ser Leu Thr Pro Thr Lys Thr Glu	290	295	300
Glu Pro Ser Thr			
305			

<210> 63

<211> 1848
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1825)
 <223> RXN01722

<400> 63

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                               Met Leu Ser Thr Met
                               1           5

cag gac gtc cca ctg tca tta acc aga atc ctc gag tac ggg tcc act 163
Gln Asp Val Pro Leu Ser Leu Thr Arg Ile Leu Glu Tyr Gly Ser Thr
                10                15                20

gtt cac ggt gat act ttg atc acc acg tgg ggc ggt gcc gat ggc att 211
Val His Gly Asp Thr Leu Ile Thr Thr Trp Gly Gly Ala Asp Gly Ile
                25                30                35

gaa caa gca cag caa act ttt agt gct gtg ggg gct aga gct gcg gct 259
Glu Gln Ala Gln Gln Thr Phe Ser Ala Val Gly Ala Arg Ala Ala Ala
                40                45                50

ttg gct cat gcg ctg cat gat tct tta ggt att act ggg gat cag cga 307
Leu Ala His Ala Leu His Asp Ser Leu Gly Ile Thr Gly Asp Gln Arg
                55                60                65

gtg gcg tcg atg ctc tat aac tgc gcg gaa cac atg gaa act atg ttt 355
Val Ala Ser Met Leu Tyr Asn Cys Ala Glu His Met Glu Thr Met Phe
                70                75                80                85

gca gtc gca tgc atg ggt gcc gtg ttt aat ccg ctg aac aag cag ttg 403
Ala Val Ala Cys Met Gly Ala Val Phe Asn Pro Leu Asn Lys Gln Leu
                90                95                100

atg aat gat cag att gtg ttc att ctc aat cac tct gaa gct gaa gtg 451
Met Asn Asp Gln Ile Val Phe Ile Leu Asn His Ser Glu Ala Glu Val
                105                110                115

gtt atc gct gat ccg cgc atg gct gaa caa ttg ggt gag atc tta aaa 499
Val Ile Ala Asp Pro Arg Met Ala Glu Gln Leu Gly Glu Ile Leu Lys
                120                125                130

gaa aca cca aaa gtt cgt gcc gtg gtg ttt att gga ccg aat gat ttc 547
Glu Thr Pro Lys Val Arg Ala Val Val Phe Ile Gly Pro Asn Asp Phe
                135                140                145

tct agc gcg gcg gcc cac atg ccg gag gga atg aag ctg tat tcc tat 595
Ser Ser Ala Ala Ala His Met Pro Glu Gly Met Lys Leu Tyr Ser Tyr
                150                155                160                165

gaa gcg ctc ctt gac ggc cgt tcc act gtt tac aac tgg ccc gag cag 643
Glu Ala Leu Leu Asp Gly Arg Ser Thr Val Tyr Asn Trp Pro Glu Gln
                170                175                180

gat gaa cgc act gct gct gca att tgc tat tcc acc ggt aca tcg gga 691

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Asp	Glu	Arg	Thr	Ala	Ala	Ala	Ile	Cys	Tyr	Ser	Thr	Gly	Thr	Ser	Gly		
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cgc	cgc	aag	ggc	gtg	gtg	tat	tcc	cac	cgc	tgc	ctt	tat	tta	cag	tgc	739	
Pro	Pro	Lys	Gly	Val	Val	Tyr	Ser	His	Arg	Ser	Leu	Tyr	Leu	Gln	Ser		
		200					205					210					
ttg	agc	ttg	cgc	acc	acg	gat	tcc	ctc	gca	gtg	gaa	cac	ggc	gaa	acg	787	
Leu	Ser	Leu	Arg	Thr	Thr	Asp	Ser	Leu	Ala	Val	Glu	His	Gly	Glu	Thr		
		215				220					225						
ttc	ctg	tgc	tgt	gtg	ccg	att	tac	cac	gtc	ctc	agc	tgg	ggc	gtg	ccg	835	
Phe	Leu	Cys	Cys	Val	Pro	Ile	Tyr	His	Val	Leu	Ser	Trp	Gly	Val	Pro		
230					235					240					245		
atc	gca	gcg	ttt	atg	tcc	ggc	act	ccc	ctg	gtg	ctt	cct	gga	ccg	gat	883	
Ile	Ala	Ala	Phe	Met	Ser	Gly	Thr	Pro	Leu	Val	Leu	Pro	Gly	Pro	Asp		
			250					255						260			
ctt	tct	gcg	ccg	aca	ttg	gca	aag	atc	att	tcc	acc	acg	ctg	cct	cgc	931	
Leu	Ser	Ala	Pro	Thr	Leu	Ala	Lys	Ile	Ile	Ser	Thr	Thr	Leu	Pro	Arg		
			265					270						275			
gtg	gcg	cat	ggc	gtg	cct	act	ctc	tgg	att	cag	ctg	atg	gtt	cac	tac	979	
Val	Ala	His	Gly	Val	Pro	Thr	Leu	Trp	Ile	Gln	Leu	Met	Val	His	Tyr		
		280					285					290					
ctg	aaa	aat	ccc	cca	gag	cgt	atg	tct	ctg	cgt	gag	cta	tac	gtg	ggc	1027	
Leu	Lys	Asn	Pro	Pro	Glu	Arg	Met	Ser	Leu	Arg	Glu	Leu	Tyr	Val	Gly		
	295					300					305						
ggc	tct	gcg	gtg	cct	cca	atc	gtg	atc	acc	atg	tgg	gag	cag	cgc	tat	1075	
Gly	Ser	Ala	Val	Pro	Pro	Ile	Val	Ile	Thr	Met	Trp	Glu	Gln	Arg	Tyr		
310					315					320					325		
ggc	gtg	gat	gtt	gtc	cac	gtg	tgg	ggc	atg	acg	gaa	acc	tcc	acc	gtg	1123	
Gly	Val	Asp	Val	Val	His	Val	Trp	Gly	Met	Thr	Glu	Thr	Ser	Thr	Val		
				330					335					340			
ggc	act	gtg	tct	cgc	cca	cca	tca	ggc	gtt	tct	ggc	gaa	agc	cgc	tgg	1171	
Gly	Thr	Val	Ser	Arg	Pro	Pro	Ser	Gly	Val	Ser	Gly	Glu	Ser	Arg	Trp		
			345					350					355				
aat	tat	cga	gtc	tcc	cag	ggc	cga	ttc	ccc	gcc	tcc	ctg	cag	tac	cgc	1219	
Asn	Tyr	Arg	Val	Ser	Gln	Gly	Arg	Phe	Pro	Ala	Ser	Leu	Gln	Tyr	Arg		
		360					365					370					
att	gtc	aac	gac	ggc	cag	gtc	atg	gcg	tcc	acc	gac	cgc	aac	gag	ggc	1267	
Ile	Val	Asn	Asp	Gly	Gln	Val	Met	Ala	Ser	Thr	Asp	Arg	Asn	Glu	Gly		
		375				380					385						
gag	att	cag	gtc	cgc	ggc	ccg	tgg	gtg	act	gca	agt	tac	ttc	cac	ccc	1315	
Glu	Ile	Gln	Val	Arg	Gly	Pro	Trp	Val	Thr	Ala	Ser	Tyr	Phe	His	Pro		
390					395					400					405		
gat	gtg	gaa	aaa	gaa	ggc	ggc	acc	gcc	tca	aca	ttc	cgc	gac	cat	gac	1363	
Asp	Val	Glu	Lys	Glu	Gly	Gly	Thr	Ala	Ser	Thr	Phe	Arg	Asp	His	Asp		
				410				415						420			
gtt	gaa	gag	gaa	aac	gat	gag	ctc	ttc	acc	gcc	gac	ggc	tgg	ctg	cgc	1411	
Val	Glu	Glu	Glu	Asn	Asp	Glu	Leu	Phe	Thr	Ala	Asp	Gly	Trp	Leu	Arg		

425	430	435	
acc ggg gac gtt gga tct gtc	acc agc gat gga ttc ctc	acc atc caa	1459
Thr Gly Asp Val Gly Ser Val	Thr Ser Asp Gly Phe Leu Thr	Ile Gln	
440	445	450	
gac cgc gcc cgc gat gtc atc cgt tct ggc ggc gag tgg att tac tcc			1507
Asp Arg Ala Arg Asp Val Ile Arg Ser Gly Gly Glu Trp Ile Tyr Ser			
455	460	465	
gct cag ctg gaa aac ctc atc gtg gct acg gaa gag gtt gtc gaa tgc			1555
Ala Gln Leu Glu Asn Leu Ile Val Ala Thr Glu Glu Val Val Glu Cys			
470	475	480	485
gcc gtc att ggc ttc ccc gat gac aag tgg gtg gaa cgt ccc ctc gca			1603
Ala Val Ile Gly Phe Pro Asp Asp Lys Trp Val Glu Arg Pro Leu Ala			
490	495	500	
gtc acc atg ctc tac ccc ggc att gaa cgc acc cgg gaa acc gcc gag			1651
Val Thr Met Leu Tyr Pro Gly Ile Glu Arg Thr Arg Glu Thr Ala Glu			
505	510	515	
cgc ctc cgc gat caa ctt cgc gac cgc cta ccc aac tgg atg ctg cca			1699
Arg Leu Arg Asp Gln Leu Arg Asp Arg Leu Pro Asn Trp Met Leu Pro			
520	525	530	
gaa tat tgg aca ttt gtt gat gag gtg gat aaa acc tcc gtc ggt aaa			1747
Glu Tyr Trp Thr Phe Val Asp Glu Val Asp Lys Thr Ser Val Gly Lys			
535	540	545	
tat gac aag aag gac ctc cgc aac cac ctg cgc aac ggc gat ttc gaa			1795
Tyr Asp Lys Lys Asp Leu Arg Asn His Leu Arg Asn Gly Asp Phe Glu			
550	555	560	565
gta att aag ctt aaa ggg cca ggt gaa aaa taacttcct atttattccg			1845
Val Ile Lys Leu Lys Gly Pro Gly Glu Lys			
570	575		
gct			1848
<210> 64			
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<212> PRT			
<213> Corynebacterium glutamicum			
<400> 64			
Met Leu Ser Thr Met Gln Asp Val Pro Leu Ser Leu Thr Arg Ile Leu			
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Glu Tyr Gly Ser Thr Val His Gly Asp Thr Leu Ile Thr Thr Trp Gly			
20	25	30	
Gly Ala Asp Gly Ile Glu Gln Ala Gln Gln Thr Phe Ser Ala Val Gly			
35	40	45	
Ala Arg Ala Ala Ala Leu Ala His Ala Leu His Asp Ser Leu Gly Ile			
50	55	60	
Thr Gly Asp Gln Arg Val Ala Ser Met Leu Tyr Asn Cys Ala Glu His			
65	70	75	80

Met Glu Thr Met Phe Ala Val Ala Cys Met Gly Ala Val Phe Asn Pro
 85 90 95
 Leu Asn Lys Gln Leu Met Asn Asp Gln Ile Val Phe Ile Leu Asn His
 100 105 110
 Ser Glu Ala Glu Val Val Ile Ala Asp Pro Arg Met Ala Glu Gln Leu
 115 120 125
 Gly Glu Ile Leu Lys Glu Thr Pro Lys Val Arg Ala Val Val Phe Ile
 130 135 140
 Gly Pro Asn Asp Phe Ser Ser Ala Ala Ala His Met Pro Glu Gly Met
 145 150 155 160
 Lys Leu Tyr Ser Tyr Glu Ala Leu Leu Asp Gly Arg Ser Thr Val Tyr
 165 170 175
 Asn Trp Pro Glu Gln Asp Glu Arg Thr Ala Ala Ala Ile Cys Tyr Ser
 180 185 190
 Thr Gly Thr Ser Gly Pro Pro Lys Gly Val Val Tyr Ser His Arg Ser
 195 200 205
 Leu Tyr Leu Gln Ser Leu Ser Leu Arg Thr Thr Asp Ser Leu Ala Val
 210 215 220
 Glu His Gly Glu Thr Phe Leu Cys Cys Val Pro Ile Tyr His Val Leu
 225 230 235 240
 Ser Trp Gly Val Pro Ile Ala Ala Phe Met Ser Gly Thr Pro Leu Val
 245 250 255
 Leu Pro Gly Pro Asp Leu Ser Ala Pro Thr Leu Ala Lys Ile Ile Ser
 260 265 270
 Thr Thr Leu Pro Arg Val Ala His Gly Val Pro Thr Leu Trp Ile Gln
 275 280 285
 Leu Met Val His Tyr Leu Lys Asn Pro Pro Glu Arg Met Ser Leu Arg
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 Glu Leu Tyr Val Gly Gly Ser Ala Val Pro Pro Ile Val Ile Thr Met
 305 310 315 320
 Trp Glu Gln Arg Tyr Gly Val Asp Val Val His Val Trp Gly Met Thr
 325 330 335
 Glu Thr Ser Thr Val Gly Thr Val Ser Arg Pro Pro Ser Gly Val Ser
 340 345 350
 Gly Glu Ser Arg Trp Asn Tyr Arg Val Ser Gln Gly Arg Phe Pro Ala
 355 360 365
 Ser Leu Gln Tyr Arg Ile Val Asn Asp Gly Gln Val Met Ala Ser Thr
 370 375 380
 Asp Arg Asn Glu Gly Glu Ile Gln Val Arg Gly Pro Trp Val Thr Ala
 385 390 395 400

Ser Tyr Phe His Pro Asp Val Glu Lys Glu Gly Gly Thr Ala Ser Thr
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Phe Arg Asp His Asp Val Glu Glu Glu Asn Asp Glu Leu Phe Thr Ala
 420 425 430

Asp Gly Trp Leu Arg Thr Gly Asp Val Gly Ser Val Thr Ser Asp Gly
 435 440 445

Phe Leu Thr Ile Gln Asp Arg Ala Arg Asp Val Ile Arg Ser Gly Gly
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Glu Trp Ile Tyr Ser Ala Gln Leu Glu Asn Leu Ile Val Ala Thr Glu
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Glu Val Val Glu Cys Ala Val Ile Gly Phe Pro Asp Asp Lys Trp Val
 485 490 495

Glu Arg Pro Leu Ala Val Thr Met Leu Tyr Pro Gly Ile Glu Arg Thr
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Arg Glu Thr Ala Glu Arg Leu Arg Asp Gln Leu Arg Asp Arg Leu Pro
 515 520 525

Asn Trp Met Leu Pro Glu Tyr Trp Thr Phe Val Asp Glu Val Asp Lys
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Thr Ser Val Gly Lys Tyr Asp Lys Lys Asp Leu Arg Asn His Leu Arg
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Asn Gly Asp Phe Glu Val Ile Lys Leu Lys Gly Pro Gly Glu Lys
 565 570 575

<210> 65
 <211> 1848
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1825)
 <223> FRXA01722

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 Met Leu Ser Thr Met
 1 5

cag gac gtc cca ctg tca tta acc aga atc ctc gag tac ggg tcc act 163
 Gln Asp Val Pro Leu Ser Leu Thr Arg Ile Leu Glu Tyr Gly Ser Thr
 10 15 20

gtt cac ggt gat act ttg atc acc acg tgg ggc ggt gcc gat ggc att 211
 Val His Gly Asp Thr Leu Ile Thr Thr Trp Gly Gly Ala Asp Gly Ile
 25 30 35

gaa caa gca cag caa act ttt agt gct gtg ggg gct aga gct gcg gct 259
 Glu Gln Ala Gln Gln Thr Phe Ser Ala Val Gly Ala Arg Ala Ala Ala

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gtg gcg tcg atg ctc tat aac tgc gcg gaa cac atg gaa act atg ttt Val Ala Ser Met Leu Tyr Asn Cys Ala Glu His Met Glu Thr Met Phe 70 75 80 85			355
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tct agc gcg gcg gcc cac atg ccg gag gga atg aag ctg tat tcc tat Ser Ser Ala Ala His Met Pro Glu Gly Met Lys Leu Tyr Ser Tyr 150 155 160 165			595
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gat gaa cgc act gct gct gca att tgc tat tcc acc ggt aca tcg gga Asp Glu Arg Thr Ala Ala Ala Ile Cys Tyr Ser Thr Gly Thr Ser Gly 185 190 195			691
ccg ccg aag ggt gtg gtg tat tcc cac cgc tcg ctt tat tta cag tcg Pro Pro Lys Gly Val Val Tyr Ser His Arg Ser Leu Tyr Leu Gln Ser 200 205 210			739
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ttc ctg tgc tgt gtg ccg att tac cac gtc ctc agc tgg ggc gtg ccg Phe Leu Cys Cys Val Pro Ile Tyr His Val Leu Ser Trp Gly Val Pro 230 235 240 245			835
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ctt tct gcg ccg aca ttg gca aag atc att tcc acc acg ctg cct cgc Leu Ser Ala Pro Thr Leu Ala Lys Ile Ile Ser Thr Thr Leu Pro Arg 265 270 275			931
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Leu Lys Asn Pro Pro Glu Arg Met Ser Leu Arg Glu Leu Tyr Val Gly	
295 300 305	
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Gly Ser Ala Val Pro Pro Ile Val Ile Thr Met Trp Glu Gln Arg Tyr	
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Gly Val Asp Val Val His Val Trp Gly Met Thr Glu Thr Ser Thr Val	
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Gly Thr Val Ser Arg Pro Pro Ser Gly Val Ser Gly Glu Ser Arg Trp	
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Asn Tyr Arg Val Ser Gln Gly Arg Phe Pro Ala Ser Leu Gln Tyr Arg	
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Ile Val Asn Asp Gly Gln Val Met Ala Ser Thr Asp Arg Asn Glu Gly	
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Glu Ile Gln Val Arg Gly Pro Trp Val Thr Ala Ser Tyr Phe His Pro	
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gat gtg gaa aaa gaa ggt ggc acc gcc tca aca ttc cgc gac cat gac	1363
Asp Val Glu Lys Glu Gly Gly Thr Ala Ser Thr Phe Arg Asp His Asp	
410 415 420	
gtt gaa gag gaa aac gat gag ctc ttc acc gcc gac ggc tgg ctg cgc	1411
Val Glu Glu Glu Asn Asp Glu Leu Phe Thr Ala Asp Gly Trp Leu Arg	
425 430 435	
acc ggg gac gtt gga tct gtc acc agc gat gga ttc ctc acc atc caa	1459
Thr Gly Asp Val Gly Ser Val Thr Ser Asp Gly Phe Leu Thr Ile Gln	
440 445 450	
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Asp Arg Ala Arg Asp Val Ile Arg Ser Gly Gly Glu Trp Ile Tyr Ser	
455 460 465	
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Ala Val Ile Gly Phe Pro Asp Asp Lys Trp Val Glu Arg Pro Leu Ala	
490 495 500	
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Val Thr Met Leu Tyr Pro Gly Ile Glu Arg Thr Arg Glu Thr Ala Glu	
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520 525 530	

gaa tat tgg aca ttt gtt gat gag gtg gat aaa acc tcc gtc ggt aaa 1747
 Glu Tyr Trp Thr Phe Val Asp Glu Val Asp Lys Thr Ser Val Gly Lys
 535 540 545

tat gac aag aag gac ctc cgc aac cac ctg cgc aac ggc gat ttc gaa 1795
 Tyr Asp Lys Lys Asp Leu Arg Asn His Leu Arg Asn Gly Asp Phe Glu
 550 555 560 565

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 Val Ile Lys Leu Lys Gly Pro Gly Xaa Lys
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gct 1848

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<211> 575

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

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 35 40 45

Ala Arg Ala Ala Ala Leu Ala His Ala Leu His Asp Ser Leu Gly Ile
 50 55 60

Thr Gly Asp Gln Arg Val Ala Ser Met Leu Tyr Asn Cys Ala Glu His
 65 70 75 80

Met Glu Thr Met Phe Ala Val Ala Cys Met Gly Ala Val Phe Asn Pro
 85 90 95

Leu Asn Lys Gln Leu Met Asn Asp Gln Ile Val Phe Ile Leu Asn His
 100 105 110

Ser Glu Ala Glu Val Val Ile Ala Asp Pro Arg Met Ala Glu Gln Leu
 115 120 125

Gly Glu Ile Leu Lys Glu Thr Pro Lys Val Arg Ala Val Val Phe Ile
 130 135 140

Gly Pro Asn Asp Phe Ser Ser Ala Ala Ala His Met Pro Glu Gly Met
 145 150 155 160

Lys Leu Tyr Ser Tyr Glu Ala Leu Leu Asp Gly Arg Ser Thr Val Tyr
 165 170 175

Asn Trp Pro Glu Gln Asp Glu Arg Thr Ala Ala Ala Ile Cys Tyr Ser
 180 185 190

Thr Gly Thr Ser Gly Pro Pro Lys Gly Val Val Tyr Ser His Arg Ser
 195 200 205

Leu Tyr Leu Gln Ser Leu Ser Leu Arg Thr Thr Asp Ser Leu Ala Val

210					215					220					
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Ser	Trp	Gly	Val	Pro 245	Ile	Ala	Ala	Phe	Met 250	Ser	Gly	Thr	Pro	Leu	Val 255
Leu	Pro	Gly	Pro 260	Asp	Leu	Ser	Ala	Pro	Thr 265	Leu	Ala	Lys	Ile	Ile	Ser 270
Thr	Thr	Leu 275	Pro	Arg	Val	Ala	His 280	Gly	Val	Pro	Thr	Leu	Trp	Ile	Gln 285
Leu	Met 290	Val	His	Tyr	Leu	Lys 295	Asn	Pro	Pro	Glu	Arg 300	Met	Ser	Leu	Arg
Glu 305	Leu	Tyr	Val	Gly	Gly 310	Ser	Ala	Val	Pro	Pro 315	Ile	Val	Ile	Thr	Met 320
Trp	Glu	Gln	Arg	Tyr 325	Gly	Val	Asp	Val	Val	His 330	Val	Trp	Gly	Met	Thr 335
Glu	Thr	Ser	Thr 340	Val	Gly	Thr	Val	Ser	Arg 345	Pro	Pro	Ser	Gly	Val	Ser 350
Gly	Glu	Ser 355	Arg	Trp	Asn	Tyr	Arg 360	Val	Ser	Gln	Gly	Arg	Phe	Pro	Ala 365
Ser 370	Leu	Gln	Tyr	Arg	Ile	Val	Asn 375	Asp	Gly	Gln	Val	Met	Ala	Ser	Thr 380
Asp 385	Arg	Asn	Glu	Gly	Glu 390	Ile	Gln	Val	Arg	Gly 395	Pro	Trp	Val	Thr	Ala 400
Ser	Tyr	Phe	His	Pro 405	Asp	Val	Glu	Lys	Glu 410	Gly	Gly	Thr	Ala	Ser	Thr 415
Phe	Arg	Asp	His 420	Asp	Val	Glu	Glu 425	Glu	Asn	Asp	Glu	Leu	Phe	Thr	Ala 430
Asp	Gly	Trp	Leu 435	Arg	Thr	Gly	Asp 440	Val	Gly	Ser	Val	Thr	Ser	Asp	Gly 445
Phe 450	Leu	Thr	Ile	Gln	Asp 455	Arg	Ala	Arg	Asp	Val	Ile 460	Arg	Ser	Gly	Gly 465
Glu 465	Trp	Ile	Tyr	Ser	Ala 470	Gln	Leu	Glu	Asn	Leu 475	Ile	Val	Ala	Xaa	Glu 480
Glu	Val	Val	Glu	Cys 485	Ala	Val	Ile	Gly	Phe 490	Pro	Asp	Asp	Lys	Trp	Val 495
Glu	Arg	Pro	Leu 500	Ala	Val	Thr	Met	Leu 505	Tyr	Pro	Gly	Ile	Glu	Arg	Thr 510
Arg	Glu	Thr	Ala 515	Glu	Arg	Leu	Arg 520	Asp	Gln	Leu	Arg	Asp	Arg	Leu	Pro 525
Asn 530	Trp	Met	Leu	Pro	Glu	Tyr 535	Trp	Thr	Phe	Val	Asp 540	Glu	Val	Asp	Lys 545

Thr Ser Val Gly Lys Tyr Asp Lys Lys Asp Leu Arg Asn His Leu Arg
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565 570 575

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<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1378)
<223> RXA01644

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Met Thr Ile Ala Asp
1 5
atc gtc gag gcc acg acc act gca ccc atc cca ttc cac atc act gcc 163
Ile Val Glu Ala Thr Thr Thr Ala Pro Ile Pro Phe His Ile Thr Ala
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ttc gat gga agc ttc act ggc cct gaa gat gct ccc tac cag ctg ttt 211
Phe Asp Gly Ser Phe Thr Gly Pro Glu Asp Ala Pro Tyr Gln Leu Phe
25 30 35
gtt gcc aac acg gat gca gta tcc tac atc gca aca gcg cca gga gat 259
Val Ala Asn Thr Asp Ala Val Ser Tyr Ile Ala Thr Ala Pro Gly Asp
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Leu Gly Leu Ala Arg Ala Tyr Leu Met Gly Asp Leu Ile Val Glu Gly
55 60 65
gag cat ccc ggc cat cct tat ggg atc ttt gat gcg ttg aag gag ttc 355
Glu His Pro Gly His Pro Tyr Gly Ile Phe Asp Ala Leu Lys Glu Phe
70 75 80 85
tac cgc tgc ttc aaa cgc cca gat gca tcc acc acc ttg cag atc atg 403
Tyr Arg Cys Phe Lys Arg Pro Asp Ala Ser Thr Thr Leu Gln Ile Met
90 95 100
tgg act ctg cgg aaa atg aat gcc tta aaa ttc cag gaa att cca cca 451
Trp Thr Leu Arg Lys Met Asn Ala Leu Lys Phe Gln Glu Ile Pro Pro
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atg gaa caa gcc cct gca tgg cgt aaa gca ctg atc aac ggg cta gca 499
Met Glu Gln Ala Pro Ala Trp Arg Lys Ala Leu Ile Asn Gly Leu Ala
120 125 130
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Ser Arg His Ser Lys Ser Arg Asp Lys Lys Ala Ile Ser Tyr His Tyr
135 140 145

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Asp Val Gly Asn Glu Phe Tyr Ser Leu Phe Leu Asp Asp Ser Met Thr	
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Tyr Thr Cys Ala Tyr Tyr Pro Thr Pro Glu Ser Ser Leu Glu Glu Ala	
170 175 180	
caa gaa aac aaa tac cgc ctc atc ttt gaa aaa ctg cgt ctg aaa gaa	691
Gln Glu Asn Lys Tyr Arg Leu Ile Phe Glu Lys Leu Arg Leu Lys Glu	
185 190 195	
ggc gat cgc ctc cta gac gtg gga tgc ggt tgg gga ggc atg gtc cgc	739
Gly Asp Arg Leu Leu Asp Val Gly Cys Gly Trp Gly Gly Met Val Arg	
200 205 210	
tac gcc gcc aaa cac ggt gtg aaa gcc atc gga gtt acg ctg tct gaa	787
Tyr Ala Ala Lys His Gly Val Lys Ala Ile Gly Val Thr Leu Ser Glu	
215 220 225	
cag caa tat gag tgg ggt caa gca gag atc aaa cgc caa ggt ttg gaa	835
Gln Gln Tyr Glu Trp Gly Gln Ala Glu Ile Lys Arg Gln Gly Leu Glu	
230 235 240 245	
gac ctc gcg gaa att cgc ttc atg gat tac cgc gat gtt cca gaa act	883
Asp Leu Ala Glu Ile Arg Phe Met Asp Tyr Arg Asp Val Pro Glu Thr	
250 255 260	
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Gly Phe Asp Ala Ile Ser Ala Ile Gly Ile Ile Glu His Ile Gly Val	
265 270 275	
aac aac tat ccc gac tac ttt gaa ttg ctc agc agc aaa ctc aaa aca	979
Asn Asn Tyr Pro Asp Tyr Phe Glu Leu Leu Ser Ser Lys Leu Lys Thr	
280 285 290	
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Gly Gly Leu Met Leu Asn His Ser Ile Thr Tyr Pro Asp Asn Arg Pro	
295 300 305	
cgc cac gca ggt gca ttt att gat cgc tac att ttc ccc gac ggt gaa	1075
Arg His Ala Gly Ala Phe Ile Asp Arg Tyr Ile Phe Pro Asp Gly Glu	
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ctc act ggc tct ggc acc ctg atc aag cac atg cag gac aac ggt ttc	1123
Leu Thr Gly Ser Gly Thr Leu Ile Lys His Met Gln Asp Asn Gly Phe	
330 335 340	
gaa gtg ctg cac gaa gaa aac ctc cgc ttt gat tac caa cgc acc ctg	1171
Glu Val Leu His Glu Glu Asn Leu Arg Phe Asp Tyr Gln Arg Thr Leu	
345 350 355	
cac gcg tgg tgc gaa aac ctc aaa gaa aat tgg gag gaa gca gtt gaa	1219
His Ala Trp Cys Glu Asn Leu Lys Glu Asn Trp Glu Glu Ala Val Glu	
360 365 370	
ctc gcc ggt gaa ccc act gca cga ctc ttt ggc ctg tac atg gca ggt	1267
Leu Ala Gly Glu Pro Thr Ala Arg Leu Phe Gly Leu Tyr Met Ala Gly	
375 380 385	
tcg gaa tgg gga ttt gcc cac aac atc gtc cag ctg cac caa gta ctg	1315

Ser Glu Trp Gly Phe Ala His Asn Ile Val Gln Leu His Gln Val Leu
 390 395 400 405

ggt gtg aaa ctc gat gag cag gga agt cgc gga gaa gtt cct gaa aga 1363
 Gly Val Lys Leu Asp Glu Gln Gly Ser Arg Gly Glu Val Pro Glu Arg
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<210> 68

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<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Thr Ala Pro Gly Asp Leu Gly Leu Ala Arg Ala Tyr Leu Met Gly Asp
 50 55 60

Leu Ile Val Glu Gly Glu His Pro Gly His Pro Tyr Gly Ile Phe Asp
 65 70 75 80

Ala Leu Lys Glu Phe Tyr Arg Cys Phe Lys Arg Pro Asp Ala Ser Thr
 85 90 95

Thr Leu Gln Ile Met Trp Thr Leu Arg Lys Met Asn Ala Leu Lys Phe
 100 105 110

Gln Glu Ile Pro Pro Met Glu Gln Ala Pro Ala Trp Arg Lys Ala Leu
 115 120 125

Ile Asn Gly Leu Ala Ser Arg His Ser Lys Ser Arg Asp Lys Lys Ala
 130 135 140

Ile Ser Tyr His Tyr Asp Val Gly Asn Glu Phe Tyr Ser Leu Phe Leu
 145 150 155 160

Asp Asp Ser Met Thr Tyr Thr Cys Ala Tyr Tyr Pro Thr Pro Glu Ser
 165 170 175

Ser Leu Glu Glu Ala Gln Glu Asn Lys Tyr Arg Leu Ile Phe Glu Lys
 180 185 190

Leu Arg Leu Lys Glu Gly Asp Arg Leu Leu Asp Val Gly Cys Gly Trp
 195 200 205

Gly Gly Met Val Arg Tyr Ala Ala Lys His Gly Val Lys Ala Ile Gly
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Val Thr Leu Ser Glu Gln Gln Tyr Glu Trp Gly Gln Ala Glu Ile Lys

<210> 69
<211> 1437
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<213> Corynebacterium glutamicum

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ttg cgc cat ctt gaa ccc att gat gtg gaa gag tgg cct. ggg gtg gcg 163
Leu Arg His Leu Glu Pro Ile Asp Val Glu Glu Trp Pro Gly Val Ala
                        10                        15                        20

tca gtg ccc aac cta qcg ttt gct ggt gca cgc gca cgg caa gca gaa 211

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Ser	Val	Pro	Asn	Leu	Ala	Phe	Ala	Gly	Ala	Arg	Ala	Arg	Gln	Ala	Glu		
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Tyr	Arg	Phe	Ala	Lys	Ala	Cys	Ser	Asn	Ala	Gly	Leu	Val	Leu	Leu	Gly		
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aat	gac	ccg	gat	ctc	att	att	gat	cat	gag	gaa	tta	ttc	tca	cgt	ttg	307	
Asn	Asp	Pro	Asp	Leu	Ile	Ile	Asp	His	Glu	Glu	Leu	Phe	Ser	Arg	Leu		
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gcc	gca	tcg	ggc	tgg	ctg	ggg	ctc	gct	gag	agc	tac	atg	gca	ggc	gag	355	
Ala	Ala	Ser	Gly	Trp	Leu	Gly	Leu	Ala	Glu	Ser	Tyr	Met	Ala	Gly	Glu		
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Trp	Arg	Ser	Glu	Arg	Leu	Ala	Asp	Val	Leu	Thr	Ala	Leu	Leu	Gly	Thr		
			90					95					100				
ggg	ttt	aaa	ccc	cgc	ggc	aaa	cta	tct	gga	tcg	ttc	acc	ctg	cca	ggg	451	
Gly	Phe	Lys	Pro	Arg	Gly	Lys	Leu	Ser	Gly	Ser	Phe	Thr	Leu	Pro	Gly		
		105					110					115					
caa	gct	gtg	gat	gcc	gga	ggc	gca	cta	ccc	aat	gaa	ctc	att	cgt	tta	499	
Gln	Ala	Val	Asp	Ala	Gly	Gly	Ala	Leu	Pro	Asn	Glu	Leu	Ile	Arg	Leu		
		120					125					130					
agt	tca	ggg	gat	ggc	atg	agc	gca	ttt	ggg	gga	gtt	ttt	gcc	tcc	ggg	547	
Ser	Ser	Gly	Asp	Gly	Met	Ser	Ala	Phe	Gly	Gly	Val	Phe	Ala	Ser	Gly		
	135					140					145						
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Val	Pro	Thr	Thr	Leu	Arg	Thr	Ala	Val	Lys	Ser	His	Val	Pro	Gly	Ala		
	150				155					160				165			
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Gly	Arg	Asn	Arg	Glu	Pro	Ala	Ser	His	Phe	Val	Asp	Ile	Thr	Lys	Ile		
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Ser	Glu	Pro	Val	Ala	Val	Glu	Arg	Glu	Asp	Leu	Gly	Glu	Ala	Gln	Arg		
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cga	gca	gcg	tcc	ttt	ttg	ctt	gac	ggc	gcc	aaa	gtt	aaa	gcc	gga	agc	739	
Arg	Ala	Ala	Ser	Phe	Leu	Leu	Asp	Gly	Ala	Lys	Val	Lys	Ala	Gly	Ser		
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cat	gtg	ttg	gag	ttt	ccc	agc	agt	ggg	gga	gct	tta	gct	att	ttg	gct	787	
His	Val	Leu	Glu	Phe	Pro	Ser	Ser	Gly	Gly	Ala	Leu	Ala	Ile	Leu	Ala		
	215					220					225						
gct	cga	cgc	cag	gga	act	gtt	gac	gct	tta	acg	gct	gat	ccc	gcg	caa	835	
Ala	Arg	Arg	Gln	Gly	Thr	Val	Asp	Ala	Leu	Thr	Ala	Asp	Pro	Ala	Gln		
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Val	Ser	Ser	Leu	Glu	Glu	Thr	Phe	Val	Leu	Ala	Gly	Val	Glu	Glu	Asp		
			250					255					260				
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Ile	His	Ile	Glu	Val	Ile	Pro	Gln	Ala	Ile	Pro	Ser	Pro	Arg	Glu	Trp		

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Gly Gly Ala Tyr Asp Ser Ile Val Ala Met Glu Lys Leu Glu Val Val			
280	285	290	
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Gly Lys His Gly Ser Lys Arg Phe Ile Lys Ala Ile Asp Arg Met Leu			
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Thr Thr Gly Gly Asn Val Ala Met Gln Ser Leu Val Ala Thr Asp Gln			
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Trp Ser Pro Val Cys Ser Glu Ala Ile Ser Leu Leu Lys Ala Tyr Ile			
330	335	340	
tgg cct gcg ctg cat tac cca act gtt gat gaa gtt cat cag ctt gtt			1171
Trp Pro Ala Leu His Tyr Pro Thr Val Asp Glu Val His Gln Leu Val			
345	350	355	
gat agg gat tct tct ctg cgc gtg gtg aag gaa aca cac ttt gcg ggc			1219
Asp Arg Asp Ser Ser Leu Arg Val Val Lys Glu Thr His Phe Ala Gly			
360	365	370	
cat tac cta aaa agc gtg cag ttg caa cgt gaa gtg ttt gaa ggc cag			1267
His Tyr Leu Lys Ser Val Gln Leu Gln Arg Glu Val Phe Glu Gly Gln			
375	380	385	
ata cgc gaa gcg gcg gca gat ggc ttt gat gcc gtc tac cgc cgc atg			1315
Ile Arg Glu Ala Ala Ala Asp Gly Phe Asp Ala Val Tyr Arg Arg Met			
390	395	400	405
tgg gtg tat cac tac gcg ctt att gaa gcc ctg tta cgc ctg gga tgt			1363
Trp Val Tyr His Tyr Ala Leu Ile Glu Ala Leu Leu Arg Leu Gly Cys			
410	415	420	
ctc aat gca gtg caa ttt gcg ttg acg aca aga aac aga agg ggg cgt			1411
Leu Asn Ala Val Gln Phe Ala Leu Thr Thr Arg Asn Arg Arg Gly Arg			
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Arg			

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<211> 438

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

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Ala	Arg	Gln	Ala	Glu	Tyr	Arg	Phe	Ala	Lys	Ala	Cys	Ser	Asn	Ala	Gly
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Leu Val Leu Leu Gly Asn Asp Pro Asp Leu Ile Ile Asp His Glu Glu
 50 55 60
 Leu Phe Ser Arg Leu Ala Ala Ser Gly Trp Leu Gly Leu Ala Glu Ser
 65 70 75 80
 Tyr Met Ala Gly Glu Trp Arg Ser Glu Arg Leu Ala Asp Val Leu Thr
 85 90 95
 Ala Leu Leu Gly Thr Gly Phe Lys Pro Arg Gly Lys Leu Ser Gly Ser
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 Phe Thr Leu Pro Gly Gln Ala Val Asp Ala Gly Gly Ala Leu Pro Asn
 115 120 125
 Glu Leu Ile Arg Leu Ser Ser Gly Asp Gly Met Ser Ala Phe Gly Gly
 130 135 140
 Val Phe Ala Ser Gly Val Pro Thr Thr Leu Arg Thr Ala Val Lys Ser
 145 150 155 160
 His Val Pro Gly Ala Gly Arg Asn Arg Glu Pro Ala Ser His Phe Val
 165 170 175
 Asp Ile Thr Lys Ile Ser Glu Pro Val Ala Val Glu Arg Glu Asp Leu
 180 185 190
 Gly Glu Ala Gln Arg Arg Ala Ala Ser Phe Leu Leu Asp Gly Ala Lys
 195 200 205
 Val Lys Ala Gly Ser His Val Leu Glu Phe Pro Ser Ser Gly Gly Ala
 210 215 220
 Leu Ala Ile Leu Ala Ala Arg Arg Gln Gly Thr Val Asp Ala Leu Thr
 225 230 235 240
 Ala Asp Pro Ala Gln Val Ser Ser Leu Glu Glu Thr Phe Val Leu Ala
 245 250 255
 Gly Val Glu Glu Asp Ile His Ile Glu Val Ile Pro Gln Ala Ile Pro
 260 265 270
 Ser Pro Arg Glu Trp Gly Gly Ala Tyr Asp Ser Ile Val Ala Met Glu
 275 280 285
 Lys Leu Glu Val Val Gly Lys His Gly Ser Lys Arg Phe Ile Lys Ala
 290 295 300
 Ile Asp Arg Met Leu Thr Thr Gly Gly Asn Val Ala Met Gln Ser Leu
 305 310 315 320
 Val Ala Thr Asp Gln Trp Ser Pro Val Cys Ser Glu Ala Ile Ser Leu
 325 330 335
 Leu Lys Ala Tyr Ile Trp Pro Ala Leu His Tyr Pro Thr Val Asp Glu
 340 345 350
 Val His Gln Leu Val Asp Arg Asp Ser Ser Leu Arg Val Val Lys Glu
 355 360 365

Thr His Phe Ala Gly His Tyr Leu Lys Ser Val Gln Leu Gln Arg Glu
370 375 380

Val Phe Glu Gly Gln Ile Arg Glu Ala Ala Ala Asp Gly Phe Asp Ala
385 390 395 400

Val Tyr Arg Arg Met Trp Val Tyr His Tyr Ala Leu Ile Glu Ala Leu
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420 425 430

Asn Arg Arg Gly Arg Arg
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<210> 71

<211> 1140

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1117)

<223> RXA01801

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Met Ser Asn Val Val
1 5

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Asn Thr Phe Val Gln Asn Ser Thr Gly Met Val Glu Leu Asn Arg Pro
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Lys Ala Leu Asn Ser Leu Asn Gln Glu Met Ile Asp Leu Val Gln Glu
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gct cta acc act tgg gct gat gat gat cag gtg cag cag gtt ctc att 259
Ala Leu Thr Thr Trp Ala Asp Asp Asp Gln Val Gln Gln Val Leu Ile
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Tyr Ser Ser Ser Glu Arg Ala Phe Cys Ala Gly Gly Asp Val Arg Ala
55 60 65

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Val Arg Glu Ser Val Leu Glu Gly Asp Val Ala Ala Gly Asp Lys Tyr
70 75 80 85

ttc atc gat gag ttc gcg atg aac aac acg ttg gga acc tat ccg aag 403
Phe Ile Asp Glu Phe Ala Met Asn Asn Thr Leu Gly Thr Tyr Pro Lys
90 95 100

ccg gtc att tct gtg atc aac ggc gtc gcg atg ggt ggc gga atg gga 451
Pro Val Ile Ser Val Ile Asn Gly Val Ala Met Gly Gly Gly Met Gly
105 110 115

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Ile Ser Met His Gly Ser His Arg Ile Val Thr Glu Lys Ala Phe Ala	
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tcg atg cct gag atg gcg atc ggc tat gtt ccc gat gtg ggc ttt act	547
Ser Met Pro Glu Met Ala Ile Gly Tyr Val Pro Asp Val Gly Phe Thr	
135 140 145	
tat ttc ggt cag cgt gca tcg tcg ctg gcc atc gcc aca ttt ttg gcg	595
Tyr Phe Gly Gln Arg Ala Ser Ser Leu Ala Ile Ala Thr Phe Leu Ala	
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Val Thr Gly Trp Arg Met Ser Pro Ala Asp Met Leu Trp Ala Gly Val	
170 175 180	
gca acg cat ttt gtt gag gat gcg cag ggg ttc att gat gcg gtc ttg	691
Ala Thr His Phe Val Glu Asp Ala Gln Gly Phe Ile Asp Ala Val Leu	
185 190 195	
aac gag tcg ctt gat ggc gcg ctg gag aaa ttc tcc acg caa cct acg	739
Asn Glu Ser Leu Asp Gly Ala Leu Glu Lys Phe Ser Thr Gln Pro Thr	
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Gly Ser Ser Glu Leu Ala Gly Val Ala Ser Gln Ile Glu Glu Thr Phe	
215 220 225	
ggg cac agc tct tgg gcg ctt atc gac gcc tcc ctc cgg tct cac ccc	835
Gly His Ser Ser Trp Ala Leu Ile Asp Ala Ser Leu Arg Ser His Pro	
230 235 240 245	
gat gct gaa ttt gtt gcc aag gtg gat ggg ctg atg gcg tcg gca gca	883
Asp Ala Glu Phe Val Ala Lys Val Asp Gly Leu Met Ala Ser Ala Ala	
250 255 260	
ccg gca tcg gtg gtg gct acc gtg aag ctg atg cat caa aac agt gag	931
Pro Ala Ser Val Val Ala Thr Val Lys Leu Met His Gln Asn Ser Glu	
265 270 275	
gcg acc act ctg cgt gaa ggc ttg gac aat gaa ttg gcg atg tct ctt	979
Ala Thr Thr Leu Arg Glu Gly Leu Asp Asn Glu Leu Ala Met Ser Leu	
280 285 290	
tat atg atc cgc cag cct gat ttt gct gaa ggt gtg cgt gca gtg ttg	1027
Tyr Met Ile Arg Gln Pro Asp Phe Ala Glu Gly Val Arg Ala Val Leu	
295 300 305	
gtt gat aaa gac cgc aat gca gcc ttc tcc cca gcc aac tac gaa gat	1075
Val Asp Lys Asp Arg Asn Ala Ala Phe Ser Pro Ala Asn Tyr Glu Asp	
310 315 320 325	
gtt gat gag tca cat ttt gtg acc ttg ttc cag cgc agt tca	1117
Val Asp Glu Ser His Phe Val Thr Leu Phe Gln Arg Ser Ser	
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taaaaccgcc aaacttttga tag	1140

<210> 72

<211> 339

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 72

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Glu Leu Asn Arg Pro Lys Ala Leu Asn Ser Leu Asn Gln Glu Met Ile
      20             25             30

Asp Leu Val Gln Glu Ala Leu Thr Thr Trp Ala Asp Asp Asp Gln Val
      35             40             45

Gln Gln Val Leu Ile Tyr Ser Ser Ser Glu Arg Ala Phe Cys Ala Gly
      50             55             60

Gly Asp Val Arg Ala Val Arg Glu Ser Val Leu Glu Gly Asp Val Ala
      65             70             75             80

Ala Gly Asp Lys Tyr Phe Ile Asp Glu Phe Ala Met Asn Asn Thr Leu
      85             90             95

Gly Thr Tyr Pro Lys Pro Val Ile Ser Val Ile Asn Gly Val Ala Met
      100            105            110

Gly Gly Gly Met Gly Ile Ser Met His Gly Ser His Arg Ile Val Thr
      115            120            125

Glu Lys Ala Phe Ala Ser Met Pro Glu Met Ala Ile Gly Tyr Val Pro
      130            135            140

Asp Val Gly Phe Thr Tyr Phe Gly Gln Arg Ala Ser Ser Leu Ala Ile
      145            150            155            160

Ala Thr Phe Leu Ala Val Thr Gly Trp Arg Met Ser Pro Ala Asp Met
      165            170            175

Leu Trp Ala Gly Val Ala Thr His Phe Val Glu Asp Ala Gln Gly Phe
      180            185            190

Ile Asp Ala Val Leu Asn Glu Ser Leu Asp Gly Ala Leu Glu Lys Phe
      195            200            205

Ser Thr Gln Pro Thr Gly Ser Ser Glu Leu Ala Gly Val Ala Ser Gln
      210            215            220

Ile Glu Glu Thr Phe Gly His Ser Ser Trp Ala Leu Ile Asp Ala Ser
      225            230            235            240

Leu Arg Ser His Pro Asp Ala Glu Phe Val Ala Lys Val Asp Gly Leu
      245            250            255

Met Ala Ser Ala Ala Pro Ala Ser Val Val Ala Thr Val Lys Leu Met
      260            265            270

His Gln Asn Ser Glu Ala Thr Thr Leu Arg Glu Gly Leu Asp Asn Glu
      275            280            285

Leu Ala Met Ser Leu Tyr Met Ile Arg Gln Pro Asp Phe Ala Glu Gly
      290            295            300

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Val Arg Ala Val Leu Val Asp Lys Asp Arg Asn Ala Ala Phe Ser Pro
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Ala Asn Tyr Glu Asp Val Asp Glu Ser His Phe Val Thr Leu Phe Gln
 325 330 335

Arg Ser Ser

<210> 73
 <211> 1086
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1063)
 <223> RXN02512

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tacagcaaca ccaaataaaa attagccgag ggagcatcgc atg aag ccg aag gat 115
 Met Lys Pro Lys Asp
 1 5

ttc tgc aca gcg gaa aat tgg gcg gag aat tta agc gca ctg ggc tat 163
 Phe Cys Thr Ala Glu Asn Trp Ala Glu Asn Leu Ser Ala Leu Gly Tyr
 10 15 20

cta gct ggt tgg cgt ttt gtc cgg atg ctc cct ttg cct att gct cgc 211
 Leu Ala Gly Trp Arg Phe Val Arg Met Leu Pro Leu Pro Ile Ala Arg
 25 30 35

cgg gtg ttt gac ctt ggg gcg gat ctg gcg tcg aaa agc gga aaa ggc 259
 Arg Val Phe Asp Leu Gly Ala Asp Leu Ala Ser Lys Ser Gly Lys Gly
 40 45 50

atg ggg cag cta cgc gct aat ctg gcg cgg gtg gtc ggt gcg gaa aac 307
 Met Gly Gln Leu Arg Ala Asn Leu Ala Arg Val Val Gly Ala Glu Asn
 55 60 65

gtt acg cag gcg ctg gtg aag caa gca acg cgc agc tat gcg cgg tat 355
 Val Thr Gln Ala Leu Val Lys Gln Ala Thr Arg Ser Tyr Ala Arg Tyr
 70 75 80 85

tgg ctg gaa gcg ttc cgg cta ccg gcg atc gcg cga gat cct gag ctg 403
 Trp Leu Glu Ala Phe Arg Leu Pro Ala Ile Ala Arg Asp Pro Glu Leu
 90 95 100

ctt gcg cgg ttg cgt aag gga act gtt ggc cta gat ttg ttg gat gaa 451
 Leu Ala Arg Leu Arg Lys Gly Thr Val Gly Leu Asp Leu Leu Asp Glu
 105 110 115

tct ttg gct gcc ggc aag ggc gta gtt ttg acg ctc cca cac agc ggc 499
 Ser Leu Ala Ala Gly Lys Gly Val Val Leu Thr Leu Pro His Ser Gly
 120 125 130

aac tgg gat atg gct ggc gct ttt ctg att agc cat cat ggg caa ttc 547
 Asn Trp Asp Met Ala Gly Ala Phe Leu Ile Ser His His Gly Gln Phe

135	140	145	
acc acc gtt gca gaa agg gtc aag ccg gaa cgc ttg ttt gaa gcg ttc			595
Thr Thr Val Ala Glu Arg Val Lys Pro Glu Arg Leu Phe Glu Ala Phe			
150	155	160	165
gtg gag ttt cga gaa agc ctt gga ttt gag gtg ctg cct ctc acc ggt			643
Val Glu Phe Arg Glu Ser Leu Gly Phe Glu Val Leu Pro Leu Thr Gly			
	170	175	180
ggc gag cgt ccg ccg ttt gaa aag ctg aaa gag cgc ctg aca tct gga			691
Gly Glu Arg Pro Pro Phe Glu Lys Leu Lys Glu Arg Leu Thr Ser Gly			
	185	190	195
ggt atc gtg tgc ctt ctt ggg gag cgt gac ctg cgg cat tcc ggc gtg			739
Gly Ile Val Cys Leu Leu Gly Glu Arg Asp Leu Arg His Ser Gly Val			
	200	205	210
gag acc act ttt ttt ggt gag aag acc tcc atg cca gca gga cct gcg			787
Glu Thr Thr Phe Phe Gly Glu Lys Thr Ser Met Pro Ala Gly Pro Ala			
	215	220	225
cag ctg gcc att gaa aca ggt gcg gcg ctg cac gtg gtg cat cca tgg			835
Gln Leu Ala Ile Glu Thr Gly Ala Ala Leu His Val Val His Pro Trp			
	230	235	240
ttc gat gac gac ggc tgg ggt ctc agc gta tcc gat gcc gtg acc gtg			883
Phe Asp Asp Asp Gly Trp Gly Leu Ser Val Ser Asp Ala Val Thr Val			
	250	255	260
gat aat tta tcc gac acg gtg cag cgg atc gca cat ctt ttt atg gca			931
Asp Asn Leu Ser Asp Thr Val Gln Arg Ile Ala His Leu Phe Met Ala			
	265	270	275
aat att acg gcg cac ccc gct gat tgg cat atg ctc caa ccc ctg tgg			979
Asn Ile Thr Ala His Pro Ala Asp Trp His Met Leu Gln Pro Leu Trp			
	280	285	290
ttt ggt gat ttg gat ccg gag cgt ctc aag cgc tct agg gag cag aca			1027
Phe Gly Asp Leu Asp Pro Glu Arg Leu Lys Arg Ser Arg Glu Gln Thr			
	295	300	305
aat gtt cac aaa ccg gtg gca tta cag gag gac aat taggtgcgaa			1073
Asn Val His Lys Pro Val Ala Leu Gln Glu Asp Asn			
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ttggaatggt ctg			1086

<210> 74

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 74

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Ser	Ala	Leu	Gly	Tyr	Leu	Ala	Gly	Trp	Arg	Phe	Val	Arg	Met	Leu	Pro
			20					25					30		

Leu Pro Ile Ala Arg Arg Val Phe Asp Leu Gly Ala Asp Leu Ala Ser
 35 40 45
 Lys Ser Gly Lys Gly Met Gly Gln Leu Arg Ala Asn Leu Ala Arg Val
 50 55 60
 Val Gly Ala Glu Asn Val Thr Gln Ala Leu Val Lys Gln Ala Thr Arg
 65 70 75 80
 Ser Tyr Ala Arg Tyr Trp Leu Glu Ala Phe Arg Leu Pro Ala Ile Ala
 85 90 95
 Arg Asp Pro Glu Leu Leu Ala Arg Leu Arg Lys Gly Thr Val Gly Leu
 100 105 110
 Asp Leu Leu Asp Glu Ser Leu Ala Ala Gly Lys Gly Val Val Leu Thr
 115 120 125
 Leu Pro His Ser Gly Asn Trp Asp Met Ala Gly Ala Phe Leu Ile Ser
 130 135 140
 His His Gly Gln Phe Thr Thr Val Ala Glu Arg Val Lys Pro Glu Arg
 145 150 155 160
 Leu Phe Glu Ala Phe Val Glu Phe Arg Glu Ser Leu Gly Phe Glu Val
 165 170 175
 Leu Pro Leu Thr Gly Gly Glu Arg Pro Pro Phe Glu Lys Leu Lys Glu
 180 185 190
 Arg Leu Thr Ser Gly Gly Ile Val Cys Leu Leu Gly Glu Arg Asp Leu
 195 200 205
 Arg His Ser Gly Val Glu Thr Thr Phe Phe Gly Glu Lys Thr Ser Met
 210 215 220
 Pro Ala Gly Pro Ala Gln Leu Ala Ile Glu Thr Gly Ala Ala Leu His
 225 230 235 240
 Val Val His Pro Trp Phe Asp Asp Asp Gly Trp Gly Leu Ser Val Ser
 245 250 255
 Asp Ala Val Thr Val Asp Asn Leu Ser Asp Thr Val Gln Arg Ile Ala
 260 265 270
 His Leu Phe Met Ala Asn Ile Thr Ala His Pro Ala Asp Trp His Met
 275 280 285
 Leu Gln Pro Leu Trp Phe Gly Asp Leu Asp Pro Glu Arg Leu Lys Arg
 290 295 300
 Ser Arg Glu Gln Thr Asn Val His Lys Pro Val Ala Leu Gln Glu Asp
 305 310 315 320
 Asn

<210> 75

<211> 1057

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> FRXA02512

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				Met	Lys	Pro	Lys	Asp	
				1				5	

ttc	tgc	aca	gcg	gaa	aat	tgg	gcg	gag	aat	tta	agc	gca	ctg	ggc	tat	163
Phe	Cys	Thr	Ala	Glu	Asn	Trp	Ala	Glu	Asn	Leu	Ser	Ala	Leu	Gly	Tyr	
			10					15						20		

cta	gct	ggt	tgg	cgt	ttt	gtc	cgg	atg	ctc	cct	ttg	cct	att	gct	cgc	211
Leu	Ala	Gly	Trp	Arg	Phe	Val	Arg	Met	Leu	Pro	Leu	Pro	Ile	Ala	Arg	
			25					30					35			

cgg	gtg	ttt	gac	ctt	ggg	gcg	gat	ctg	gcg	tcg	aaa	agc	gga	aaa	ggc	259
Arg	Val	Phe	Asp	Leu	Gly	Ala	Asp	Leu	Ala	Ser	Lys	Ser	Gly	Lys	Gly	
		40					45					50				

atg	ggg	cag	cta	cgc	gct	aat	ctg	gcg	cgg	gtg	gtc	ggt	gcg	gaa	aac	307
Met	Gly	Gln	Leu	Arg	Ala	Asn	Leu	Ala	Arg	Val	Val	Gly	Ala	Glu	Asn	
	55					60					65					

gtt	acg	cag	gcg	ctg	gtg	aag	caa	gca	acg	cgc	agc	tat	gcg	cgg	tat	355
Val	Thr	Gln	Ala	Leu	Val	Lys	Gln	Ala	Thr	Arg	Ser	Tyr	Ala	Arg	Tyr	
70					75					80					85	

tgg	ctg	gaa	gcg	ttc	cgg	cta	ccg	gcg	atc	gcg	cga	gat	cct	gag	ctg	403
Trp	Leu	Glu	Ala	Phe	Arg	Leu	Pro	Ala	Ile	Ala	Arg	Asp	Pro	Glu	Leu	
			90						95					100		

ctt	gcg	cgg	ttg	cgt	aag	gga	act	gtt	ggc	cta	gat	ttg	ttg	gat	gaa	451
Leu	Ala	Arg	Leu	Arg	Lys	Gly	Thr	Val	Gly	Leu	Asp	Leu	Leu	Asp	Glu	
			105					110					115			

tct	ttg	gct	gcc	ggc	aag	ggc	gta	gtt	ttg	acg	ctc	cca	cac	agc	ggc	499
Ser	Leu	Ala	Ala	Gly	Lys	Gly	Val	Val	Leu	Thr	Leu	Pro	His	Ser	Gly	
	120					125						130				

aac	tgg	gat	atg	gct	ggc	gct	ttt	ctg	att	agc	cat	cat	ggg	caa	ttc	547
Asn	Trp	Asp	Met	Ala	Gly	Ala	Phe	Leu	Ile	Ser	His	His	Gly	Gln	Phe	
	135					140					145					

acc	acc	gtt	gca	gaa	agg	gtc	aag	ccg	gaa	cgc	ttg	ttt	gaa	gcg	ttc	595
Thr	Thr	Val	Ala	Glu	Arg	Val	Lys	Pro	Glu	Arg	Leu	Phe	Glu	Ala	Phe	
150					155				160						165	

gtg	gag	ttt	cga	gaa	agc	ctt	gga	ttt	gag	gtg	ctg	cct	ctc	acc	ggc	643
Val	Glu	Phe	Arg	Glu	Ser	Leu	Gly	Phe	Glu	Val	Leu	Pro	Leu	Thr	Gly	
			170					175						180		

ggc	gag	cgt	ccg	ccg	ttt	gaa	aag	ctg	aaa	gag	cgc	ctg	aca	tct	gga	691
Gly	Glu	Arg	Pro	Pro	Phe	Glu	Lys	Leu	Lys	Glu	Arg	Leu	Thr	Ser	Gly	
			185					190					195			

ggt atc gtg tgc ctt ctt ggg gag cgt gac ctg cgg cat tcc ggc gtg 739
 Gly Ile Val Cys Leu Leu Gly Glu Arg Asp Leu Arg His Ser Gly Val
 200 205 210
 gag acc act ttt ttt ggt gag aag acc tcc atg cca gca gga cct gcg 787
 Glu Thr Thr Phe Phe Gly Glu Lys Thr Ser Met Pro Ala Gly Pro Ala
 215 220 225
 cag ctg gcc att gaa aca ggt gcg gcg ctg cac gtg gtg cat cca tgg 835
 Gln Leu Ala Ile Glu Thr Gly Ala Ala Leu His Val Val His Pro Trp
 230 235 240 245
 ttc gat gac gac ggc tgg ggt ctc agc gta tcc gat gcc gtg acc gtg 883
 Phe Asp Asp Asp Gly Trp Gly Leu Ser Val Ser Asp Ala Val Thr Val
 250 255 260
 gat aat tta tcc gac acg gtg cag cgg atc gca cat ctt ttt atg gca 931
 Asp Asn Leu Ser Asp Thr Val Gln Arg Ile Ala His Leu Phe Met Ala
 265 270 275
 aat att acg gcg cac ccc gct gat tgg cat atg ctc caa ccc ctg tgg 979
 Asn Ile Thr Ala His Pro Ala Asp Trp His Met Leu Gln Pro Leu Trp
 280 285 290
 ttt ggt gat ttg gat ccg gag cgt ctc aag cgc tct agg gag cag aca 1027
 Phe Gly Asp Leu Asp Pro Glu Arg Leu Lys Arg Ser Arg Glu Gln Thr
 295 300 305
 aat gtt cac aaa ccg gtg gca tta cag gag 1057
 Asn Val His Lys Pro Val Ala Leu Gln Glu
 310 315

<210> 76
 <211> 319
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 76
 Met Lys Pro Lys Asp Phe Cys Thr Ala Glu Asn Trp Ala Glu Asn Leu
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 Ser Ala Leu Gly Tyr Leu Ala Gly Trp Arg Phe Val Arg Met Leu Pro
 20 25 30
 Leu Pro Ile Ala Arg Arg Val Phe Asp Leu Gly Ala Asp Leu Ala Ser
 35 40 45
 Lys Ser Gly Lys Gly Met Gly Gln Leu Arg Ala Asn Leu Ala Arg Val
 50 55 60
 Val Gly Ala Glu Asn Val Thr Gln Ala Leu Val Lys Gln Ala Thr Arg
 65 70 75 80
 Ser Tyr Ala Arg Tyr Trp Leu Glu Ala Phe Arg Leu Pro Ala Ile Ala
 85 90 95
 Arg Asp Pro Glu Leu Leu Ala Arg Leu Arg Lys Gly Thr Val Gly Leu
 100 105 110

Asp Leu Leu Asp Glu Ser Leu Ala Ala Gly Lys Gly Val Val Leu Thr
 115 120 125
 Leu Pro His Ser Gly Asn Trp Asp Met Ala Gly Ala Phe Leu Ile Ser
 130 135 140
 His His Gly Gln Phe Thr Thr Val Ala Glu Arg Val Lys Pro Glu Arg
 145 150 155 160
 Leu Phe Glu Ala Phe Val Glu Phe Arg Glu Ser Leu Gly Phe Glu Val
 165 170 175
 Leu Pro Leu Thr Gly Gly Glu Arg Pro Pro Phe Glu Lys Leu Lys Glu
 180 185 190
 Arg Leu Thr Ser Gly Gly Ile Val Cys Leu Leu Gly Glu Arg Asp Leu
 195 200 205
 Arg His Ser Gly Val Glu Thr Thr Phe Phe Gly Glu Lys Thr Ser Met
 210 215 220
 Pro Ala Gly Pro Ala Gln Leu Ala Ile Glu Thr Gly Ala Ala Leu His
 225 230 235 240
 Val Val His Pro Trp Phe Asp Asp Asp Gly Trp Gly Leu Ser Val Ser
 245 250 255
 Asp Ala Val Thr Val Asp Asn Leu Ser Asp Thr Val Gln Arg Ile Ala
 260 265 270
 His Leu Phe Met Ala Asn Ile Thr Ala His Pro Ala Asp Trp His Met
 275 280 285
 Leu Gln Pro Leu Trp Phe Gly Asp Leu Asp Pro Glu Arg Leu Lys Arg
 290 295 300
 Ser Arg Glu Gln Thr Asn Val His Lys Pro Val Ala Leu Gln Glu
 305 310 315

<210> 77
 <211> 1389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1366)
 <223> RXA00899

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ccggtgacgc caccgcatcc aacaagaaat caacgacctc atg gaa gac gtc cac 115
 Met Glu Asp Val His
 1 5

gac gac gtc ccc gac atc ccc acc gga atg gat gtc tcc gcg gaa gtt 163
 Asp Asp Val Pro Asp Ile Pro Thr Gly Met Asp Val Ser Ala Glu Val
 10 15 20

gaa tct gtc atc aaa ctc aac cgc cgc ctc acc cgc atg cca gca gtg	211
Glu Ser Val Ile Lys Leu Asn Arg Arg Leu Thr Arg Met Pro Ala Val	
25 30 35	
acc ggc gga aac aac ggc ttc tac tcc gac tac cgt gaa tcc ctc aaa	259
Thr Gly Gly Asn Asn Gly Phe Tyr Ser Asp Tyr Arg Glu Ser Leu Lys	
40 45 50	
cgg atg acc gcc gca atc gac gaa gcc gaa gaa tac atc tac gtc gag	307
Arg Met Thr Ala Ala Ile Asp Glu Ala Glu Glu Tyr Ile Tyr Val Glu	
55 60 65	
atc tac atc atg gcc tgg gat tcc tac acc caa cca ttc ttc gca gca	355
Ile Tyr Ile Met Ala Trp Asp Ser Tyr Thr Gln Pro Phe Phe Ala Ala	
70 75 80 85	
ctc gaa cga gcc cac aac cgc ggc gtc aaa gtc cga ctc ctt ttc gac	403
Leu Glu Arg Ala His Asn Arg Gly Val Lys Val Arg Leu Leu Phe Asp	
90 95 100	
cac gtc ggc agc tgg aaa tac ccc ggc tac cac cgc ctc aaa aaa gaa	451
His Val Gly Ser Trp Lys Tyr Pro Gly Tyr His Arg Leu Lys Lys Glu	
105 110 115	
ctc aac cgc atg ggc ttc gcc tgg tac ctc atg ctc ccc ctc caa ccc	499
Leu Asn Arg Met Gly Phe Ala Trp Tyr Leu Met Leu Pro Leu Gln Pro	
120 125 130	
tgg cga cgc cgc ttc cgc cga ccc gac ctg cgc aac cac cgc aaa atg	547
Trp Arg Arg Arg Phe Arg Arg Pro Asp Leu Arg Asn His Arg Lys Met	
135 140 145	
ctc atc atc gac ggc cac acc gca ttc atg ggc tcc caa aat ctc atc	595
Leu Ile Ile Asp Gly His Thr Ala Phe Met Gly Ser Gln Asn Leu Ile	
150 155 160 165	
gcc ccg agt tac cta caa aag aaa aac atc aaa ctc ggc cgc gaa tgg	643
Ala Pro Ser Tyr Leu Gln Lys Lys Asn Ile Lys Leu Gly Arg Glu Trp	
170 175 180	
aaa gac ctc atg gtc gaa ctc acc ggc ccc atc gtc tcc tcc atg gaa	691
Lys Asp Leu Met Val Glu Leu Thr Gly Pro Ile Val Ser Ser Met Glu	
185 190 195	
atg atc ttc gcc ggc gac tgg tac gtc gaa tcc aac gaa gcc ctc gac	739
Met Ile Phe Ala Gly Asp Trp Tyr Val Glu Ser Asn Glu Ala Leu Asp	
200 205 210	
atc cgc gac cac gca gaa gcc cac ggc tac atc ggc aac act caa aaa	787
Ile Arg Asp His Ala Glu Ala His Gly Tyr Ile Gly Asn Thr Gln Lys	
215 220 225	
gac tcc gcc acc aac ctc gtg cag ctc atc ccc tcc ggc cct ggt tac	835
Asp Ser Ala Thr Asn Leu Val Gln Leu Ile Pro Ser Gly Pro Gly Tyr	
230 235 240 245	
acc aca gaa ccc aac ctg cgc atg ttc aac tcc atc gtt cac cac gcc	883
Thr Thr Glu Pro Asn Leu Arg Met Phe Asn Ser Ile Val His His Ala	
250 255 260	
aaa gaa cga ctc atc ttg tgc agc ccc tac ttc atc ccc gac gaa tcc	931

Lys Glu Arg Leu Ile Leu Cys Ser Pro Tyr Phe Ile Pro Asp Glu Ser
 265 270 275
 ctc ctc gaa gcc gtc acc tca gcc tgc tac cgc gga gta acc gtc gaa 979
 Leu Leu Glu Ala Val Thr Ser Ala Cys Tyr Arg Gly Val Thr Val Glu
 280 285 290
 cta ttc gtc tct gaa caa gcc gac caa ttc gcc atc gac cac gcc caa 1027
 Leu Phe Val Ser Glu Gln Ala Asp Gln Phe Ala Ile Asp His Ala Gln
 295 300 305
 tcc tcc tac tac cag gca ctc ctt gaa gcc ggc gtg aaa atc tac caa 1075
 Ser Ser Tyr Tyr Gln Ala Leu Leu Glu Ala Gly Val Lys Ile Tyr Gln
 310 315 320 325
 ttc ccc aaa ccc gac gtc ctc cac acc aag tac atg atc gcc gac ccc 1123
 Phe Pro Lys Pro Asp Val Leu His Thr Lys Tyr Met Ile Ala Asp Pro
 330 335 340
 gac gac acc acc ggc aac gaa gcc ctc gga gtc ctc gga tcc tcc aac 1171
 Asp Asp Thr Thr Gly Asn Glu Ala Leu Gly Val Leu Gly Ser Ser Asn
 345 350 355
 ctc gac atc cgc agc ttt ggc ctc aac tac gaa atc tcc ctg atg atc 1219
 Leu Asp Ile Arg Ser Phe Gly Leu Asn Tyr Glu Ile Ser Leu Met Ile
 360 365 370
 gcc aaa ggc aac ctc atc cac gaa ctc aac gcc ctc acc gac cgt tac 1267
 Ala Lys Gly Asn Leu Ile His Glu Leu Asn Ala Leu Thr Asp Arg Tyr
 375 380 385
 cgc aca gta agt ttc aag ctc acc ttg gat aag tgg aac cag cgc agt 1315
 Arg Thr Val Ser Phe Lys Leu Thr Leu Asp Lys Trp Asn Gln Arg Ser
 390 395 400 405
 tgg cgg cgc cgc tac gtg gac aat gtc atg cgt ttg acc tcg gcg ctg 1363
 Trp Arg Arg Arg Tyr Val Asp Asn Val Met Arg Leu Thr Ser Ala Leu
 410 415 420
 cag tagtttggcg cgtttggagt gcg 1389
 Gln

<210> 78

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 78

Met Glu Asp Val His Asp Asp Val Pro Asp Ile Pro Thr Gly Met Asp
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Val Ser Ala Glu Val Glu Ser Val Ile Lys Leu Asn Arg Arg Leu Thr
 20 25 30

Arg Met Pro Ala Val Thr Gly Gly Asn Asn Gly Phe Tyr Ser Asp Tyr
 35 40 45

Arg Glu Ser Leu Lys Arg Met Thr Ala Ala Ile Asp Glu Ala Glu Glu
 50 55 60

Tyr Ile Tyr Val Glu Ile Tyr Ile Met Ala Trp Asp Ser Tyr Thr Gln
 65 70 75 80
 Pro Phe Phe Ala Ala Leu Glu Arg Ala His Asn Arg Gly Val Lys Val
 85 90 95
 Arg Leu Leu Phe Asp His Val Gly Ser Trp Lys Tyr Pro Gly Tyr His
 100 105 110
 Arg Leu Lys Lys Glu Leu Asn Arg Met Gly Phe Ala Trp Tyr Leu Met
 115 120 125
 Leu Pro Leu Gln Pro Trp Arg Arg Arg Phe Arg Arg Pro Asp Leu Arg
 130 135 140
 Asn His Arg Lys Met Leu Ile Ile Asp Gly His Thr Ala Phe Met Gly
 145 150 155 160
 Ser Gln Asn Leu Ile Ala Pro Ser Tyr Leu Gln Lys Lys Asn Ile Lys
 165 170 175
 Leu Gly Arg Glu Trp Lys Asp Leu Met Val Glu Leu Thr Gly Pro Ile
 180 185 190
 Val Ser Ser Met Glu Met Ile Phe Ala Gly Asp Trp Tyr Val Glu Ser
 195 200 205
 Asn Glu Ala Leu Asp Ile Arg Asp His Ala Glu Ala His Gly Tyr Ile
 210 215 220
 Gly Asn Thr Gln Lys Asp Ser Ala Thr Asn Leu Val Gln Leu Ile Pro
 225 230 235 240
 Ser Gly Pro Gly Tyr Thr Thr Glu Pro Asn Leu Arg Met Phe Asn Ser
 245 250 255
 Ile Val His His Ala Lys Glu Arg Leu Ile Leu Cys Ser Pro Tyr Phe
 260 265 270
 Ile Pro Asp Glu Ser Leu Leu Glu Ala Val Thr Ser Ala Cys Tyr Arg
 275 280 285
 Gly Val Thr Val Glu Leu Phe Val Ser Glu Gln Ala Asp Gln Phe Ala
 290 295 300
 Ile Asp His Ala Gln Ser Ser Tyr Tyr Gln Ala Leu Leu Glu Ala Gly
 305 310 315 320
 Val Lys Ile Tyr Gln Phe Pro Lys Pro Asp Val Leu His Thr Lys Tyr
 325 330 335
 Met Ile Ala Asp Pro Asp Asp Thr Thr Gly Asn Glu Ala Leu Gly Val
 340 345 350
 Leu Gly Ser Ser Asn Leu Asp Ile Arg Ser Phe Gly Leu Asn Tyr Glu
 355 360 365
 Ile Ser Leu Met Ile Ala Lys Gly Asn Leu Ile His Glu Leu Asn Ala
 370 375 380

Leu Thr Asp Arg Tyr Arg Thr Val Ser Phe Lys Leu Thr Leu Asp Lys
 385 390 395 400

Trp Asn Gln Arg Ser Trp Arg Arg Arg Tyr Val Asp Asn Val Met Arg
 405 410 415

Leu Thr Ser Ala Leu Gln
 420

<210> 79
 <211> 1452
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1429)
 <223> RXN00819

<400> 79
 gatgaggttc gtccgggaat cctcaaagac aatgcggtga aggtacttgg cctagccgct 60
 agcactgagc gcggatctca agcagaaaag gtcgtgcaac atg cgt gat ccc att 115
 Met Arg Asp Pro Ile
 1 5

caa ggt gct gtt att cct tct gat ctt ttt ggt ttc gca gaa gtt ctc 163
 Gln Gly Ala Val Ile Pro Ser Asp Leu Phe Gly Phe Ala Glu Val Leu
 10 15 20

acc gaa gcc gaa cgc gca gtt ctt ctg gaa acc cgc agg gtg ctt gag 211
 Thr Glu Ala Glu Arg Ala Val Leu Leu Glu Thr Arg Arg Val Leu Glu
 25 30 35

gaa gag gtg aag cct tat att aat gag gcc tgg gat aag gca gtc ttc 259
 Glu Glu Val Lys Pro Tyr Ile Asn Glu Ala Trp Asp Lys Ala Val Phe
 40 45 50

ccc gat gag atc gtg cag ccc ctc caa gat ctg caa ttg ctt gat ccg 307
 Pro Asp Glu Ile Val Gln Pro Leu Gln Asp Leu Gln Leu Leu Asp Pro
 55 60 65

cct gca ctt cgg gaa gca ggg gag tcg gtt cga gac att ttc act ggt 355
 Pro Ala Leu Arg Glu Ala Gly Glu Ser Val Arg Asp Ile Phe Thr Gly
 70 75 80 85

ttc cgc aat ttt gaa ctc gcg cgc tgt gac atc aat gtt ggt acc tat 403
 Phe Arg Asn Phe Glu Leu Ala Arg Cys Asp Ile Asn Val Gly Thr Tyr
 90 95 100

tac aac gca tct gct ggt ctc ttc cga acg gcc tgc atg gtt ggt ggc 451
 Tyr Asn Ala Ser Ala Gly Leu Phe Arg Thr Ala Cys Met Val Gly Gly
 105 110 115

tcc ccg gag cag gcg cag cga ttg gat gcg cag atc aaa tct ggt gag 499
 Ser Pro Glu Gln Ala Gln Arg Leu Asp Ala Gln Ile Lys Ser Gly Glu
 120 125 130

gtc aag ggc gtt ttt gca ctg acg gaa cct gat cat ggc tct gat atc 547
 Val Lys Gly Val Phe Ala Leu Thr Glu Pro Asp His Gly Ser Asp Ile

135	140	145	
gca ggt ggt ctg gca acc acg gcc act aag gac gca gac acc ggc gag Ala Gly Gly Leu Ala Thr Thr Ala Thr Lys Asp Ala Asp Thr Gly Glu 150 155 160 165			595
tgg att atc aat ggt gaa aaa cgg tgg atc ggt ggt gct tcc act gct Trp Ile Ile Asn Gly Glu Lys Arg Trp Ile Gly Gly Ala Ser Thr Ala 170 175 180			643
gat ttg atc gct acc ttc gcc agg gat aca gcc gat aac cag gtg aaa Asp Leu Ile Ala Thr Phe Ala Arg Asp Thr Ala Asp Asn Gln Val Lys 185 190 195			691
tgc ttc ctc gtg gca cct cag gca gag ggc gtg tcc atg gag att att Cys Phe Leu Val Ala Pro Gln Ala Glu Gly Val Ser Met Glu Ile Ile 200 205 210			739
gat cgc aaa gcc tca ctg cgc atc atg caa aat gca cac att acc tat Asp Arg Lys Ala Ser Leu Arg Ile Met Gln Asn Ala His Ile Thr Tyr 215 220 225			787
aac aat gtc cgg gtg tct ggg gat gcg cgg ctg cac aac atc aat tct Asn Asn Val Arg Val Ser Gly Asp Ala Arg Leu His Asn Ile Asn Ser 230 235 240 245			835
ttc aag gat gtt tgc gaa tgc ctg cgc cgt atg cgt tcc gat gtg gcg Phe Lys Asp Val Ser Glu Cys Leu Arg Arg Met Arg Ser Asp Val Ala 250 255 260			883
tgg atg gcg gtc ggt gcg cag gca ggt gcc tat gaa gca gcc gtg aag Trp Met Ala Val Gly Ala Gln Ala Gly Ala Tyr Glu Ala Ala Val Lys 265 270 275			931
tat gtg cgc agc agg gaa cag ttt ggc cgt ccg atc gcg ggg ttc cag Tyr Val Arg Ser Arg Glu Gln Phe Gly Arg Pro Ile Ala Gly Phe Gln 280 285 290			979
ttg att cag gaa aag ctc gcg ctc atg ctg ggc aat ctc acg gcg tgc Leu Ile Gln Glu Lys Leu Ala Leu Met Leu Gly Asn Leu Thr Ala Ser 295 300 305			1027
ctg ggc atg atg gtc aaa ctc acc gat cag cag cag gcg gga att ttc Leu Gly Met Met Val Lys Leu Thr Asp Gln Gln Gln Ala Gly Ile Phe 310 315 320 325			1075
aaa gag gaa aac tcc gcg ctg gcg aaa atg ttt acc tcg ctc aaa ctt Lys Glu Glu Asn Ser Ala Leu Ala Lys Met Phe Thr Ser Leu Lys Leu 330 335 340			1123
cgg gag acc gct agt tgg gcg cgg gaa atc tgc gga ggc aac ggc atc Arg Glu Thr Ala Ser Trp Ala Arg Glu Ile Cys Gly Gly Asn Gly Ile 345 350 355			1171
att ttg gac aac gat gtt gcc cgg ttc cat gcc gat gca gaa gcc gtc Ile Leu Asp Asn Asp Val Ala Arg Phe His Ala Asp Ala Glu Ala Val 360 365 370			1219
tat tca tat gaa ggc acc cac gaa atc aat gca ctc atc gtt ggn cgn Tyr Ser Tyr Glu Gly Thr His Glu Ile Asn Ala Leu Ile Val Gly Arg 375 380 385			1267

ncc att ctg ggn cnt ctn ttc ttt tta tat tat nac nct ttt gag gag 1315
 Xaa Ile Leu Gly Xaa Leu Phe Phe Leu Tyr Tyr Xaa Xaa Phe Glu Glu
 390 395 400 405

gat ctt cat gac tac ttc cac cac ccc aaa cca tcg ttt ctt tcg aag 1363
 Asp Leu His Asp Tyr Phe His His Pro Lys Pro Ser Phe Leu Ser Lys
 410 415 420

acg cac caa ccc tca ccg gcc agg acc tgg gct ttt cgc agt ggc gca 1411
 Thr His Gln Pro Ser Pro Ala Arg Thr Trp Ala Phe Arg Ser Gly Ala
 425 430 435

ctg tca ccc agg aga tgg tgaacacctt ggcgagcgca act 1452
 Leu Ser Pro Arg Arg Trp
 440

<210> 80

<211> 443

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

Met Arg Asp Pro Ile Gln Gly Ala Val Ile Pro Ser Asp Leu Phe Gly
 1 5 10 15

Phe Ala Glu Val Leu Thr Glu Ala Glu Arg Ala Val Leu Leu Glu Thr
 20 25 30

Arg Arg Val Leu Glu Glu Glu Val Lys Pro Tyr Ile Asn Glu Ala Trp
 35 40 45

Asp Lys Ala Val Phe Pro Asp Glu Ile Val Gln Pro Leu Gln Asp Leu
 50 55 60

Gln Leu Leu Asp Pro Pro Ala Leu Arg Glu Ala Gly Glu Ser Val Arg
 65 70 75 80

Asp Ile Phe Thr Gly Phe Arg Asn Phe Glu Leu Ala Arg Cys Asp Ile
 85 90 95

Asn Val Gly Thr Tyr Tyr Asn Ala Ser Ala Gly Leu Phe Arg Thr Ala
 100 105 110

Cys Met Val Gly Gly Ser Pro Glu Gln Ala Gln Arg Leu Asp Ala Gln
 115 120 125

Ile Lys Ser Gly Glu Val Lys Gly Val Phe Ala Leu Thr Glu Pro Asp
 130 135 140

His Gly Ser Asp Ile Ala Gly Gly Leu Ala Thr Thr Ala Thr Lys Asp
 145 150 155 160

Ala Asp Thr Gly Glu Trp Ile Ile Asn Gly Glu Lys Arg Trp Ile Gly
 165 170 175

Gly Ala Ser Thr Ala Asp Leu Ile Ala Thr Phe Ala Arg Asp Thr Ala
 180 185 190

Asp Asn Gln Val Lys Cys Phe Leu Val Ala Pro Gln Ala Glu Gly Val

195	200	205
Ser Met Glu Ile Ile Asp Arg Lys Ala Ser Leu Arg Ile Met Gln Asn 210 215 220		
Ala His Ile Thr Tyr Asn Asn Val Arg Val Ser Gly Asp Ala Arg Leu 225 230 235 240		
His Asn Ile Asn Ser Phe Lys Asp Val Ser Glu Cys Leu Arg Arg Met 245 250 255		
Arg Ser Asp Val Ala Trp Met Ala Val Gly Ala Gln Ala Gly Ala Tyr 260 265 270		
Glu Ala Ala Val Lys Tyr Val Arg Ser Arg Glu Gln Phe Gly Arg Pro 275 280 285		
Ile Ala Gly Phe Gln Leu Ile Gln Glu Lys Leu Ala Leu Met Leu Gly 290 295 300		
Asn Leu Thr Ala Ser Leu Gly Met Met Val Lys Leu Thr Asp Gln Gln 305 310 315 320		
Gln Ala Gly Ile Phe Lys Glu Glu Asn Ser Ala Leu Ala Lys Met Phe 325 330 335		
Thr Ser Leu Lys Leu Arg Glu Thr Ala Ser Trp Ala Arg Glu Ile Cys 340 345 350		
Gly Gly Asn Gly Ile Ile Leu Asp Asn Asp Val Ala Arg Phe His Ala 355 360 365		
Asp Ala Glu Ala Val Tyr Ser Tyr Glu Gly Thr His Glu Ile Asn Ala 370 375 380		
Leu Ile Val Gly Arg Xaa Ile Leu Gly Xaa Leu Phe Phe Leu Tyr Tyr 385 390 395 400		
Xaa Xaa Phe Glu Glu Asp Leu His Asp Tyr Phe His His Pro Lys Pro 405 410 415		
Ser Phe Leu Ser Lys Thr His Gln Pro Ser Pro Ala Arg Thr Trp Ala 420 425 430		
Phe Arg Ser Gly Ala Leu Ser Pro Arg Arg Trp 435 440		

<210> 81
 <211> 1030
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (18)..(1007)
 <223> FRXA00819

<400> 81
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 Met Val Gly Gly Ser Pro Glu Gln Ala Gln Arg Leu

	1	5	10	
gat gcg cag atc aaa tct ggt gag gtc aag ggc gtt ttt gca ctg acg				101
Asp Ala Gln Ile Lys Ser Gly Glu Val Lys Gly Val Phe Ala Leu Thr	15	20	25	
gaa cct gat cat ggc tct gat atc gca ggt ggt ctg gca acc acg gcc				149
Glu Pro Asp His Gly Ser Asp Ile Ala Gly Gly Leu Ala Thr Thr Ala	30	35	40	
act aag gac gca gac acc ggc gag tgg att atc aat ggt gaa aaa cgg				197
Thr Lys Asp Ala Asp Thr Gly Glu Trp Ile Ile Asn Gly Glu Lys Arg	45	50	55	60
tgg atc ggt ggt gct tcc act gct gat ttg atc gct acc ttc gcc agg				245
Trp Ile Gly Gly Ala Ser Thr Ala Asp Leu Ile Ala Thr Phe Ala Arg	65	70	75	
gat aca gcc gat aac cag gtg aaa tgc ttc ctc gtg gca cct cag gca				293
Asp Thr Ala Asp Asn Gln Val Lys Cys Phe Leu Val Ala Pro Gln Ala	80	85	90	
gag ggc gtg tcc atg gag att att gat cgc aaa gcc tca ctg cgc atc				341
Glu Gly Val Ser Met Glu Ile Ile Asp Arg Lys Ala Ser Leu Arg Ile	95	100	105	
atg caa aat gca cac att acc tat aac aat gtc cgg gtg tct ggg gat				389
Met Gln Asn Ala His Ile Thr Tyr Asn Asn Val Arg Val Ser Gly Asp	110	115	120	
gcg cgg ctg cac aac atc aat tct ttc aag gat gtt tcg gaa tgc ctg				437
Ala Arg Leu His Asn Ile Asn Ser Phe Lys Asp Val Ser Glu Cys Leu	125	130	135	140
cgc cgt atg cgt tcc gat gtg gcg tgg atg gcg gtc ggt gcg cag gca				485
Arg Arg Met Arg Ser Asp Val Ala Trp Met Ala Val Gly Ala Gln Ala	145	150	155	
ggt gcc tat gaa gca gcc gtg aag tat gtg cgc agc agg gaa cag ttt				533
Gly Ala Tyr Glu Ala Ala Val Lys Tyr Val Arg Ser Arg Glu Gln Phe	160	165	170	
ggc cgt ccg atc gcg ggg ttc cag ttg att cag gaa aag ctc gcg ctc				581
Gly Arg Pro Ile Ala Gly Phe Gln Leu Ile Gln Glu Lys Leu Ala Leu	175	180	185	
atg ctg ggc aat ctc acg gcg tcg ctg ggc atg atg gtc aaa ctc acc				629
Met Leu Gly Asn Leu Thr Ala Ser Leu Gly Met Met Val Lys Leu Thr	190	195	200	
gat cag cag cag gcg gga att ttc aaa gag gaa aac tcc gcg ctg gcg				677
Asp Gln Gln Gln Ala Gly Ile Phe Lys Glu Glu Asn Ser Ala Leu Ala	205	210	215	220
aaa atg ttt acc tcg ctc aaa ctt cgg gag acc gct agt tgg gcg cgg				725
Lys Met Phe Thr Ser Leu Lys Leu Arg Glu Thr Ala Ser Trp Ala Arg	225	230	235	
gaa atc tgc gga ggc aac ggc atc att ttg gac aac gat gtt gcc cgg				773
Glu Ile Cys Gly Gly Asn Gly Ile Ile Leu Asp Asn Asp Val Ala Arg	240	245	250	

ttc cat gcc gat gca gaa gcc gtc tat tca tat gaa ggc acc cac gaa 821
 Phe His Ala Asp Ala Glu Ala Val Tyr Ser Tyr Glu Gly Thr His Glu
 255 260 265

atc aat gca ctc atc gtt ggn cgn ncc att ctg ggn cnt ctn ttc ttt 869
 Ile Asn Ala Leu Ile Val Gly Arg Xaa Ile Leu Gly Xaa Leu Phe Phe
 270 275 280

tta tat tat nac nct ttt gag gag gat ctt cat gac tac ttc cac cac 917
 Leu Tyr Tyr Xaa Xaa Phe Glu Glu Asp Leu His Asp Tyr Phe His His
 285 290 295 300

ccc aaa cca tcg ttt ctt tcg aag acg cac caa ccc tca ccg gcc agg 965
 Pro Lys Pro Ser Phe Leu Ser Lys Thr His Gln Pro Ser Pro Ala Arg
 305 310 315

acc tgg gct ttt cgc agt ggc gca ctg tca ccc agg aga tgg 1007
 Thr Trp Ala Phe Arg Ser Gly Ala Leu Ser Pro Arg Arg Trp
 320 325 330

tgaacacctt cgcggacgca act 1030

<210> 82
 <211> 330
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 82
 Met Val Gly Gly Ser Pro Glu Gln Ala Gln Arg Leu Asp Ala Gln Ile
 1 5 10 15

Lys Ser Gly Glu Val Lys Gly Val Phe Ala Leu Thr Glu Pro Asp His
 20 25 30

Gly Ser Asp Ile Ala Gly Gly Leu Ala Thr Thr Ala Thr Lys Asp Ala
 35 40 45

Asp Thr Gly Glu Trp Ile Ile Asn Gly Glu Lys Arg Trp Ile Gly Gly
 50 55 60

Ala Ser Thr Ala Asp Leu Ile Ala Thr Phe Ala Arg Asp Thr Ala Asp
 65 70 75 80

Asn Gln Val Lys Cys Phe Leu Val Ala Pro Gln Ala Glu Gly Val Ser
 85 90 95

Met Glu Ile Ile Asp Arg Lys Ala Ser Leu Arg Ile Met Gln Asn Ala
 100 105 110

His Ile Thr Tyr Asn Asn Val Arg Val Ser Gly Asp Ala Arg Leu His
 115 120 125

Asn Ile Asn Ser Phe Lys Asp Val Ser Glu Cys Leu Arg Arg Met Arg
 130 135 140

Ser Asp Val Ala Trp Met Ala Val Gly Ala Gln Ala Gly Ala Tyr Glu
 145 150 155 160

Ala Ala Val Lys Tyr Val Arg Ser Arg Glu Gln Phe Gly Arg Pro Ile

165										170					175						
Ala	Gly	Phe	Gln	Leu	Ile	Gln	Glu	Lys	Leu	Ala	Leu	Met	Leu	Gly	Asn						
			180					185					190								
Leu	Thr	Ala	Ser	Leu	Gly	Met	Met	Val	Lys	Leu	Thr	Asp	Gln	Gln	Gln						
		195				200						205									
Ala	Gly	Ile	Phe	Lys	Glu	Glu	Asn	Ser	Ala	Leu	Ala	Lys	Met	Phe	Thr						
	210					215					220										
Ser	Leu	Lys	Leu	Arg	Glu	Thr	Ala	Ser	Trp	Ala	Arg	Glu	Ile	Cys	Gly						
225					230					235				240							
Gly	Asn	Gly	Ile	Ile	Leu	Asp	Asn	Asp	Val	Ala	Arg	Phe	His	Ala	Asp						
			245						250					255							
Ala	Glu	Ala	Val	Tyr	Ser	Tyr	Glu	Gly	Thr	His	Glu	Ile	Asn	Ala	Leu						
		260						265					270								
Ile	Val	Gly	Arg	Xaa	Ile	Leu	Gly	Xaa	Leu	Phe	Phe	Leu	Tyr	Tyr	Xaa						
	275						280					285									
Xaa	Phe	Glu	Glu	Asp	Leu	His	Asp	Tyr	Phe	His	His	Pro	Lys	Pro	Ser						
	290					295					300										
Phe	Leu	Ser	Lys	Thr	His	Gln	Pro	Ser	Pro	Ala	Arg	Thr	Trp	Ala	Phe						
305					310					315					320						
Arg	Ser	Gly	Ala	Leu	Ser	Pro	Arg	Arg	Trp												
			325						330												

<210> 83

<211> 391

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> FRXA01766

<400> 83

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agcactgagc	gcggatctca	agcagaaaag	gtcgtgcaac	atg	cgt	gat	ccc	att	115
				Met	Arg	Asp	Pro	Ile	
				1				5	

caa	ggt	gct	ggt	att	cct	tct	gat	ctt	ttt	ggt	ttc	gca	gaa	ggt	ctc	163
Gln	Gly	Ala	Val	Ile	Pro	Ser	Asp	Leu	Phe	Gly	Phe	Ala	Glu	Val	Leu	
			10						15					20		

acc	gaa	gcc	gaa	cgc	gca	ggt	ctt	ctg	gaa	acc	cgc	agg	gtg	ctt	gag	211
Thr	Glu	Ala	Glu	Arg	Ala	Val	Leu	Leu	Glu	Thr	Arg	Arg	Val	Leu	Glu	
			25					30					35			

gaa	gag	gtg	aag	cct	tat	att	aat	gag	gcc	tgg	gat	aag	gca	gtc	ttc	259
Glu	Glu	Val	Lys	Pro	Tyr	Ile	Asn	Glu	Ala	Trp	Asp	Lys	Ala	Val	Phe	
			40				45					50				

ccc gat gag atc gtg cag ccc ctc caa gat ctg caa ttg ctt gat ccg 307
 Pro Asp Glu Ile Val Gln Pro Leu Gln Asp Leu Gln Leu Leu Asp Pro
 55 60 65

cct gca ctt cgg gaa gca ggg gag tcg gtt cga gac att ttc act ggt 355
 Pro Ala Leu Arg Glu Ala Gly Glu Ser Val Arg Asp Ile Phe Thr Gly
 70 75 80 85

ttc cgc aat ttt gaa ctc gcg cgc tgt gac atc aat 391
 Phe Arg Asn Phe Glu Leu Ala Arg Cys Asp Ile Asn
 90 95

<210> 84
 <211> 97
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 84
 Met Arg Asp Pro Ile Gln Gly Ala Val Ile Pro Ser Asp Leu Phe Gly
 1 5 10 15
 Phe Ala Glu Val Leu Thr Glu Ala Glu Arg Ala Val Leu Leu Glu Thr
 20 25 30
 Arg Arg Val Leu Glu Glu Glu Val Lys Pro Tyr Ile Asn Glu Ala Trp
 35 40 45
 Asp Lys Ala Val Phe Pro Asp Glu Ile Val Gln Pro Leu Gln Asp Leu
 50 55 60
 Gln Leu Leu Asp Pro Pro Ala Leu Arg Glu Ala Gly Glu Ser Val Arg
 65 70 75 80
 Asp Ile Phe Thr Gly Phe Arg Asn Phe Glu Leu Ala Arg Cys Asp Ile
 85 90 95

Asn

<210> 85
 <211> 1659
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1636)
 <223> RXN01762

<400> 85
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 cttttaatga cttcaaactg gatctaaagc acaaaggaga atg aaa gtg aac ctc 115
 Met Lys Val Asn Leu
 1 5
 gga ata gga agc tac cca cga cgc agg gca act gtt cga cca gag tcc 163
 Gly Ile Gly Ser Tyr Pro Arg Arg Arg Ala Thr Val Arg Pro Glu Ser

	10	15	20	
act gca atc gaa ttc gaa ggc acc agc atc acc tac gga gaa ttc agc				211
Thr Ala Ile Glu Phe Glu Gly Thr Ser Ile Thr Tyr Gly Glu Phe Ser	25	30	35	
aaa cga gtc aat cgg ctt gga cat gct ctt cta gac ctc ggc gtt gcg				259
Lys Arg Val Asn Arg Leu Gly His Ala Leu Leu Asp Leu Gly Val Ala	40	45	50	
cac caa gat cga gta gct tat gtc gga ttc aac cac cct gcc ctg cta				307
His Gln Asp Arg Val Ala Tyr Val Gly Phe Asn His Pro Ala Leu Leu	55	60	65	
gaa gtg ttc ttt tca acg aac ctc att ggg gca aca ccc gtg ctt gtt				355
Glu Val Phe Phe Ser Thr Asn Leu Ile Gly Ala Thr Pro Val Leu Val	70	75	80	85
aac cct cgc cta tcg gca aac gaa atc gat tac atc atc caa gac agc				403
Asn Pro Arg Leu Ser Ala Asn Glu Ile Asp Tyr Ile Ile Gln Asp Ser	90	95	100	
ggg ggc agc atc gtg ttt tac gga atc gac ctc atc gag cac gcc act				451
Gly Ala Ser Ile Val Phe Tyr Gly Ile Asp Leu Ile Glu His Ala Thr	105	110	115	
tac ctc caa gaa ctc cat cca gag atc atc atg gtg gcc gtt gaa ggc				499
Tyr Leu Gln Glu Leu His Pro Glu Ile Ile Met Val Ala Val Glu Gly	120	125	130	
gat gag ggt cca ggt ttg cgt cga aaa gcg ctt att gaa gcg gcg agc				547
Asp Glu Gly Pro Gly Leu Arg Arg Lys Ala Leu Ile Glu Ala Ala Ser	135	140	145	
gac gcc gac atc gac cta gaa gtc agc gat gat gac ctg gtg ctg ctc				595
Asp Ala Asp Ile Asp Leu Glu Val Ser Asp Asp Asp Leu Val Leu Leu	150	155	160	165
atg tac acc tcc gga acc act ggc cgc cca aag ggc gcc atg tta tcc				643
Met Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys Gly Ala Met Leu Ser	170	175	180	
cac cga aac ctc ttc ttt aac tac ttc aat gcc ctg ctc agc cag gaa				691
His Arg Asn Leu Phe Phe Asn Tyr Phe Asn Ala Leu Leu Ser Gln Glu	185	190	195	
att gaa caa ggc gcg gta ctt tta tcc act gcg ccg tta ttc cac atc				739
Ile Glu Gln Gly Ala Val Leu Leu Ser Thr Ala Pro Leu Phe His Ile	200	205	210	
gcg ggc ctc aac atg acc acc atc ccg gtg atg atg aag ggc gga aag				787
Ala Gly Leu Asn Met Thr Thr Ile Pro Val Met Met Lys Gly Gly Lys	215	220	225	
gtg atc atc cac cgc gaa ttc cgg gca gag cac gtc ctc gac gaa atc				835
Val Ile Ile His Arg Glu Phe Arg Ala Glu His Val Leu Asp Glu Ile	230	235	240	245
gaa cgc tcc aag gta tcc gaa tcc ttc atg gtg cca gcg atg atc gac				883
Glu Arg Ser Lys Val Ser Glu Ser Phe Met Val Pro Ala Met Ile Asp	250	255	260	

atg ttg tcc aac cac cca tca ttt gcc gaa cgc gac ctt tct tcc ctt	931
Met Leu Ser Asn His Pro Ser Phe Ala Glu Arg Asp Leu Ser Ser Leu	
265 270 275	
cgc gcc atc atg gtg ggc ggc tct ccc ctt agc gaa cgt gcg ctg cga	979
Arg Ala Ile Met Val Gly Gly Ser Pro Leu Ser Glu Arg Ala Leu Arg	
280 285 290	
atc tgg caa gga cgc gac gta aaa att gtc caa ggc ttc ggc atg aca	1027
Ile Trp Gln Gly Arg Asp Val Lys Ile Val Gln Gly Phe Gly Met Thr	
295 300 305	
gaa acc gca ccg ggc gcc tgt atc ctc gag gca aca gac aca agc aca	1075
Glu Thr Ala Pro Gly Ala Cys Ile Leu Glu Ala Thr Asp Thr Ser Thr	
310 315 320 325	
cac ctt gga acc gca ggt cga gcc cac ttc ttc acc gac atc aaa cta	1123
His Leu Gly Thr Ala Gly Arg Ala His Phe Phe Thr Asp Ile Lys Leu	
330 335 340	
gtg gac ccg aaa acc ggc gaa gaa gtc ccc acc gga gag gcc ggc gaa	1171
Val Asp Pro Lys Thr Gly Glu Glu Val Pro Thr Gly Glu Ala Gly Glu	
345 350 355	
gtt ctc atc cgc gga cca cat gtg atg acc gga tac tgg aac cga cca	1219
Val Leu Ile Arg Gly Pro His Val Met Thr Gly Tyr Trp Asn Arg Pro	
360 365 370	
gaa gac acc gcc agc gca cta caa aat ggc tgg tac cac tcc gga gat	1267
Glu Asp Thr Ala Ser Ala Leu Gln Asn Gly Trp Tyr His Ser Gly Asp	
375 380 385	
atc gcc atc aaa gat gaa gac ggc tac tac acc atc aaa gac cgc atc	1315
Ile Ala Ile Lys Asp Glu Asp Gly Tyr Tyr Thr Ile Lys Asp Arg Ile	
390 395 400 405	
aaa gac atg tac atc tcc ggc ggc gaa aac att tac ccc gca gaa gtc	1363
Lys Asp Met Tyr Ile Ser Gly Gly Glu Asn Ile Tyr Pro Ala Glu Val	
410 415 420	
gaa caa gca ctc cag gaa ctg gaa gca gtc ctt gat gcc gca gtc atc	1411
Glu Gln Ala Leu Gln Glu Leu Glu Ala Val Leu Asp Ala Ala Val Ile	
425 430 435	
gga gtc ccc gat gaa cga tgg ggc gaa act ggc atc gcc ttt gtc tcc	1459
Gly Val Pro Asp Glu Arg Trp Gly Glu Thr Gly Ile Ala Phe Val Ser	
440 445 450	
atc cga gaa agc tac ctg acc aac cca cca acc gga ccg gaa cta cga	1507
Ile Arg Glu Ser Tyr Leu Thr Asn Pro Pro Thr Gly Pro Glu Leu Arg	
455 460 465	
gaa cta cta ggc agt gtc cta gcc aga tac aaa ctt cca cga gaa atc	1555
Glu Leu Leu Gly Ser Val Leu Ala Arg Tyr Lys Leu Pro Arg Glu Ile	
470 475 480 485	
cac atc atc gaa gaa ctc ccc cgc aac gcc aca ggc aaa atc caa aag	1603
His Ile Ile Glu Glu Leu Pro Arg Asn Ala Thr Gly Lys Ile Gln Lys	
490 495 500	

aac atc ctg cga gac ttc acc atc ccc gtt tca taaaccccc aacgtcactt 1656
 Asn Ile Leu Arg Asp Phe Thr Ile Pro Val Ser
 505 510

tga

1659

<210> 86

<211> 512

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Met Lys Val Asn Leu Gly Ile Gly Ser Tyr Pro Arg Arg Arg Ala Thr
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Val Arg Pro Glu Ser Thr Ala Ile Glu Phe Glu Gly Thr Ser Ile Thr
 20 25 30

Tyr Gly Glu Phe Ser Lys Arg Val Asn Arg Leu Gly His Ala Leu Leu
 35 40 45

Asp Leu Gly Val Ala His Gln Asp Arg Val Ala Tyr Val Gly Phe Asn
 50 55 60

His Pro Ala Leu Leu Glu Val Phe Phe Ser Thr Asn Leu Ile Gly Ala
 65 70 75 80

Thr Pro Val Leu Val Asn Pro Arg Leu Ser Ala Asn Glu Ile Asp Tyr
 85 90 95

Ile Ile Gln Asp Ser Gly Ala Ser Ile Val Phe Tyr Gly Ile Asp Leu
 100 105 110

Ile Glu His Ala Thr Tyr Leu Gln Glu Leu His Pro Glu Ile Ile Met
 115 120 125

Val Ala Val Glu Gly Asp Glu Gly Pro Gly Leu Arg Arg Lys Ala Leu
 130 135 140

Ile Glu Ala Ala Ser Asp Ala Asp Ile Asp Leu Glu Val Ser Asp Asp
 145 150 155 160

Asp Leu Val Leu Leu Met Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys
 165 170 175

Gly Ala Met Leu Ser His Arg Asn Leu Phe Phe Asn Tyr Phe Asn Ala
 180 185 190

Leu Leu Ser Gln Glu Ile Glu Gln Gly Ala Val Leu Leu Ser Thr Ala
 195 200 205

Pro Leu Phe His Ile Ala Gly Leu Asn Met Thr Thr Ile Pro Val Met
 210 215 220

Met Lys Gly Gly Lys Val Ile Ile His Arg Glu Phe Arg Ala Glu His
 225 230 235 240

Val Leu Asp Glu Ile Glu Arg Ser Lys Val Ser Glu Ser Phe Met Val
 245 250 255

Pro Ala Met Ile Asp Met Leu Ser Asn His Pro Ser Phe Ala Glu Arg
 260 265 270
 Asp Leu Ser Ser Leu Arg Ala Ile Met Val Gly Gly Ser Pro Leu Ser
 275 280 285
 Glu Arg Ala Leu Arg Ile Trp Gln Gly Arg Asp Val Lys Ile Val Gln
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 Gly Phe Gly Met Thr Glu Thr Ala Pro Gly Ala Cys Ile Leu Glu Ala
 305 310 315 320
 Thr Asp Thr Ser Thr His Leu Gly Thr Ala Gly Arg Ala His Phe Phe
 325 330 335
 Thr Asp Ile Lys Leu Val Asp Pro Lys Thr Gly Glu Glu Val Pro Thr
 340 345 350
 Gly Glu Ala Gly Glu Val Leu Ile Arg Gly Pro His Val Met Thr Gly
 355 360 365
 Tyr Trp Asn Arg Pro Glu Asp Thr Ala Ser Ala Leu Gln Asn Gly Trp
 370 375 380
 Tyr His Ser Gly Asp Ile Ala Ile Lys Asp Glu Asp Gly Tyr Tyr Thr
 385 390 395 400
 Ile Lys Asp Arg Ile Lys Asp Met Tyr Ile Ser Gly Gly Glu Asn Ile
 405 410 415
 Tyr Pro Ala Glu Val Glu Gln Ala Leu Gln Glu Leu Glu Ala Val Leu
 420 425 430
 Asp Ala Ala Val Ile Gly Val Pro Asp Glu Arg Trp Gly Glu Thr Gly
 435 440 445
 Ile Ala Phe Val Ser Ile Arg Glu Ser Tyr Leu Thr Asn Pro Pro Thr
 450 455 460
 Gly Pro Glu Leu Arg Glu Leu Leu Gly Ser Val Leu Ala Arg Tyr Lys
 465 470 475 480
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<210> 87
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1363)
 <223> FRXA01762

<400> 87

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								Met	Lys	Val	Asn	Leu	5			
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gga	ata	gga	agc	tac	cca	cga	cgc	agg	gca	act	ggt	cga	cca	gag	tcc	163
Gly	Ile	Gly	Ser	Tyr	Pro	Arg	Arg	Arg	Ala	Thr	Val	Arg	Pro	Glu	Ser	20
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Thr	Ala	Ile	Glu	Phe	Glu	Gly	Thr	Ser	Ile	Thr	Tyr	Gly	Glu	Phe	Ser	35
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Lys	Arg	Val	Asn	Arg	Leu	Gly	His	Ala	Leu	Leu	Asp	Leu	Gly	Val	Ala	50
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His	Gln	Asp	Arg	Val	Ala	Tyr	Val	Gly	Phe	Asn	His	Pro	Ala	Leu	Leu	65
	55					60										
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Glu	Val	Phe	Phe	Ser	Thr	Asn	Leu	Ile	Gly	Ala	Thr	Pro	Val	Leu	Val	85
	70					75				80						
aac	cct	cgc	cta	tcg	gca	aac	gaa	atc	gat	tac	atc	atc	caa	gac	agc	403
Asn	Pro	Arg	Leu	Ser	Ala	Asn	Glu	Ile	Asp	Tyr	Ile	Ile	Gln	Asp	Ser	95
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ggt	gcg	agc	atc	gtg	ttt	tac	gga	atc	gac	ctc	atc	gag	cac	gcc	act	451
Gly	Ala	Ser	Ile	Val	Phe	Tyr	Gly	Ile	Asp	Leu	Ile	Glu	His	Ala	Thr	110
			105					110					115			
tac	ctc	caa	gaa	ctc	cat	cca	gag	atc	atc	atg	gtg	gcc	ggt	gaa	ggc	499
Tyr	Leu	Gln	Glu	Leu	His	Pro	Glu	Ile	Ile	Met	Val	Ala	Val	Glu	Gly	120
		120					125					130				
gat	gag	ggt	cca	ggt	ttg	cgt	cga	aaa	gcg	ctt	att	gaa	gcg	gcg	agc	547
Asp	Glu	Gly	Pro	Gly	Leu	Arg	Arg	Lys	Ala	Leu	Ile	Glu	Ala	Ala	Ser	135
						140					145					
gac	gcc	gac	atc	gac	cta	gaa	gtc	agc	gat	gat	gac	ctg	gtg	ctg	ctc	595
Asp	Ala	Asp	Ile	Asp	Leu	Glu	Val	Ser	Asp	Asp	Asp	Leu	Val	Leu	Leu	150
					155					160					165	
atg	tac	acc	tcc	gga	acc	act	ggc	cgc	cca	aag	ggc	gcc	atg	tta	tcc	643
Met	Tyr	Thr	Ser	Gly	Thr	Thr	Gly	Arg	Pro	Lys	Gly	Ala	Met	Leu	Ser	170
				170					175					180		
cac	cga	aac	ctc	ttc	ttt	aac	tac	ttc	aat	gcc	ctg	ctc	agc	cag	gaa	691
His	Arg	Asn	Leu	Phe	Phe	Asn	Tyr	Phe	Asn	Ala	Leu	Leu	Ser	Gln	Glu	185
			185					190					195			
att	gaa	caa	ggc													

Ala Gly Leu Asn Met Thr Thr Ile Pro Val Met Met Lys Gly Gly Lys	
215 220 225	
gtg atc atc cac cgc gaa ttc cgg gca gag cac gtc ctc gac gaa atc	835
Val Ile Ile His Arg Glu Phe Arg Ala Glu His Val Leu Asp Glu Ile	
230 235 240 245	
gaa cgc tcc aag gta tcc gaa tcc ttc atg gtg cca gcg atg atc gac	883
Glu Arg Ser Lys Val Ser Glu Ser Phe Met Val Pro Ala Met Ile Asp	
250 255 260	
atg ttg tcc aac cac cca tca ttt gcc gaa cgc gac ctt tct tcc ctt	931
Met Leu Ser Asn His Pro Ser Phe Ala Glu Arg Asp Leu Ser Ser Leu	
265 270 275	
cgc gcc atc atg gtg ggc ggc tct ccc ctt agc gaa cgt gcg ctg cga	979
Arg Ala Ile Met Val Gly Gly Ser Pro Leu Ser Glu Arg Ala Leu Arg	
280 285 290	
atc tgg caa gga cgc gac gta aaa att gtc caa ggc ttc ggc atg aca	1027
Ile Trp Gln Gly Arg Asp Val Lys Ile Val Gln Gly Phe Gly Met Thr	
295 300 305	
gaa acc gca ccg ggc gcc tgt atc ctc gag gca aca gac aca agc aca	1075
Glu Thr Ala Pro Gly Ala Cys Ile Leu Glu Ala Thr Asp Thr Ser Thr	
310 315 320 325	
cac ctt gga acc gca ggt cga gcc cac ttc ttc acc gac atc aaa cta	1123
His Leu Gly Thr Ala Gly Arg Ala His Phe Phe Thr Asp Ile Lys Leu	
330 335 340	
gtg gac ccg aaa acc ggc gaa gaa gtc ccc acc gga gag gcc ggc gaa	1171
Val Asp Pro Lys Thr Gly Glu Glu Val Pro Thr Gly Glu Ala Gly Glu	
345 350 355	
gtt ctc atc cgc gga cca cat gtg atg acc gga tac tgg aac cga cca	1219
Val Leu Ile Arg Gly Pro His Val Met Thr Gly Tyr Trp Asn Arg Pro	
360 365 370	
gaa gac acc gcc agc gca cta caa aat ggc tgg tac cac tcc gga gat	1267
Glu Asp Thr Ala Ser Ala Leu Gln Asn Gly Trp Tyr His Ser Gly Asp	
375 380 385	
atc gcc atc aaa gat gaa gac ggc tac tac acc atc aaa gac cgc atc	1315
Ile Ala Ile Lys Asp Glu Asp Gly Tyr Tyr Thr Ile Lys Asp Arg Ile	
390 395 400 405	
aaa gac atg tac atc tcc ggc ggc gaa aac att tac ccc gca gaa gtc	1363
Lys Asp Met Tyr Ile Ser Gly Gly Glu Asn Ile Tyr Pro Ala Glu Val	
410 415 420	
taagtaccc	1372
<210> 88	
<211> 421	
<212> PRT	
<213> Corynebacterium glutamicum	
<400> 88	
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Tyr Gly Glu Phe Ser Lys Arg Val Asn Arg Leu Gly His Ala Leu Leu	35	40	45
Asp Leu Gly Val Ala His Gln Asp Arg Val Ala Tyr Val Gly Phe Asn	50	55	60
His Pro Ala Leu Leu Glu Val Phe Phe Ser Thr Asn Leu Ile Gly Ala	65	70	75
Thr Pro Val Leu Val Asn Pro Arg Leu Ser Ala Asn Glu Ile Asp Tyr	85	90	95
Ile Ile Gln Asp Ser Gly Ala Ser Ile Val Phe Tyr Gly Ile Asp Leu	100	105	110
Ile Glu His Ala Thr Tyr Leu Gln Glu Leu His Pro Glu Ile Ile Met	115	120	125
Val Ala Val Glu Gly Asp Glu Gly Pro Gly Leu Arg Arg Lys Ala Leu	130	135	140
Ile Glu Ala Ala Ser Asp Ala Asp Ile Asp Leu Glu Val Ser Asp Asp	145	150	155
Asp Leu Val Leu Leu Met Tyr Thr Ser Gly Thr Thr Gly Arg Pro Lys	165	170	175
Gly Ala Met Leu Ser His Arg Asn Leu Phe Phe Asn Tyr Phe Asn Ala	180	185	190
Leu Leu Ser Gln Glu Ile Glu Gln Gly Ala Val Leu Leu Ser Thr Ala	195	200	205
Pro Leu Phe His Ile Ala Gly Leu Asn Met Thr Thr Ile Pro Val Met	210	215	220
Met Lys Gly Gly Lys Val Ile Ile His Arg Glu Phe Arg Ala Glu His	225	230	235
Val Leu Asp Glu Ile Glu Arg Ser Lys Val Ser Glu Ser Phe Met Val	245	250	255
Pro Ala Met Ile Asp Met Leu Ser Asn His Pro Ser Phe Ala Glu Arg	260	265	270
Asp Leu Ser Ser Leu Arg Ala Ile Met Val Gly Gly Ser Pro Leu Ser	275	280	285
Glu Arg Ala Leu Arg Ile Trp Gln Gly Arg Asp Val Lys Ile Val Gln	290	295	300
Gly Phe Gly Met Thr Glu Thr Ala Pro Gly Ala Cys Ile Leu Glu Ala	305	310	315
Thr Asp Thr Ser Thr His Leu Gly Thr Ala Gly Arg Ala His Phe Phe	325	330	335

Thr Asp Ile Lys Leu Val Asp Pro Lys Thr Gly Glu Glu Val Pro Thr
340 345 350

Gly Glu Ala Gly Glu Val Leu Ile Arg Gly Pro His Val Met Thr Gly
355 360 365

Tyr Trp Asn Arg Pro Glu Asp Thr Ala Ser Ala Leu Gln Asn Gly Trp
370 375 380

Tyr His Ser Gly Asp Ile Ala Ile Lys Asp Glu Asp Gly Tyr Tyr Thr
385 390 395 400

Ile Lys Asp Arg Ile Lys Asp Met Tyr Ile Ser Gly Gly Glu Asn Ile
405 410 415

Tyr Pro Ala Glu Val
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<210> 89

<211> 867

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(844)

<223> RXA00681

<400> 89

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agccatgcmc actcagtagc agcacatggg gtggatacac atg cct agt cca cgc 115
Met Pro Ser Pro Arg
1 5

act gtt ctt atc act ggt gcc gct ggc ggt ttg ggt cgg gca ttc gct 163
Thr Val Leu Ile Thr Gly Ala Ala Gly Gly Leu Gly Arg Ala Phe Ala
10 15 20

gaa ggt ttc gca gcc caa gga gac cgt atc gcg gtg gcg gat atc aat 211
Glu Gly Phe Ala Ala Gln Gly Asp Arg Ile Ala Val Ala Asp Ile Asn
25 30 35

ctg gat ggg gcg caa gag acc gtt gac aag ctg aaa gca ttg ggc gca 259
Leu Asp Gly Ala Gln Glu Thr Val Asp Lys Leu Lys Ala Leu Gly Ala
40 45 50

gat gcc gca gcc ttt gaa gtt gat gtc acg tct ttg gag tcc acc gag 307
Asp Ala Ala Ala Phe Glu Val Asp Val Thr Ser Leu Glu Ser Thr Glu
55 60 65

gcc cta gcc gcc ggt gcc gct gag ttt ggc ggt ggc cga att gat gtc 355
Ala Leu Ala Ala Gly Ala Ala Glu Phe Gly Gly Arg Ile Asp Val
70 75 80 85

ctt att aat aac gca gcg ata tat gcg aca gtg act cgt tca ccg ttt 403
Leu Ile Asn Asn Ala Ala Ile Tyr Ala Thr Val Thr Arg Ser Pro Phe
90 95 100

gag gat att gac cct gcg gag tgg gat ttg gtc atg gga gtc aat ctc 451
 Glu Asp Ile Asp Pro Ala Glu Trp Asp Leu Val Met Gly Val Asn Leu
 105 110 115
 aaa ggc ccg tgg ttg gtg acg cgt tct gtg agt ccg ttt ttg tcc gat 499
 Lys Gly Pro Trp Leu Val Thr Arg Ser Val Ser Pro Phe Leu Ser Asp
 120 125 130
 aat gcc cgt gtg gtc aat ctt tcc agc gcg act gtg ttt tca gga tct 547
 Asn Ala Arg Val Val Asn Leu Ser Ser Ala Thr Val Phe Ser Gly Ser
 135 140 145
 gca cac tgg gcg cac tac gtg gca tcc aaa ggt ggg gtc att gct tta 595
 Ala His Trp Ala His Tyr Val Ala Ser Lys Gly Gly Val Ile Ala Leu
 150 155 160 165
 acc agg gtg ctt gct aaa gag ctg ggt ggt cgt ggg atc acg gtc aat 643
 Thr Arg Val Leu Ala Lys Glu Leu Gly Gly Arg Gly Ile Thr Val Asn
 170 175 180
 gcg gtt gcg cct ggg ttt acg ctg act gaa gcc agc ttg gga ctc atg 691
 Ala Val Ala Pro Gly Phe Thr Leu Thr Glu Ala Ser Leu Gly Leu Met
 185 190 195
 gat agc gcg gaa acg tac ggt gtc gat cgc gga tcc atc aag cgc gca 739
 Asp Ser Ala Glu Thr Tyr Gly Val Asp Arg Gly Ser Ile Lys Arg Ala
 200 205 210
 agc caa ccg aaa gac atc gtc ggc acc acc atg ttt ctt gca tcc cca 787
 Ser Gln Pro Lys Asp Ile Val Gly Thr Thr Met Phe Leu Ala Ser Pro
 215 220 225
 gaa gcc gaa tac atc act ggg caa aca ctc atc gtt gat ggt ggc cga 835
 Glu Ala Glu Tyr Ile Thr Gly Gln Thr Leu Ile Val Asp Gly Gly Arg
 230 235 240 245
 cag ttc atc taagtactaa aagttctaag gag 867
 Gln Phe Ile

<210> 90

<211> 248

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

Met Pro Ser Pro Arg Thr Val Leu Ile Thr Gly Ala Ala Gly Gly Leu
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Gly Arg Ala Phe Ala Glu Gly Phe Ala Ala Gln Gly Asp Arg Ile Ala
 20 25 30

Val Ala Asp Ile Asn Leu Asp Gly Ala Gln Glu Thr Val Asp Lys Leu
 35 40 45

Lys Ala Leu Gly Ala Asp Ala Ala Ala Phe Glu Val Asp Val Thr Ser
 50 55 60

Leu Glu Ser Thr Glu Ala Leu Ala Ala Gly Ala Ala Glu Phe Gly Gly
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<210> 91
<211> 837
<212> DNA
<213> Corynebacterium glutamicum
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                                     Met Asp Leu Lys Leu
                                     1                               5

ggt ggc caa gtc ata ctt gtt gtt ggc ggt gca gga act att ggt tct 163
Gly Gly Gln Val Ile Leu Val Val Gly Gly Ala Gly Thr Ile Gly Ser
                               10                               15                               20

gaa gtt gta aaa ctc tta act gaa gaa ggc gca acc gcg gta gcg gcg 211
Glu Val Val Lys Leu Leu Thr Glu Glu Gly Ala Thr Ala Val Ala Ala
                               25                               30                               35

tcg aga agc acg ccc tta tct att gac gct tcg gat gaa gcg tcc gtc 259

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Ser	Arg	Ser	Thr	Pro	Leu	Ser	Ile	Asp	Ala	Ser	Asp	Glu	Ala	Ser	Val		
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Arg	Ala	Gly	Ile	Asp	Gln	Val	Ile	Ala	Glu	His	Gly	Arg	Leu	Asp	Gly		
	55					60					65						
ctg	gtt	gtt	tct	tct	gca	ccc	gct	gcg	caa	acg	ctc	agc	gcg	gag	aca	355	
Leu	Val	Val	Ser	Ser	Ala	Pro	Ala	Ala	Gln	Thr	Leu	Ser	Ala	Glu	Thr		
	70				75					80					85		
gca	gat	gat	ccg	gac	act	gtg	ttg	gct	gct	att	gaa	ggc	aaa	gcc	atc	403	
Ala	Asp	Asp	Pro	Asp	Thr	Val	Leu	Ala	Ala	Ile	Glu	Gly	Lys	Ala	Ile		
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acg	ttt	atg	aag	gct	gca	acc	gtg	gcg	ctc	gag	aag	atg	cgt	gag	gct	451	
Thr	Phe	Met	Lys	Ala	Ala	Thr	Val	Ala	Leu	Glu	Lys	Met	Arg	Glu	Ala		
			105					110					115				
gga	cat	ggg	cgc	atc	gtt	gca	ctt	tcc	ggc	atg	aac	tca	tac	aaa	aca	499	
Gly	His	Gly	Arg	Ile	Val	Ala	Leu	Ser	Gly	Met	Asn	Ser	Tyr	Lys	Thr		
		120					125					130					
ttg	agt	act	act	gcg	tcg	gcg	cga	aat	gct	gcg	ctg	aat	gtc	gtg	gtg	547	
Leu	Ser	Thr	Thr	Ala	Ser	Ala	Arg	Asn	Ala	Ala	Leu	Asn	Val	Val	Val		
	135					140					145						
aaa	aat	ttg	gcg	gat	cgt	cac	gcg	ggc	acc	gga	att	aca	gta	aat	gcg	595	
Lys	Asn	Leu	Ala	Asp	Arg	His	Ala	Gly	Thr	Gly	Ile	Thr	Val	Asn	Ala		
	150				155					160					165		
att	agc	ccg	gga	ttc	gtg	gta	gct	gag	cca	gac	gct	gag	gta	aac	cgc	643	
Ile	Ser	Pro	Gly	Phe	Val	Val	Ala	Glu	Pro	Asp	Ala	Glu	Val	Asn	Arg		
				170					175					180			
gca	aat	ggt	gac	acc	acg	tgg	agg	agg	tcg	cgg	agg	cga	tcg	cgt	ttt	691	
Ala	Asn	Gly	Asp	Thr	Thr	Trp	Arg	Arg	Ser	Arg	Arg	Arg	Ser	Arg	Phe		
			185					190					195				
tgt	tgt	cgc	cgc	gca	ccg	cat	caa	ttt	ctg	gag	aga	tta	ttt	cgg	tgg	739	
Cys	Cys	Arg	Arg	Ala	Pro	His	Gln	Phe	Leu	Glu	Arg	Leu	Phe	Arg	Trp		
		200					205					210					
gac	ata	agg	cga	agg	gca	tca	tcc	ttc	ctt	agc	tcg	cgt	gag	ctt	ccc	787	
Asp	Ile	Arg	Arg	Arg	Ala	Ser	Ser	Phe	Leu	Ser	Ser	Arg	Glu	Leu	Pro		
	215					220					225						
aag	cgt	aag	cac	ccc	cgt	gtg	agg	gca	taacggccgt	tctgttaaag						834	
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att																	837

<210> 92

<211> 238

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

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Thr Ala Val Ala	Ala Ser Arg Ser	Thr Pro Leu Ser	Ile Asp Ala Ser
35		40	45
Asp Glu Ala Ser	Val Arg Ala Gly	Ile Asp Gln Val	Ile Ala Glu His
50		55	60
Gly Arg Leu Asp	Gly Leu Val Val	Ser Ser Ala Pro	Ala Ala Gln Thr
65		70	75
Leu Ser Ala Glu	Thr Ala Asp Asp	Pro Asp Thr Val	Leu Ala Ala Ile
	85	90	95
Glu Gly Lys Ala	Ile Thr Phe Met	Lys Ala Ala Thr	Val Ala Leu Glu
	100	105	110
Lys Met Arg Glu	Ala Gly His Gly	Arg Ile Val Ala	Leu Ser Gly Met
	115	120	125
Asn Ser Tyr Lys	Thr Leu Ser Thr	Thr Ala Ser Ala	Arg Asn Ala Ala
	130	135	140
Leu Asn Val Val	Val Lys Asn Leu	Ala Asp Arg His	Ala Gly Thr Gly
	145	150	155
Ile Thr Val Asn	Ala Ile Ser Pro	Gly Phe Val Val	Ala Glu Pro Asp
	165	170	175
Ala Glu Val Asn	Arg Ala Asn Gly	Asp Thr Thr Trp	Arg Arg Ser Arg
	180	185	190
Arg Arg Ser Arg	Phe Cys Cys Arg	Arg Ala Pro His	Gln Phe Leu Glu
	195	200	205
Arg Leu Phe Arg	Trp Asp Ile Arg	Arg Arg Ala Ser	Ser Phe Leu Ser
	210	215	220
Ser Arg Glu Leu	Pro Lys Arg Lys	His Pro Arg Val	Arg Ala
	225	230	235

<210> 93

<211> 329

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(306)

<223> RXA02133

<400> 93

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gta gca gca ttc aac cgt gtg ctt cgc ttg gaa acc cac cag cag acc	96
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Val Ala Ala Phe Asn Arg Val Leu Arg Leu Glu Thr His Gln Gln Thr
      20                      25                      30

ctt cgc gta tct gag atc gat cca ggt cga gtt gcc acg gaa gaa ttc 144
Leu Arg Val Ser Glu Ile Asp Pro Gly Arg Val Ala Thr Glu Glu Phe
      35                      40                      45

tcc ctc gtt cgt ttc ggc gga gat aaa gaa cgc gca gaa gca gtc tat 192
Ser Leu Val Arg Phe Gly Gly Asp Lys Glu Arg Ala Glu Ala Val Tyr
      50                      55                      60

gac gac gtc ctc aac ctc acc gct gaa gac atc gca gag tct gtg cgt 240
Asp Asp Val Leu Asn Leu Thr Ala Glu Asp Ile Ala Glu Ser Val Arg
      65                      70                      75                      80

tgg gtc gcg agc ctt cca aag cac atg aac att gac cgc atg cgt att 288
Trp Val Ala Ser Leu Pro Lys His Met Asn Ile Asp Arg Met Arg Ile
      85                      90                      95

aca cct cgc gat cag gtc taaaacccgc actcttttga aat 329
Thr Pro Arg Asp Gln Val
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<210> 94
 <211> 102
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 94
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Val Ala Ala Phe Asn Arg Val Leu Arg Leu Glu Thr His Gln Gln Thr
      20                      25                      30

Leu Arg Val Ser Glu Ile Asp Pro Gly Arg Val Ala Thr Glu Glu Phe
      35                      40                      45

Ser Leu Val Arg Phe Gly Gly Asp Lys Glu Arg Ala Glu Ala Val Tyr
      50                      55                      60

Asp Asp Val Leu Asn Leu Thr Ala Glu Asp Ile Ala Glu Ser Val Arg
      65                      70                      75                      80

Trp Val Ala Ser Leu Pro Lys His Met Asn Ile Asp Arg Met Arg Ile
      85                      90                      95

Thr Pro Arg Asp Gln Val
      100

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<210> 95
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 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
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 <222> (101)..(1324)
 <223> RXN01114

<400> 95

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                                         Met Asn Pro Gln Asp
                                         1 5

att gtc atc tgt tcc cca ttg cgc acc cca gtt ggt gct tac ggc gga 163
Ile Val Ile Cys Ser Pro Leu Arg Thr Pro Val Gly Ala Tyr Gly Gly
                        10 15 20

tcc ttc acc ggc gtc cct gtt gaa gaa ttg gcc acc acc gtg atc aac 211
Ser Phe Thr Gly Val Pro Val Glu Glu Leu Ala Thr Thr Val Ile Asn
                        25 30 35

gcg atc gtt gag gca acc ggc atc acc ggc gac gat gtg gac gat ctg 259
Ala Ile Val Glu Ala Thr Gly Ile Thr Gly Asp Asp Val Asp Asp Leu
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atc ctc ggc cag gca tcc ccc aac ggt gcg gct cca gca ctg ggc cgt 307
Ile Leu Gly Gln Ala Ser Pro Asn Gly Ala Ala Pro Ala Leu Gly Arg
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gtt gtt gct cta gat tcc aag ctt ggc caa aac gtt cca ggc atg cag 355
Val Val Ala Leu Asp Ser Lys Leu Gly Gln Asn Val Pro Gly Met Gln
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ctt gat cgc cgc tgt ggt tcc ggc ctg cag gca atc gtc acc gct gct 403
Leu Asp Arg Arg Cys Gly Ser Gly Leu Gln Ala Ile Val Thr Ala Ala
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gca cac gtt gca tcc ggc gct gct gat ctg atc atc gca ggt ggc gca 451
Ala His Val Ala Ser Gly Ala Ala Asp Leu Ile Ile Ala Gly Gly Ala
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gaa tcc atg agc cgc gtt gag tac acc gtg tcc ggc gat atc cgt tgg 499
Glu Ser Met Ser Arg Val Glu Tyr Thr Val Ser Gly Asp Ile Arg Trp
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ggt gtc aag ggc ggc gac atg cag ctt cgt gac cgc ctt gca gaa gca 547
Gly Val Lys Gly Gly Asp Met Gln Leu Arg Asp Arg Leu Ala Glu Ala
                        135 140 145

cgc gaa acc gct ggc gga cgc aac cac ccg atc cct ggt ggc atg atc 595
Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile Pro Gly Gly Met Ile
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gag acc gct gag aac ctg cgt cgc gaa tac ggc atc tcc cgc gag gag 643
Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly Ile Ser Arg Glu Glu
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cag gac aag atc tcc gca gcg tcc cag cag cgt tgg ggc aag gct gct 691
Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg Trp Gly Lys Ala Ala
                        185 190 195

gat gcg ggg ctt ttc gac gac gag atc gtg cca gtc acc gtc cct gcc 739
Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro Val Thr Val Pro Ala
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aag aag cgc ggc cag gag cca acc atc gtt tct cga gac gag cat ggt 787

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Lys	Lys	Arg	Gly	Gln	Glu	Pro	Thr	Ile	Val	Ser	Arg	Asp	Glu	His	Gly		
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cga	cca	gga	aca	acc	gtc	gaa	aag	ctt	gct	gct	ttg	cgc	ccc	atc	atg	835	
Arg	Pro	Gly	Thr	Thr	Val	Glu	Lys	Leu	Ala	Ala	Leu	Arg	Pro	Ile	Met		
230					235					240					245		
ggc	cgc	cag	gat	gcg	gaa	gca	acc	gtc	acc	gct	ggc	aac	gcg	tcc	ggc	883	
Gly	Arg	Gln	Asp	Ala	Glu	Ala	Thr	Val	Thr	Ala	Gly	Asn	Ala	Ser	Gly		
				250						255					260		
caa	aat	gat	ggc	gct	gct	gcc	gtc	atc	gtg	acc	act	cgc	gcc	aag	gcc	931	
Gln	Asn	Asp	Gly	Ala	Ala	Ala	Val	Ile	Val	Thr	Thr	Arg	Ala	Lys	Ala		
			265						270						275		
gag	gag	aag	ggc	ctg	cgc	cca	gtc	atg	cgt	ttg	gct	ggc	tgg	tct	gtg	979	
Glu	Glu	Lys	Gly	Leu	Arg	Pro	Val	Met	Arg	Leu	Ala	Gly	Trp	Ser	Val		
		280						285					290				
gct	gct	gtt	ccc	cca	gag	acc	atg	ggt	att	gga	cct	gtt	cct	gcc	acc	1027	
Ala	Ala	Val	Pro	Pro	Glu	Thr	Met	Gly	Ile	Gly	Pro	Val	Pro	Ala	Thr		
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aag	aag	gtc	ctg	gat	cgt	ttg	ggc	ctt	acc	ctg	gag	gac	atc	ggc	gcg	1075	
Lys	Lys	Val	Leu	Asp	Arg	Leu	Gly	Leu	Thr	Leu	Glu	Asp	Ile	Gly	Ala		
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Ile	Glu	Leu	Asn	Glu	Ala	Phe	Ala	Ala	Gln	Ala	Leu	Ser	Val	Leu	Lys		
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Glu	Trp	Asn	Ile	Ser	Trp	Glu	Asp	Glu	Arg	Val	Asn	Pro	Leu	Gly	Ser		
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ggt	att	tcc	atg	gga	cac	cca	gtc	ggt	gcc	acc	ggt	gct	cgc	atg	gca	1219	
Gly	Ile	Ser	Met	Gly	His	Pro	Val	Gly	Ala	Thr	Gly	Ala	Arg	Met	Ala		
		360							365						370		
gta	acc	ttg	gct	cac	cgc	atg	cag	cgt	gaa	aac	act	cag	tac	gga	ctg	1267	
Val	Thr	Leu	Ala	His	Arg	Met	Gln	Arg	Glu	Asn	Thr	Gln	Tyr	Gly	Leu		
		375					380										
gcc	acc	atg	tgc	atc	ggt	ggc	ggc	cag	ggt	ctt	gca	gct	gtc	ttt	gaa	1315	
Ala	Thr	Met	Cys	Ile	Gly	Gly	Gly	Gln	Gly	Leu	Ala	Ala	Val	Phe	Glu		
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Lys	Glu	Asn															

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<212> PRT

<213> Corynebacterium glutamicum

<400> 96

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 Thr Thr Val Ile Asn Ala Ile Val Glu Ala Thr Gly Ile Thr Gly Asp
 35 40 45
 Asp Val Asp Asp Leu Ile Leu Gly Gln Ala Ser Pro Asn Gly Ala Ala
 50 55 60
 Pro Ala Leu Gly Arg Val Val Ala Leu Asp Ser Lys Leu Gly Gln Asn
 65 70 75 80
 Val Pro Gly Met Gln Leu Asp Arg Arg Cys Gly Ser Gly Leu Gln Ala
 85 90 95
 Ile Val Thr Ala Ala Ala His Val Ala Ser Gly Ala Ala Asp Leu Ile
 100 105 110
 Ile Ala Gly Gly Ala Glu Ser Met Ser Arg Val Glu Tyr Thr Val Ser
 115 120 125
 Gly Asp Ile Arg Trp Gly Val Lys Gly Gly Asp Met Gln Leu Arg Asp
 130 135 140
 Arg Leu Ala Glu Ala Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile
 145 150 155 160
 Pro Gly Gly Met Ile Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly
 165 170 175
 Ile Ser Arg Glu Glu Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg
 180 185 190
 Trp Gly Lys Ala Ala Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro
 195 200 205
 Val Thr Val Pro Ala Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser
 210 215 220
 Arg Asp Glu His Gly Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala
 225 230 235 240
 Leu Arg Pro Ile Met Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala
 245 250 255
 Gly Asn Ala Ser Gly Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr
 260 265 270
 Thr Arg Ala Lys Ala Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu
 275 280 285
 Ala Gly Trp Ser Val Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly
 290 295 300
 Pro Val Pro Ala Thr Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu
 305 310 315 320
 Glu Asp Ile Gly Ala Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala
 325 330 335
 Leu Ser Val Leu Lys Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val

340 345 350
 Asn Pro Leu Gly Ser Gly Ile Ser Met Gly His Pro Val Gly Ala Thr
 355 360 365
 Gly Ala Arg Met Ala Val Thr Leu Ala His Arg Met Gln Arg Glu Asn
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 Thr Gln Tyr Gly Leu Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu
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 <223> FRXA01114

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 cct ggt ggc atg atc gag acc gct gag aac ctg cgt cgc gaa tac ggc 96
 Pro Gly Gly Met Ile Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly
 20 25 30
 atc tcc cgc gag gag cag gac aag atc tcc gca gcg tcc cag cag cgt 144
 Ile Ser Arg Glu Glu Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg
 35 40 45
 tgg ggc aag gct gct gat gcg ggg ctt ttc gac gac gag atc gtg cca 192
 Trp Gly Lys Ala Ala Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro
 50 55 60
 gtc acc gtc cct gcc aag aag cgc ggc cag gag cca acc atc gtt tct 240
 Val Thr Val Pro Ala Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser
 65 70 75 80
 cga gac gag cat ggt cga cca gga aca acc gtc gaa aag ctt gct gct 288
 Arg Asp Glu His Gly Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala
 85 90 95
 ttg cgc ccc atc atg ggc cgc cag gat gcg gaa gca acc gtc acc gct 336
 Leu Arg Pro Ile Met Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala
 100 105 110
 ggc aac gcg tcc ggc caa aat gat ggc gct gct gcc gtc atc gtg acc 384
 Gly Asn Ala Ser Gly Gln Asn Asp Gly Ala Ala Val Ile Val Thr
 115 120 125
 act cgc gcc aag gcc gag gag aag ggc ctg cgc cca gtc atg cgt ttg 432
 Thr Arg Ala Lys Ala Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu
 130 135 140

gct ggc tgg tct gtg gct gct gtt ccc cca gag acc atg ggt att gga 480
 Ala Gly Trp Ser Val Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly
 145 150 155 160
 cct gtt cct gcc acc aag aag gtc ctg gat cgt ttg ggc ctt acc ctg 528
 Pro Val Pro Ala Thr Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu
 165 170 175
 gag gac atc ggc gcg atc gaa ctc aac gaa gct ttc gca gct cag gca 576
 Glu Asp Ile Gly Ala Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala
 180 185 190
 ctg tct gtg ctg aag gaa tgg aac att tct tgg gaa gat gag cgc gtc 624
 Leu Ser Val Leu Lys Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val
 195 200 205
 aac cca ctg ggt tcc ggt att tcc atg gga cac cca gtc ggt gcc acc 672
 Asn Pro Leu Gly Ser Gly Ile Ser Met Gly His Pro Val Gly Ala Thr
 210 215 220
 ggt gct cgc atg gca gta acc ttg gct cac cgc atg cag cgt gaa aac 720
 Gly Ala Arg Met Ala Val Thr Leu Ala His Arg Met Gln Arg Glu Asn
 225 230 235 240
 act cag tac gga ctg gcc acc atg tgc atc ggt ggc ggc cag ggt ctt 768
 Thr Gln Tyr Gly Leu Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu
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 <213> Corynebacterium glutamicum

<400> 98
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 20 25 30
 Ile Ser Arg Glu Glu Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg
 35 40 45
 Trp Gly Lys Ala Ala Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro
 50 55 60
 Val Thr Val Pro Ala Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser
 65 70 75 80
 Arg Asp Glu His Gly Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala
 85 90 95
 Leu Arg Pro Ile Met Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala
 100 105 110

Gly Asn Ala Ser Gly Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr
 115 120 125

Thr Arg Ala Lys Ala Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu
 130 135 140

Ala Gly Trp Ser Val Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly
 145 150 155 160

Pro Val Pro Ala Thr Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu
 165 170 175

Glu Asp Ile Gly Ala Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala
 180 185 190

Leu Ser Val Leu Lys Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val
 195 200 205

Asn Pro Leu Gly Ser Gly Ile Ser Met Gly His Pro Val Gly Ala Thr
 210 215 220

Gly Ala Arg Met Ala Val Thr Leu Ala His Arg Met Gln Arg Glu Asn
 225 230 235 240

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 <223> RXA01894

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 Met Pro Lys Pro Lys
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aat aat gcg ggt cga gat ctc aaa gct gcc att gct gtg ggg atc gga 163
 Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala Ile Ala Val Gly Ile Gly
 10 15 20

ctg ggg gtc ctg gtt ctt ttg ggg att gtc cta agc cca tgg ggt tgg 211
 Leu Gly Val Leu Val Leu Leu Gly Ile Val Leu Ser Pro Trp Gly Trp
 25 30 35

tac atc ctc gtt gca ggt ttt atg gct gca gca aca tgg gaa gtt ggt 259
 Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val Gly
 40 45 50

agc aga ctt aaa gaa ggc ggc tat cat ttg cca ctg ccg att atg atc 307

Ser	Arg	Leu	Lys	Glu	Gly	Gly	Tyr	His	Leu	Pro	Leu	Pro	Ile	Met	Ile	
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Ile	Gly	Gly	Gln	Ala	Ile	Ile	Trp	Leu	Ser	Trp	Pro	Phe	Gly	Thr	Met	
70					75					80					85	
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Gly	Ile	Leu	Ala	Ser	Phe	Val	Ala	Thr	Val	Leu	Val	Leu	Met	Tyr	Phe	
				90					95					100		
cga	att	ttc	tac	aat	ggc	acg	gaa	aaa	gaa	gcc	cgc	aac	tat	ttg	agg	451
Arg	Ile	Phe	Tyr	Asn	Gly	Thr	Glu	Lys	Glu	Ala	Arg	Asn	Tyr	Leu	Arg	
			105					110					115			
gac	acc	tct	gtg	ggc	atc	ttc	gtg	ctc	acc	tgg	att	cca	ttg	ttc	gga	499
Asp	Thr	Ser	Val	Gly	Ile	Phe	Val	Leu	Thr	Trp	Ile	Pro	Leu	Phe	Gly	
		120					125					130				
agc	ttc	gct	gcg	atg	ctg	tcg	ctg	atg	caa	aac	aat	tcc	atc	ccg	ggt	547
Ser	Phe	Ala	Ala	Met	Leu	Ser	Leu	Met	Gln	Asn	Asn	Ser	Ile	Pro	Gly	
	135					140					145					
aca	tat	ttc	att	ttg	acg	ttc	atg	ctg	tgt	gtg	atc	gca	tcg	gat	gtg	595
Thr	Tyr	Phe	Ile	Leu	Thr	Phe	Met	Leu	Cys	Val	Ile	Ala	Ser	Asp	Val	
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Gly	Gly	Tyr	Ile	Ala	Gly	Val	Phe	Phe	Gly	Ser	His	Pro	Met	Ala	Pro	
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ttg	gtg	agt	ccg	aag	aag	tct	tgg	gaa	ggc	ttt	gcc	ggc	tcc	att	gtc	691
Leu	Val	Ser	Pro	Lys	Lys	Ser	Trp	Glu	Gly	Phe	Ala	Gly	Ser	Ile	Val	
			185					190					195			
tta	gga	tcg	gtc	act	ggt	gca	ctc	agt	gtt	cac	ttc	ctg	ctc	gat	cac	739
Leu	Gly	Ser	Val	Thr	Gly	Ala	Leu	Ser	Val	His	Phe	Leu	Leu	Asp	His	
		200					205					210				
cac	tgg	tgg	atg	ggt	gtg	atc	ttg	ggt	tgt	gcc	cta	ggt	gtg	tgc	gcc	787
His	Trp	Trp	Met	Gly	Val	Ile	Leu	Gly	Cys	Ala	Leu	Val	Val	Cys	Ala	
	215					220					225					
acg	ttg	ggt	gac	ttg	ggt	gag	tcg	cag	ttc	aaa	cgc	gat	ttg	ggc	atc	835
Thr	Leu	Gly	Asp	Leu	Val	Glu	Ser	Gln	Phe	Lys	Arg	Asp	Leu	Gly	Ile	
230					235					240					245	
aag	gat	atg	tcg	aac	ctt	ctt	cca	ggc	cac	ggc	gga	ttg	atg	gac	cgt	883
Lys	Asp	Met	Ser	Asn	Leu	Leu	Pro	Gly	His	Gly	Gly	Leu	Met	Asp	Arg	
				250					255					260		
ttg	gat	ggc	atg	ctc	ccg	gcc	gcg	atg	gtg	acg	tgg	ttg	atc	ctg	agt	931
Leu	Asp	Gly	Met	Leu	Pro	Ala	Ala	Met	Val	Thr	Trp	Leu	Ile	Leu	Ser	
			265					270					275			
gtg	atc	agc	agc	tcg	tat	ccg	tcg	taaagcttgg	gccagcttata	agt						978
Val	Ile	Ser	Ser	Ser	Tyr	Pro	Ser									
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 <213> Corynebacterium glutamicum

<400> 100

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Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala
      35           40           45

Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro
      50           55           60

Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp
 65           70           75           80

Pro Phe Gly Thr Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu
      85           90           95

Val Leu Met Tyr Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala
      100          105          110

Arg Asn Tyr Leu Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp
      115          120          125

Ile Pro Leu Phe Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn
      130          135          140

Asn Ser Ile Pro Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val
      145          150          155          160

Ile Ala Ser Asp Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser
      165          170          175

His Pro Met Ala Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe
      180          185          190

Ala Gly Ser Ile Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His
      195          200          205

Phe Leu Leu Asp His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala
      210          215          220

Leu Val Val Cys Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys
      225          230          235          240

Arg Asp Leu Gly Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly
      245          250          255

Gly Leu Met Asp Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr
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Trp Leu Ile Leu Ser Val Ile Ser Ser Ser Tyr Pro Ser
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 <223> RXA02599

<400> 101

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                                         Met Asp Gln Leu Ile
                                         1           5

ctc gac gca ttt atc ggc ttg aga gtg act tgg ctg agt ccg gtg att 163
Leu Asp Ala Phe Ile Gly Leu Arg Val Thr Trp Leu Ser Pro Val Ile
                10                15                20

att ttg ttc acc cag ctc acc ggg cca aca ctg atg ttt gtg tat gcg 211
Ile Leu Phe Thr Gln Leu Thr Gly Pro Thr Leu Met Phe Val Tyr Ala
                25                30                35

ctt gtg tgg ggc ttg ttg cgc aag agc gcc act gcc ccg atc gcg gtg 259
Leu Val Trp Gly Leu Leu Arg Lys Ser Ala Thr Ala Pro Ile Ala Val
                40                45                50

ggg ctg gct aat ctg atc agt cat ttt ctc aag agg gcg ttt gaa cgg 307
Gly Leu Ala Asn Leu Ile Ser His Phe Leu Lys Arg Ala Phe Glu Arg
                55                60                65

cct cga cca aat aca gca gag cac ttg gtt gta gaa act aac ttt tca 355
Pro Arg Pro Asn Thr Ala Glu His Leu Val Val Glu Thr Asn Phe Ser
                70                75                80                85

ttc cct tct ggt cat gct gtg ggc gct gca gca tgt gcc gtg gca gtg 403
Phe Pro Ser Gly His Ala Val Gly Ala Ala Cys Ala Val Ala Val
                90                95                100

ggg tac tcc gtg aac cgg tgg tgg aaa ctc acg ctg tgg gta atc gcg 451
Gly Tyr Ser Val Asn Arg Trp Trp Lys Leu Thr Leu Trp Val Ile Ala
                105                110                115

ctg ctt gtg ggg ctg tct cgg ttg tat gtc ggt gtg cat tgg ccc agc 499
Leu Leu Val Gly Leu Ser Arg Leu Tyr Val Gly Val His Trp Pro Ser
                120                125                130

gat gtg ctt gcc ggc tgg gcc atc ggt gcg ttg act tca gtg gtg gtg 547
Asp Val Leu Ala Gly Trp Ala Ile Gly Ala Leu Thr Ser Val Val Val
                135                140                145

ttt acc agc tgg aac ctc ctc cag cgc cgc tgaaaccact gctgaaagtg 597
Phe Thr Ser Trp Asn Leu Leu Gln Arg Arg
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gta 600

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Met Phe Val Tyr Ala Leu Val Trp Gly Leu Leu Arg Lys Ser Ala Thr
 35 40 45

Ala Pro Ile Ala Val Gly Leu Ala Asn Leu Ile Ser His Phe Leu Lys
 50 55 60

Arg Ala Phe Glu Arg Pro Arg Pro Asn Thr Ala Glu His Leu Val Val
 65 70 75 80

Glu Thr Asn Phe Ser Phe Pro Ser Gly His Ala Val Gly Ala Ala Ala
 85 90 95

Cys Ala Val Ala Val Gly Tyr Ser Val Asn Arg Trp Trp Lys Leu Thr
 100 105 110

Leu Trp Val Ile Ala Leu Leu Val Gly Leu Ser Arg Leu Tyr Val Gly
 115 120 125

Val His Trp Pro Ser Asp Val Leu Ala Gly Trp Ala Ile Gly Ala Leu
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 145 150 155

<210> 103

<211> 999

<212> DNA

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<220>

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<222> (101)..(976)

<223> RXN02638

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 Met Val Lys Arg Phe
 1 5

ggc ttt ttc gta gag gat tcc ctg cct aag gtt ccg ctg cat ccc gaa 163
 Gly Phe Phe Val Glu Asp Ser Leu Pro Lys Val Pro Leu His Pro Glu
 10 15 20

gag tca cgg gag acg ttt tat ggg cgc atc atc att agt gct gtg cgg 211
 Glu Ser Arg Glu Thr Phe Tyr Gly Arg Ile Ile Ile Ser Ala Val Arg
 25 30 35

acg gtg atg aaa gcc cag gat gtg cag att tcc atc ttc ggt gcg gag 259

Thr	Val	Met	Lys	Ala	Gln	Asp	Val	Gln	Ile	Ser	Ile	Phe	Gly	Ala	Glu		
		40					45					50					
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Asn	Ile	Pro	Thr	Thr	Gly	Gly	Ala	Leu	Phe	Ala	Ser	Thr	Thr	Leu	Val		
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att	atg	act	tca	ttc	tgg	gtg	gta	tcc	ccc	gca	ttc	gtg	cgg	ggg	aag	355	
Ile	Met	Thr	Ser	Phe	Trp	Val	Val	Ser	Pro	Ala	Phe	Val	Arg	Gly	Lys		
	70				75				80						85		
cgc	ctg	gtt	cga	ttc	atg	gcg	aag	aag	gaa	att	ttc	gac	acc	cca	gtt	403	
Arg	Leu	Val	Arg	Phe	Met	Ala	Lys	Lys	Glu	Ile	Phe	Asp	Thr	Pro	Val		
				90					95					100			
gtc	ggc	acc	ctc	atg	cgc	tgg	atg	aag	cac	gtc	tct	gtg	gac	cgc	tcc	451	
Val	Gly	Thr	Leu	Met	Arg	Trp	Met	Lys	His	Val	Ser	Val	Asp	Arg	Ser		
			105					110					115				
gca	ggt	gcc	ggt	tcc	atg	gaa	gat	gcg	cgg	aag	cgt	ctc	gac	gcc	ggc	499	
Ala	Gly	Ala	Gly	Ser	Met	Glu	Asp	Ala	Arg	Lys	Arg	Leu	Asp	Ala	Gly		
		120					125					130					
agc	ctc	gtc	ggt	atc	ttc	cct	gag	gcg	acg	gtg	tca	cgg	tcc	ttt	gaa	547	
Ser	Leu	Val	Gly	Ile	Phe	Pro	Glu	Ala	Thr	Val	Ser	Arg	Ser	Phe	Glu		
	135					140					145						
atc	aag	gaa	cta	aaa	act	ggc	gcc	gtc	cgc	atc	gcc	gac	agc	gct	aac	595	
Ile	Lys	Glu	Leu	Lys	Thr	Gly	Ala	Val	Arg	Ile	Ala	Asp	Ser	Ala	Asn		
	150				155					160					165		
gtt	ccg	ctg	ctg	cca	ctt	att	att	tgg	ggc	ggc	cag	cgc	atc	atc	acc	643	
Val	Pro	Leu	Leu	Pro	Leu	Ile	Ile	Trp	Gly	Gly	Gln	Arg	Ile	Ile	Thr		
				170					175					180			
aaa	gac	atc	gag	cgc	gac	ttc	ggc	cgc	tcc	cac	atc	ccc	gta	ttc	atc	691	
Lys	Asp	Ile	Glu	Arg	Asp	Phe	Gly	Arg	Ser	His	Ile	Pro	Val	Phe	Ile		
			185					190					195				
agc	gtg	ggt	gaa	ccc	gtc	gac	gcc	agc	ggc	gat	ccc	gac	gaa	gca	acg	739	
Ser	Val	Gly	Glu	Pro	Val	Asp	Ala	Ser	Gly	Asp	Pro	Asp	Glu	Ala	Thr		
		200					205					210					
gaa	cgc	ctc	tac	gag	gct	atg	aaa	aag	ctt	ctc	gac	gaa	acc	cgc	acc	787	
Glu	Arg	Leu	Tyr	Glu	Ala	Met	Lys	Lys	Leu	Leu	Asp	Glu	Thr	Arg	Thr		
	215					220					225						
gcc	tac	gaa	caa	aag	tat	ggc	cca	ttc	gaa	ggt	gga	gaa	ttg	tgg	cgc	835	
Ala	Tyr	Glu	Gln	Lys	Tyr	Gly	Pro	Phe	Glu	Gly	Gly	Glu	Leu	Trp	Arg		
	230				235					240				245			
ccg	aaa	tcc	ctc	ggc	ggc	ggc	gcc	cca	acg	ttg	gag	cag	gcg	aaa	atg	883	
Pro	Lys	Ser	Leu	Gly	Gly	Gly	Ala	Pro	Thr	Leu	Glu	Gln	Ala	Lys	Met		
				250					255					260			
ttg	gaa	atc	gcc	gaa	cgg	gaa	cgt	cga	caa	gca	aaa	cgc	gcg	gca	aag	931	
Leu	Glu	Ile	Ala	Glu	Arg	Glu	Arg	Arg	Gln	Ala	Lys	Arg	Ala	Ala	Lys		
			265				270						275				
gtc	gcc	aag	aaa	cgc	acc	acc	ttt	ata	agg	aaa	atc	ttt	aaa	aaa		976	
Val	Ala	Lys	Lys	Arg	Thr	Thr	Phe	Ile	Arg	Lys	Ile	Phe	Lys	Lys			

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285

290

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<212> PRT

<213> Corynebacterium glutamicum

<400> 104

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Pro	Leu	His	Pro	Glu	Glu	Ser	Arg	Glu	Thr	Phe	Tyr	Gly	Arg	Ile	Ile
			20					25					30		

Ile	Ser	Ala	Val	Arg	Thr	Val	Met	Lys	Ala	Gln	Asp	Val	Gln	Ile	Ser
		35					40					45			

Ile	Phe	Gly	Ala	Glu	Asn	Ile	Pro	Thr	Thr	Gly	Gly	Ala	Leu	Phe	Ala
	50					55					60				

Ser	Thr	Thr	Leu	Val	Ile	Met	Thr	Ser	Phe	Trp	Val	Val	Ser	Pro	Ala
65					70					75					80

Phe	Val	Arg	Gly	Lys	Arg	Leu	Val	Arg	Phe	Met	Ala	Lys	Lys	Glu	Ile
				85					90					95	

Phe	Asp	Thr	Pro	Val	Val	Gly	Thr	Leu	Met	Arg	Trp	Met	Lys	His	Val
			100					105					110		

Ser	Val	Asp	Arg	Ser	Ala	Gly	Ala	Gly	Ser	Met	Glu	Asp	Ala	Arg	Lys
		115					120					125			

Arg	Leu	Asp	Ala	Gly	Ser	Leu	Val	Gly	Ile	Phe	Pro	Glu	Ala	Thr	Val
	130					135					140				

Ser	Arg	Ser	Phe	Glu	Ile	Lys	Glu	Leu	Lys	Thr	Gly	Ala	Val	Arg	Ile
145					150					155					160

Ala	Asp	Ser	Ala	Asn	Val	Pro	Leu	Leu	Pro	Leu	Ile	Ile	Trp	Gly	Gly
				165					170					175	

Gln	Arg	Ile	Ile	Thr	Lys	Asp	Ile	Glu	Arg	Asp	Phe	Gly	Arg	Ser	His
		180						185					190		

Ile	Pro	Val	Phe	Ile	Ser	Val	Gly	Glu	Pro	Val	Asp	Ala	Ser	Gly	Asp
	195						200					205			

Pro	Asp	Glu	Ala	Thr	Glu	Arg	Leu	Tyr	Glu	Ala	Met	Lys	Lys	Leu	Leu
	210					215					220				

Asp	Glu	Thr	Arg	Thr	Ala	Tyr	Glu	Gln	Lys	Tyr	Gly	Pro	Phe	Glu	Gly
225					230					235					240

Gly	Glu	Leu	Trp	Arg	Pro	Lys	Ser	Leu	Gly	Gly	Gly	Ala	Pro	Thr	Leu
				245					250					255	

Glu	Gln	Ala	Lys	Met	Leu	Glu	Ile	Ala	Glu	Arg	Glu	Arg	Arg	Gln	Ala
			260					265						270	

Lys Arg Ala Ala Lys Val Ala Lys Lys Arg Thr Thr Phe Ile Arg Lys
 275 280 285

Ile Phe Lys Lys
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<210> 105

<211> 534

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (8)..(511)

<223> FRXA02638

<400> 105

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 Met Ala Arg Lys Arg Leu Asn Ala Gly Ser Leu Val Gly Ile
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ttc cct gag gcg acg gtg tca cgg tcc ttt gaa atc aag gaa cta aaa 97
 Phe Pro Glu Ala Thr Val Ser Arg Ser Phe Glu Ile Lys Glu Leu Lys
 15 20 25 30

act ggc gcc gtc cgc atc gcc gac agc gct aac gtt ccg ctg ctg cca 145
 Thr Gly Ala Val Arg Ile Ala Asp Ser Ala Asn Val Pro Leu Leu Pro
 35 40 45

ctt att att tgg ggc ggc cag cgc atc atc acc aaa gac atc gag cgc 193
 Leu Ile Ile Trp Gly Gly Gln Arg Ile Ile Thr Lys Asp Ile Glu Arg
 50 55 60

gac ttc ggc cgc tcc cac atc ccc gta ttc atc agc gtg ggt gaa ccc 241
 Asp Phe Gly Arg Ser His Ile Pro Val Phe Ile Ser Val Gly Glu Pro
 65 70 75

gtc gac gcc agc ggc gat ccc gac gaa gca acg gaa cgc ctc tac gag 289
 Val Asp Ala Ser Gly Asp Pro Asp Glu Ala Thr Glu Arg Leu Tyr Glu
 80 85 90

gct atg aaa aag ctt ctc gac gaa acc cgc acc gcc tac gaa caa aag 337
 Ala Met Lys Lys Leu Leu Asp Glu Thr Arg Thr Ala Tyr Glu Gln Lys
 95 100 105 110

tat ggc cca ttc gaa ggt gga gaa ttg tgg cgc ccg aaa tcc ctc ggc 385
 Tyr Gly Pro Phe Glu Gly Gly Glu Leu Trp Arg Pro Lys Ser Leu Gly
 115 120 125

ggc ggc gcc cca acg ttg gag cag gcg aaa atg ttg gaa atc gcc gaa 433
 Gly Gly Ala Pro Thr Leu Glu Gln Ala Lys Met Leu Glu Ile Ala Glu
 130 135 140

cgg gaa cgt cga caa gca aaa cgc gcg gca aag gtc gcc aag aaa cgc 481
 Arg Glu Arg Arg Gln Ala Lys Arg Ala Ala Lys Val Ala Lys Lys Arg
 145 150 155

acc acc ttt ata agg aaa atc ttt aaa aaa tgattgcact ggggttcagcg 531
 Thr Thr Phe Ile Arg Lys Ile Phe Lys Lys

160

165

ccc

534

<210> 106

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

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Glu Ala Thr Val Ser Arg Ser Phe Glu Ile Lys Glu Leu Lys Thr Gly
 20 25 30

Ala Val Arg Ile Ala Asp Ser Ala Asn Val Pro Leu Leu Pro Leu Ile
 35 40 45

Ile Trp Gly Gly Gln Arg Ile Ile Thr Lys Asp Ile Glu Arg Asp Phe
 50 55 60

Gly Arg Ser His Ile Pro Val Phe Ile Ser Val Gly Glu Pro Val Asp
 65 70 75 80

Ala Ser Gly Asp Pro Asp Glu Ala Thr Glu Arg Leu Tyr Glu Ala Met
 85 90 95

Lys Lys Leu Leu Asp Glu Thr Arg Thr Ala Tyr Glu Gln Lys Tyr Gly
 100 105 110

Pro Phe Glu Gly Gly Glu Leu Trp Arg Pro Lys Ser Leu Gly Gly Gly
 115 120 125

Ala Pro Thr Leu Glu Gln Ala Lys Met Leu Glu Ile Ala Glu Arg Glu
 130 135 140

Arg Arg Gln Ala Lys Arg Ala Ala Lys Val Ala Lys Lys Arg Thr Thr
 145 150 155 160

Phe Ile Arg Lys Ile Phe Lys Lys
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<210> 107

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(637)

<223> RXA00856

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 Val Ser Asp Val Ser
 1 5

gca ggc gta aat ggc gca caa gat cca agc aat caa gcg gtc aag cct 163
 Ala Gly Val Asn Gly Ala Gln Asp Pro Ser Asn Gln Ala Val Lys Pro
 10 15 20
 tcc aac tgg aac ctt ccg aac ttc ttg acc agc ttg cgt atc att gtc 211
 Ser Asn Trp Asn Leu Pro Asn Phe Leu Thr Ser Leu Arg Ile Ile Val
 25 30 35
 atc cct ttg ttt gcg tgg ctt acg ctt aaa ggt gag acg gaa aac aat 259
 Ile Pro Leu Phe Ala Trp Leu Thr Leu Lys Gly Glu Thr Glu Asn Asn
 40 45 50
 gct ttt gcc tgg tgg gcg ttg gtt gtt ttc att ttg ctc atg atc acc 307
 Ala Phe Ala Trp Trp Ala Leu Val Val Phe Ile Leu Leu Met Ile Thr
 55 60 65
 gac aag ctt gac ggc gat att gcg cga gca cgt ggc ctg gtc act gac 355
 Asp Lys Leu Asp Gly Asp Ile Ala Arg Ala Arg Gly Leu Val Thr Asp
 70 75 80 85
 ttt ggc aag atc gcg gat ccg att gcc gat aag gcg ttg atg acc aca 403
 Phe Gly Lys Ile Ala Asp Pro Ile Ala Asp Lys Ala Leu Met Thr Thr
 90 95 100
 gca ttt gtc tgt ttc aac atc atc ggc att ttg ccc tgg tgg gtc act 451
 Ala Phe Val Cys Phe Asn Ile Ile Gly Ile Leu Pro Trp Trp Val Thr
 105 110 115
 gcg ttg att gtg ctt cga gag ttc ggc att acc atc tgg cgt ttc ttc 499
 Ala Leu Ile Val Leu Arg Glu Phe Gly Ile Thr Ile Trp Arg Phe Phe
 120 125 130
 caa ctg cgc gct gga aat gtt gtg cct gca tca aag ggg ggc aag ctt 547
 Gln Leu Arg Ala Gly Asn Val Val Pro Ala Ser Lys Gly Gly Lys Leu
 135 140 145
 aag act gct ctg cag act gtt gcc gtt gct ctg tat ctg tgc cct ttc 595
 Lys Thr Ala Leu Gln Thr Val Ala Val Ala Leu Tyr Leu Cys Pro Phe
 150 155 160 165
 cca agt tgg atg gat att cca agc cag atc gtc atg tat gca 637
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<210> 108

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

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 Leu Arg Ile Ile Val Ile Pro Leu Phe Ala Trp Leu Thr Leu Lys Gly
 35 40 45

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									atg	ctg	gga	ctt	cat				115
									Met	Leu	Gly	Leu	His				
									1				5				
gga cgt aag cct gcg cag gtt att gtt gag cct gtt gcc aaa ttg atg																	163
Gly	Arg	Lys	Pro	Ala	Gln	Val	Ile	Val	Glu	Pro	Val	Ala	Lys	Leu	Met		
				10					15					20			
atc aag ttg aag gtg acg cct aat cag ctc acc tta gtc agc gct ggc																	211
Ile	Lys	Leu	Lys	Val	Thr	Pro	Asn	Gln	Leu	Thr	Leu	Val	Ser	Ala	Gly		
			25					30					35				
ctc acc gtt ggg gtg gct ttg ctg ctg att cct acg ggg cat ttg att																	259
Leu	Thr	Val	Gly	Val	Ala	Leu	Leu	Leu	Ile	Pro	Thr	Gly	His	Leu	Ile		
		40					45					50					
tgg gcg gca gtt ttg acg ggc ctg ttt gcg gct ttc gac atg att gat																	307
Trp	Ala	Ala	Val	Leu	Thr	Gly	Leu	Phe	Ala	Ala	Phe	Asp	Met	Ile	Asp		
	55					60					65						

ggc acg gtt gct cgc atg caa ggt ggt ggc acc aaa ttt ggt gcc acc 355
 Gly Thr Val Ala Arg Met Gln Gly Gly Gly Thr Lys Phe Gly Ala Thr
 70 75 80 85
 ttg gat gcc acg tgt gac cgc atc act gat ggt gca cta ttt ggt gcg 403
 Leu Asp Ala Thr Cys Asp Arg Ile Thr Asp Gly Ala Leu Phe Gly Ala
 90 95 100
 att acc tgg tgg ctg gtg tat tcc tac gat gca cca cag gca ttg gtc 451
 Ile Thr Trp Trp Leu Val Tyr Ser Tyr Asp Ala Pro Gln Ala Leu Val
 105 110 115
 gct gcc tcc ttg gtt tgt ttg gtt gcc tcc cag gtg atc tct tac gtg 499
 Ala Ala Ser Leu Val Cys Leu Val Ala Ser Gln Val Ile Ser Tyr Val
 120 125 130
 aaa gcc agg gga gag gcc tcc gga ttc acc atg gac ggc ggt ctc gtg 547
 Lys Ala Arg Gly Glu Ala Ser Gly Phe Thr Met Asp Gly Gly Leu Val
 135 140 145
 gaa cgc cct gag cgt ctg att gtc agc ctt gtt ggt ttg ggg ctg acc 595
 Glu Arg Pro Glu Arg Leu Ile Val Ser Leu Val Gly Leu Gly Leu Thr
 150 155 160 165
 gga atg ggc gtt cca tat gcc atc gat gtg gca ctg tgg gcc ctt gca 643
 Gly Met Gly Val Pro Tyr Ala Ile Asp Val Ala Leu Trp Ala Leu Ala
 170 175 180
 gct ggc agt att tac act gtt gtg cag cgc ttg gtc atg gct gga aag 691
 Ala Gly Ser Ile Tyr Thr Val Val Gln Arg Leu Val Met Ala Gly Lys
 185 190 195
 tcc cca ttg gct aag gaa ttt acc aag gca cca gca ggt gcg aag gca 739
 Ser Pro Leu Ala Lys Glu Phe Thr Lys Ala Pro Ala Gly Ala Lys Ala
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 Asp Tyr Ser Asn Thr Lys
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<210> 110

<211> 219

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 110

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 20 25 30
 Leu Val Ser Ala Gly Leu Thr Val Gly Val Ala Leu Leu Ile Pro
 35 40 45
 Thr Gly His Leu Ile Trp Ala Ala Val Leu Thr Gly Leu Phe Ala Ala
 50 55 60
 Phe Asp Met Ile Asp Gly Thr Val Ala Arg Met Gln Gly Gly Gly Thr
 65 70 75 80

ctg gag gtc gcc cca ttc ggc atc gac gtt gtt gtc atc gaa ccg ggc 355
 Leu Glu Val Ala Pro Phe Gly Ile Asp Val Val Val Ile Glu Pro Gly
 70 75 80 85
 ggc atc gcc acc gag tgg gga gga atc gct gcc gac aat ctc gac gca 403
 Gly Ile Ala Thr Glu Trp Gly Gly Ile Ala Ala Asp Asn Leu Asp Ala
 90 95 100
 gtg tcg aaa gac agc gca tac aag cgc cag gct gac gca gta tcg aag 451
 Val Ser Lys Asp Ser Ala Tyr Lys Arg Gln Ala Asp Ala Val Ser Lys
 105 110 115
 tcg ttg cga tct gag gcg aac agc aac cgc aac tca cca ccg tcg gtt 499
 Ser Leu Arg Ser Glu Ala Asn Ser Asn Arg Asn Ser Pro Pro Ser Val
 120 125 130
 gtc gcc gat gcg att gga aag gcc gtg acg gca cgt cac ccc aag acc 547
 Val Ala Asp Ala Ile Gly Lys Ala Val Thr Ala Arg His Pro Lys Thr
 135 140 145
 cgc tat gcc atc ggc ttc ggt gcc aaa ccg ctg att gcc tcg cgc aac 595
 Arg Tyr Ala Ile Gly Phe Gly Ala Lys Pro Leu Ile Ala Ser Arg Asn
 150 155 160 165
 atc ctc acc gat cgc cag ttc gac cca gtg atc act cga gcg act ggc 643
 Ile Leu Thr Asp Arg Gln Phe Asp Pro Val Ile Thr Arg Ala Thr Gly
 170 175 180
 gtc ccc cgc gac tgaccactct tctgcgcccg tca 678
 Val Pro Arg Asp
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<210> 112

<211> 185

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 112

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 20 25 30
 Trp Gly Thr Ile Val Asn Ile Thr Ser Met Gly Gly Lys Ile Tyr Thr
 35 40 45
 Pro Leu Gly Gly Trp Tyr His Gly Thr Lys Phe Ala Leu Glu Ala Leu
 50 55 60
 Ser Asp Ala Leu Arg Leu Glu Val Ala Pro Phe Gly Ile Asp Val Val
 65 70 75 80
 Val Ile Glu Pro Gly Gly Ile Ala Thr Glu Trp Gly Gly Ile Ala Ala
 85 90 95
 Asp Asn Leu Asp Ala Val Ser Lys Asp Ser Ala Tyr Lys Arg Gln Ala
 100 105 110

Asp Ala Val Ser Lys Ser Leu Arg Ser Glu Ala Asn Ser Asn Arg Asn
 115 120 125

Ser Pro Pro Ser Val Val Ala Asp Ala Ile Gly Lys Ala Val Thr Ala
 130 135 140

Arg His Pro Lys Thr Arg Tyr Ala Ile Gly Phe Gly Ala Lys Pro Leu
 145 150 155 160

Ile Ala Ser Arg Asn Ile Leu Thr Asp Arg Gln Phe Asp Pro Val Ile
 165 170 175

Thr Arg Ala Thr Gly Val Pro Arg Asp
 180 185

<210> 113
 <211> 406
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(406)
 <223> FRXA02836

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gcttcagacg ggatccaccc cctcgagatg gacgtcaccg atg aca atc gat gaa 115
 Met Thr Ile Asp Glu
 1 5

ggc cgt cgc cag ttc gag gtc aat gta ttc ggc gcg atg gcc ctc acc 163
 Gly Arg Arg Gln Phe Glu Val Asn Val Phe Gly Ala Met Ala Leu Thr
 10 15 20

cga ctc gtc ctg ccc cac atg cag aaa caa aag tgg ggg acg atc gtg 211
 Arg Leu Val Leu Pro His Met Gln Lys Gln Lys Trp Gly Thr Ile Val
 25 30 35

aac atc acà tcg atg ggc ggg aag atc tac acg cct ctc ggc ggc tgg 259
 Asn Ile Thr Ser Met Gly Gly Lys Ile Tyr Thr Pro Leu Gly Gly Trp
 40 45 50

tat cac ggc acc aag ttc gcc ctc gag gcc ctc tcg gac gcc ctc cgc 307
 Tyr His Gly Thr Lys Phe Ala Leu Glu Ala Leu Ser Asp Ala Leu Arg
 55 60 65

ctg gag gtc gcc cca ttc ggc atc gac gtt gtt gtc atc gaa ccg ggc 355
 Leu Glu Val Ala Pro Phe Gly Ile Asp Val Val Val Ile Glu Pro Gly
 70 75 80 85

ggc atc gcc acc gag tgg gga gga atc gct gcc gac aat ctc gac gca 403
 Gly Ile Ala Thr Glu Trp Gly Gly Ile Ala Ala Asp Asn Leu Asp Ala
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gtg 406
 Val

<210> 114
<211> 102
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 114

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20 25 30

Trp Gly Thr Ile Val Asn Ile Thr Ser Met Gly Gly Lys Ile Tyr Thr
35 40 45

Pro Leu Gly Gly Trp Tyr His Gly Thr Lys Phe Ala Leu Glu Ala Leu
50 55 60

Ser Asp Ala Leu Arg Leu Glu Val Ala Pro Phe Gly Ile Asp Val Val
65 70 75 80

Val Ile Glu Pro Gly Gly Ile Ala Thr Glu Trp Gly Gly Ile Ala Ala
85 90 95

Asp Asn Leu Asp Ala Val
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<212> DNA
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<223> RXA02578
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aaacagcccac acctttccgc taaactcgca tggtgaaata atg tct acc caa tca 115
Met Ser Thr Gln Ser
1 5

tat gca ccc atc cgc cat cgc gga ttc atc agc tca ctc gag gga cta 163
Tyr Ala Pro Ile Arg His Arg Gly Phe Ile Ser Ser Leu Glu Gly Leu
10 15 20

cgc gca atc gcc tcc ctg gga gtc ttg gcg acc cac gtt gca ttc caa 211
 Arg Ala Ile Ala Ser Leu Gly Val Leu Ala Thr His Val Ala Phe Gln
 25 30 35

acc tcc gtc gac ccc gcc agc aac atc ggt gca gta ctc gcg cgt ttc 259
Thr Ser Val Asp Pro Ala Ser Asn Ile Gly Ala Val Leu Ala Arg Phe
40 45 50

gac ttt ttc gtc gcc gtc ttc ttc gcc ctc tcc gcc ttc gtt ctt tgg 307
Asp Phe Phe Val Ala Val Phe Phe Ala Leu Ser Ala Phe Val Leu Trp
55 60 65

cga cgc cgc gcc ggg caa cca gtg gga ctg tac tac ctc aaa cgc cta	355
Arg Arg Arg Ala Gly Gln Pro Val Gly Leu Tyr Tyr Leu Lys Arg Leu	
70 75 80 85	
gcc cgc atc atg ccc gca tac tgg gca acg gtc att gca gtc ctg ctg	403
Ala Arg Ile Met Pro Ala Tyr Trp Ala Thr Val Ile Ala Val Leu Leu	
90 95 100	
ttt att ccc acc ggc ccc tgg tta gcc aac ctg acg atg acc caa atc	451
Phe Ile Pro Thr Gly Pro Trp Leu Ala Asn Leu Thr Met Thr Gln Ile	
105 110 115	
tac tgg cca gac ggg ctc atg aca ggc ctc acc cac ctt tgg tcc ctg	499
Tyr Trp Pro Asp Gly Leu Met Thr Gly Leu Thr His Leu Trp Ser Leu	
120 125 130	
tgc gtg gaa gtg gcg ttt tac ctg gtg atg ccg ctt ctc gcg tgg gtg	547
Cys Val Glu Val Ala Phe Tyr Leu Val Met Pro Leu Leu Ala Trp Val	
135 140 145	
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Leu Asp Arg Phe Gly Arg Pro Val Arg Ile Leu Leu Ile Val Gly Gly	
150 155 160 165	
gca gtg ttg agt ctg gcg tgg ccg tgg att ccc ctt gtg gag cat gcg	643
Ala Val Leu Ser Leu Ala Trp Pro Trp Ile Pro Leu Val Glu His Ala	
170 175 180	
ttg gac gag ggg tgg gcg aac atg cag atc tgg cca ccc gct tac gct	691
Leu Asp Glu Gly Trp Ala Asn Met Gln Ile Trp Pro Pro Ala Tyr Ala	
185 190 195	
tgc tgg ttt gca gtc ggc atg atc gcc gca gaa att gaa gga gtt cga	739
Cys Trp Phe Ala Val Gly Met Ile Ala Ala Glu Ile Glu Gly Val Arg	
200 205 210	
ttc cca cgg gtt ccg agc ttt gtg tgg gtg ggt tta gct tta gtg gtc	787
Phe Pro Arg Val Pro Ser Phe Val Trp Val Gly Leu Ala Leu Val Val	
215 220 225	
gct tgg atc gcg ggc caa gaa tgg ttc gga cca cta ggt tta gtg cac	835
Ala Trp Ile Ala Gly Gln Glu Trp Phe Gly Pro Leu Gly Leu Val His	
230 235 240 245	
ccc agc ccc tgg gaa ttc aac tta aga gtc ctc gcg ggc aca ctt ttc	883
Pro Ser Pro Trp Glu Phe Asn Leu Arg Val Leu Ala Gly Thr Leu Phe	
250 255 260	
gct gta ttt ctg gtg gtt ccc tac gcg ctg ggt acg ccc tct cgg ctt	931
Ala Val Phe Leu Val Val Pro Tyr Ala Leu Gly Thr Pro Ser Arg Leu	
265 270 275	
ctt gat tcc agt tgg atg aaa acg ctc ggc acc tgg tgg tat tcc atc	979
Leu Asp Ser Ser Trp Met Lys Thr Leu Gly Thr Trp Ser Tyr Ser Ile	
280 285 290	
ttc ctc tgg cac ctt ccc gtg ctg acg att gtg ttc cca ctg ctc ggg	1027
Phe Leu Trp His Leu Pro Val Leu Thr Ile Val Phe Pro Leu Leu Gly	
295 300 305	

ttg cct tta ttt agt gga aat ttc ctg ttg gtg ttc atc gtg acg gtc 1075
 Leu Pro Leu Phe Ser Gly Asn Phe Leu Leu Val Phe Ile Val Thr Val
 310 315 320 325

ttg ttg acg atc cca gtt gcc gcc atc agc tac acc ttc atc gaa gag 1123
 Leu Leu Thr Ile Pro Val Ala Ala Ile Ser Tyr Thr Phe Ile Glu Glu
 330 335 340

ccc atc agc ggt gga ccc ggc gcg cca ttc agg ctg ggg gtc gtt agg 1171
 Pro Ile Ser Gly Gly Pro Gly Ala Pro Phe Arg Leu Gly Val Val Arg
 345 350 355

att cac cat ttt tct ggg ggt agg tct gga aaa tgatgaattg gcaccacgtc 1224
 Ile His His Phe Ser Gly Gly Arg Ser Gly Lys
 360 365

aag 1227

<210> 116

<211> 368

<212> PRT

<213> Corynebacterium glutamicum

<400> 116

Met Ser Thr Gln Ser Tyr Ala Pro Ile Arg His Arg Gly Phe Ile Ser
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Ser Leu Glu Gly Leu Arg Ala Ile Ala Ser Leu Gly Val Leu Ala Thr
 20 25 30

His Val Ala Phe Gln Thr Ser Val Asp Pro Ala Ser Asn Ile Gly Ala
 35 40 45

Val Leu Ala Arg Phe Asp Phe Phe Val Ala Val Phe Phe Ala Leu Ser
 50 55 60

Ala Phe Val Leu Trp Arg Arg Ala Gly Gln Pro Val Gly Leu Tyr
 65 70 75 80

Tyr Leu Lys Arg Leu Ala Arg Ile Met Pro Ala Tyr Trp Ala Thr Val
 85 90 95

Ile Ala Val Leu Leu Phe Ile Pro Thr Gly Pro Trp Leu Ala Asn Leu
 100 105 110

Thr Met Thr Gln Ile Tyr Trp Pro Asp Gly Leu Met Thr Gly Leu Thr
 115 120 125

His Leu Trp Ser Leu Cys Val Glu Val Ala Phe Tyr Leu Val Met Pro
 130 135 140

Leu Leu Ala Trp Val Leu Asp Arg Phe Gly Arg Pro Val Arg Ile Leu
 145 150 155 160

Leu Ile Val Gly Gly Ala Val Leu Ser Leu Ala Trp Pro Trp Ile Pro
 165 170 175

Leu Val Glu His Ala Leu Asp Glu Gly Trp Ala Asn Met Gln Ile Trp
 180 185 190

Pro Pro Ala Tyr Ala Cys Trp Phe Ala Val Gly Met Ile Ala Ala Glu
 195 200 205
 Ile Glu Gly Val Arg Phe Pro Arg Val Pro Ser Phe Val Trp Val Gly
 210 215 220
 Leu Ala Leu Val Val Ala Trp Ile Ala Gly Gln Glu Trp Phe Gly Pro
 225 230 235 240
 Leu Gly Leu Val His Pro Ser Pro Trp Glu Phe Asn Leu Arg Val Leu
 245 250 255
 Ala Gly Thr Leu Phe Ala Val Phe Leu Val Val Pro Tyr Ala Leu Gly
 260 265 270
 Thr Pro Ser Arg Leu Leu Asp Ser Ser Trp Met Lys Thr Leu Gly Thr
 275 280 285
 Trp Ser Tyr Ser Ile Phe Leu Trp His Leu Pro Val Leu Thr Ile Val
 290 295 300
 Phe Pro Leu Leu Gly Leu Pro Leu Phe Ser Gly Asn Phe Leu Leu Val
 305 310 315 320
 Phe Ile Val Thr Val Leu Leu Thr Ile Pro Val Ala Ala Ile Ser Tyr
 325 330 335
 Thr Phe Ile Glu Glu Pro Ile Ser Gly Gly Pro Gly Ala Pro Phe Arg
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 Leu Gly Val Val Arg Ile His His Phe Ser Gly Gly Arg Ser Gly Lys
 355 360 365

<210> 117
 <211> 924
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(901)
 <223> RXA02150

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 taaaaagtgg ttttggtagc ttcgcagcaa aatacacatc gtg ggt aac gta ttc 115
 Val Gly Asn Val Phe
 1 5
 tta gaa gtt cct aca gca gta aag cgc gaa gaa ggg gta aac cca aac 163
 Leu Glu Val Pro Thr Ala Val Lys Arg Glu Glu Gly Val Asn Pro Asn
 10 15 20
 atc atg aaa aac aac tgg tat cgg ctt ttc aag tat gtg cta att ggc 211
 Ile Met Lys Asn Asn Trp Tyr Arg Leu Phe Lys Tyr Val Leu Ile Gly
 25 30 35

ccg ttt ttg cgt gtg tac aac cgc ccg gag atc gaa ggc aaa gaa aac	259
Pro Phe Leu Arg Val Tyr Asn Arg Pro Glu Ile Glu Gly Lys Glu Asn	
40 45 50	
atc cct gca gaa ggt gcc gcg atc atg gcg tcc aac cac gaa gca gtg	307
Ile Pro Ala Glu Gly Ala Ala Ile Met Ala Ser Asn His Glu Ala Val	
55 60 65	
atg gat tcc ttt tat ttt ccc ctg ctg tgc cca cgg cag ctg acc ttc	355
Met Asp Ser Phe Tyr Phe Pro Leu Leu Cys Pro Arg Gln Leu Thr Phe	
70 75 80 85	
cca gcg aag gcc gaa tac ttc aca tca cca ggt att aaa ggc aag atg	403
Pro Ala Lys Ala Glu Tyr Phe Thr Ser Pro Gly Ile Lys Gly Lys Met	
90 95 100	
cag aag tgg ttt ttt act tct gtg ggg caa gta ccc ctg gac cgc acc	451
Gln Lys Trp Phe Phe Thr Ser Val Gly Gln Val Pro Leu Asp Arg Thr	
105 110 115	
gca gat aat gcc atg gat tct ttg atg aat acc gcc aaa atg gtg ctg	499
Ala Asp Asn Ala Met Asp Ser Leu Met Asn Thr Ala Lys Met Val Leu	
120 125 130	
gat cgg gga gac ctc ttc ggt att tac cct gaa gga tct cgt tcg ccc	547
Asp Arg Gly Asp Leu Phe Gly Ile Tyr Pro Glu Gly Ser Arg Ser Pro	
135 140 145	
gat ggt cgc atc tac aag ggc aaa acc gga atg gcc tat gtt gcg atg	595
Asp Gly Arg Ile Tyr Lys Gly Lys Thr Gly Met Ala Tyr Val Ala Met	
150 155 160 165	
gaa act ggt acg aca gtt atc ccc gtt gcc atg att ggc agc cgg gac	643
Glu Thr Gly Thr Thr Val Ile Pro Val Ala Met Ile Gly Ser Arg Asp	
170 175 180	
gcg aac cct atc gga agt tgg ttt ccg aaa ccc gca aaa gtc agg atc	691
Ala Asn Pro Ile Gly Ser Trp Phe Pro Lys Pro Ala Lys Val Arg Ile	
185 190 195	
aag gta gga agc cca att gat ccc ctc gca ttc gtc aaa gaa cat ggg	739
Lys Val Gly Ser Pro Ile Asp Pro Leu Ala Phe Val Lys Glu His Gly	
200 205 210	
ttg aag cct gga acc tac gaa gca gcg cgc aag ctg aca gat cac gtt	787
Leu Lys Pro Gly Thr Tyr Glu Ala Ala Arg Lys Leu Thr Asp His Val	
215 220 225	
atg ttc att ctt gct gat ctc act ggt cag ccg tat gtt gat gcg tac	835
Met Phe Ile Leu Ala Asp Leu Thr Gly Gln Pro Tyr Val Asp Ala Tyr	
230 235 240 245	
tct aaa gat gtg aaa aac gct ctg gag gaa gga aaa gga tac ccg gag	883
Ser Lys Asp Val Lys Asn Ala Leu Glu Glu Gly Lys Gly Tyr Pro Glu	
250 255 260	
ggc aca gct cct tca cag taatcggggtc ttttctgtta aaa	924
Gly Thr Ala Pro Ser Gln	
265	

<210> 118
 <211> 267
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 118

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Gly	Val	Asn	Pro	Asn	Ile	Met	Lys	Asn	Asn	Trp	Tyr	Arg	Leu	Phe	Lys
			20					25					30		
Tyr	Val	Leu	Ile	Gly	Pro	Phe	Leu	Arg	Val	Tyr	Asn	Arg	Pro	Glu	Ile
		35					40					45			
Glu	Gly	Lys	Glu	Asn	Ile	Pro	Ala	Glu	Gly	Ala	Ala	Ile	Met	Ala	Ser
	50					55					60				
Asn	His	Glu	Ala	Val	Met	Asp	Ser	Phe	Tyr	Phe	Pro	Leu	Leu	Cys	Pro
65					70					75					80
Arg	Gln	Leu	Thr	Phe	Pro	Ala	Lys	Ala	Glu	Tyr	Phe	Thr	Ser	Pro	Gly
				85					90					95	
Ile	Lys	Gly	Lys	Met	Gln	Lys	Trp	Phe	Phe	Thr	Ser	Val	Gly	Gln	Val
			100					105					110		
Pro	Leu	Asp	Arg	Thr	Ala	Asp	Asn	Ala	Met	Asp	Ser	Leu	Met	Asn	Thr
		115					120					125			
Ala	Lys	Met	Val	Leu	Asp	Arg	Gly	Asp	Leu	Phe	Gly	Ile	Tyr	Pro	Glu
	130					135					140				
Gly	Ser	Arg	Ser	Pro	Asp	Gly	Arg	Ile	Tyr	Lys	Gly	Lys	Thr	Gly	Met
145					150					155					160
Ala	Tyr	Val	Ala	Met	Glu	Thr	Gly	Thr	Thr	Val	Ile	Pro	Val	Ala	Met
				165					170					175	
Ile	Gly	Ser	Arg	Asp	Ala	Asn	Pro	Ile	Gly	Ser	Trp	Phe	Pro	Lys	Pro
			180					185					190		
Ala	Lys	Val	Arg	Ile	Lys	Val	Gly	Ser	Pro	Ile	Asp	Pro	Leu	Ala	Phe
		195					200					205			
Val	Lys	Glu	His	Gly	Leu	Lys	Pro	Gly	Thr	Tyr	Glu	Ala	Ala	Arg	Lys
	210					215					220				
Leu	Thr	Asp	His	Val	Met	Phe	Ile	Leu	Ala	Asp	Leu	Thr	Gly	Gln	Pro
225					230					235					240
Tyr	Val	Asp	Ala	Tyr	Ser	Lys	Asp	Val	Lys	Asn	Ala	Leu	Glu	Glu	Gly
				245					250					255	
Lys	Gly	Tyr	Pro	Glu	Gly	Thr	Ala	Pro	Ser	Gln					
			260					265							

<210> 119
 <211> 504

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(481)

<223> RXA00607

<400> 119

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ccatcaaccc cgcaggcgat aacaaagagg aggcaaaccg atg att ctc gca ctg 115
 Met Ile Leu Ala Leu
 1 5

aca gtc gcg ata ctt ttc ggt gga ggt gtc tac ctc att cag caa cgc 163
 Thr Val Ala Ile Leu Phe Gly Gly Gly Val Tyr Leu Ile Gln Gln Arg
 10 15 20

gga atg gtg cgc atc gtc ttc ggc atg tca ctg atc ggc cac gca gcg 211
 Gly Met Val Arg Ile Val Phe Gly Met Ser Leu Ile Gly His Ala Ala
 25 30 35

aac ctg acc atc ctg tac gcc ggt gtg ccc acg tgg cgc ggc gaa gcc 259
 Asn Leu Thr Ile Leu Tyr Ala Gly Val Pro Thr Trp Arg Gly Glu Ala
 40 45 50

ttc ccc gac agg acc ccg ctt acc gac gcc gcc gat cca ctc ccc cag 307
 Phe Pro Asp Arg Thr Pro Leu Thr Asp Ala Ala Asp Pro Leu Pro Gln
 55 60 65

gcc ttc gtc ctc acc gcc atc gtc atc gcg atg gcc acc aca acc atc 355
 Ala Phe Val Leu Thr Ala Ile Val Ile Ala Met Ala Thr Thr Thr Ile
 70 75 80 85

atg ttg gcc ttg gca gca ctg gga cgc agc gac gac acc cgg tcc atc 403
 Met Leu Ala Leu Ala Ala Leu Gly Arg Ser Asp Asp Thr Arg Ser Ile
 90 95 100

gaa cca gat gac gat caa tcg cct ttg act act agc gct cgt tca gtc 451
 Glu Pro Asp Asp Asp Gln Ser Pro Leu Thr Thr Ser Ala Arg Ser Val
 105 110 115

acc aac cca aca gat cag gag gat aaa gct taaatggcca tggatgttct 501
 Thr Asn Pro Thr Asp Gln Glu Asp Lys Ala
 120 125

cct 504

<210> 120

<211> 127

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

Met Ile Leu Ala Leu Thr Val Ala Ile Leu Phe Gly Gly Gly Val Tyr
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Leu Ile Gln Gln Arg Gly Met Val Arg Ile Val Phe Gly Met Ser Leu
 20 25 30

Ile Gly His Ala Ala Asn Leu Thr Ile Leu Tyr Ala Gly Val Pro Thr
 35 40 45
 Trp Arg Gly Glu Ala Phe Pro Asp Arg Thr Pro Leu Thr Asp Ala Ala
 50 55 60
 Asp Pro Leu Pro Gln Ala Phe Val Leu Thr Ala Ile Val Ile Ala Met
 65 70 75 80
 Ala Thr Thr Thr Ile Met Leu Ala Leu Ala Ala Leu Gly Arg Ser Asp
 85 90 95
 Asp Thr Arg Ser Ile Glu Pro Asp Asp Asp Gln Ser Pro Leu Thr Thr
 100 105 110
 Ser Ala Arg Ser Val Thr Asn Pro Thr Asp Gln Glu Asp Lys Ala
 115 120 125

<210> 121
 <211> 1119
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1096)
 <223> RXA02397

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 tagaaaccag agacaagctt aagaaggaca ggggccggcc atg aat gat ttc gaa 115
 Met Asn Asp Phe Glu
 1 5
 aca acc atc gat cgg atc tct aaa gaa caa gat ccc gca gcc cga agc 163
 Thr Thr Ile Asp Arg Ile Ser Lys Glu Gln Asp Pro Ala Ala Arg Ser
 10 15 20
 cgc gtg gaa cag ttc att gtg gaa aca gta cgt gca cta ccc aac ttg 211
 Arg Val Glu Gln Phe Ile Val Glu Thr Val Arg Ala Leu Pro Asn Leu
 25 30 35
 acc acc aaa caa ggt gca tcg ttg gct atc caa ctt ctt gat gcg gta 259
 Thr Thr Lys Gln Gly Ala Ser Leu Ala Ile Gln Leu Leu Asp Ala Val
 40 45 50
 cag ctc gcg gat gcg gcg gga acc aag ggg ggt gcg tcg aca agc aat 307
 Gln Leu Ala Asp Ala Ala Gly Thr Lys Gly Gly Ala Ser Thr Ser Asn
 55 60 65
 gct tca tcg ctg cct gac acc ttt gac gcg ctg acc agc ctg att ggc 355
 Ala Ser Ser Leu Pro Asp Thr Phe Asp Ala Leu Thr Ser Leu Ile Gly
 70 75 80 85
 aag ctc gat gtg cgc agc gat tct gaa tgg cgc tcg ttt ggg ttc cag 403
 Lys Leu Asp Val Arg Ser Asp Ser Glu Trp Arg Ser Phe Gly Phe Gln
 90 95 100

cct tct gaa act gcg cac ccg cta atg atc gct atc cct gag att gag	451
Pro Ser Glu Thr Ala His Pro Leu Met Ile Ala Ile Pro Glu Ile Glu	
105 110 115	
att ttt tat cag cac acc gat gtg gag ccg gga agc gat gac gcc gtg	499
Ile Phe Tyr Gln His Thr Asp Val Glu Pro Gly Ser Asp Asp Ala Val	
120 125 130	
gcg ccg gac ttt cag gaa aat cag gat atg tgg cgc agg cgt ctg gga	547
Ala Pro Asp Phe Gln Glu Asn Gln Asp Met Trp Arg Arg Arg Leu Gly	
135 140 145	
tct gtc acc gaa cca aac ctt ata tat aaa gag ttt tcc gga ccc ggc	595
Ser Val Thr Glu Pro Asn Leu Ile Tyr Lys Glu Phe Ser Gly Pro Gly	
150 155 160 165	
aaa gcg cag cgt gcc gta gaa atg ctg ggc aat ctg tgg aag atc ggc	643
Lys Ala Gln Arg Ala Val Glu Met Leu Gly Asn Leu Trp Lys Ile Gly	
170 175 180	
gtg gtg gtg agt agg aat acg gaa agt cgc ctt ggg tta act cgt gtg	691
Val Val Val Ser Arg Asn Thr Glu Ser Arg Leu Gly Leu Thr Arg Val	
185 190 195	
gaa tac acc ccc acc cct ggc gaa gta ccc gtg ccg ctg atg tcg gag	739
Glu Tyr Thr Pro Thr Pro Gly Glu Val Pro Val Pro Leu Met Ser Glu	
200 205 210	
aag aac tgt tgg tac agc att cgg gtg tct gaa acc att ggt gag aac	787
Lys Asn Cys Trp Tyr Ser Ile Arg Val Ser Glu Thr Ile Gly Glu Asn	
215 220 225	
cag gtt ccg gaa att gtg cgc tgc tta ggc gag att ttc tgt ggc tat	835
Gln Val Pro Glu Ile Val Arg Cys Leu Gly Glu Ile Phe Cys Gly Tyr	
230 235 240 245	
ctt ccc cag atg tgg ctg aaa gaa cca gta aag gcc ggc aag ttg cga	883
Leu Pro Gln Met Trp Leu Lys Glu Pro Val Lys Ala Gly Lys Leu Arg	
250 255 260	
atc caa gaa tcg gaa gca gca gcg tat atc gcg atg gcg cga cta gat	931
Ile Gln Glu Ser Glu Ala Ala Ala Tyr Ile Ala Met Ala Arg Leu Asp	
265 270 275	
ctt tcc cca cgc acc ggc aac acc act tgg acc aac agc tat att tcc	979
Leu Ser Pro Arg Thr Gly Asn Thr Thr Trp Thr Asn Ser Tyr Ile Ser	
280 285 290	
acg cgt cct ctg tcc ccc gct ttt agg tgg gac gtg gtg ctg gag gct	1027
Thr Arg Pro Leu Ser Pro Ala Phe Arg Trp Asp Val Val Leu Glu Ala	
295 300 305	
tcc cac caa ttg gag aac ctg ctg cgt gga gac aca ggg ccg gtc act	1075
Ser His Gln Leu Glu Asn Leu Leu Arg Gly Asp Thr Gly Pro Val Thr	
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gcc aca caa tcg gca gct ggt taacccaaaag ttcacgtgga gat	1119
Ala Thr Gln Ser Ala Ala Gly	
330	

<210> 122
 <211> 332
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 122

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Ala Leu Pro Asn Leu Thr Thr Lys Gln Gly Ala Ser Leu Ala Ile Gln
      35           40           45

Leu Leu Asp Ala Val Gln Leu Ala Asp Ala Ala Gly Thr Lys Gly Gly
      50           55           60

Ala Ser Thr Ser Asn Ala Ser Ser Leu Pro Asp Thr Phe Asp Ala Leu
      65           70           75           80

Thr Ser Leu Ile Gly Lys Leu Asp Val Arg Ser Asp Ser Glu Trp Arg
      85           90           95

Ser Phe Gly Phe Gln Pro Ser Glu Thr Ala His Pro Leu Met Ile Ala
      100          105          110

Ile Pro Glu Ile Glu Ile Phe Tyr Gln His Thr Asp Val Glu Pro Gly
      115          120          125

Ser Asp Asp Ala Val Ala Pro Asp Phe Gln Glu Asn Gln Asp Met Trp
      130          135          140

Arg Arg Arg Leu Gly Ser Val Thr Glu Pro Asn Leu Ile Tyr Lys Glu
      145          150          155          160

Phe Ser Gly Pro Gly Lys Ala Gln Arg Ala Val Glu Met Leu Gly Asn
      165          170          175

Leu Trp Lys Ile Gly Val Val Val Ser Arg Asn Thr Glu Ser Arg Leu
      180          185          190

Gly Leu Thr Arg Val Glu Tyr Thr Pro Thr Pro Gly Glu Val Pro Val
      195          200          205

Pro Leu Met Ser Glu Lys Asn Cys Trp Tyr Ser Ile Arg Val Ser Glu
      210          215          220

Thr Ile Gly Glu Asn Gln Val Pro Glu Ile Val Arg Cys Leu Gly Glu
      225          230          235          240

Ile Phe Cys Gly Tyr Leu Pro Gln Met Trp Leu Lys Glu Pro Val Lys
      245          250          255

Ala Gly Lys Leu Arg Ile Gln Glu Ser Glu Ala Ala Ala Tyr Ile Ala
      260          265          270

Met Ala Arg Leu Asp Leu Ser Pro Arg Thr Gly Asn Thr Thr Trp Thr
      275          280          285

Asn Ser Tyr Ile Ser Thr Arg Pro Leu Ser Pro Ala Phe Arg Trp Asp

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290 295 300

Val Val Leu Glu Ala Ser His Gln Leu Glu Asn Leu Leu Arg Gly Asp
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Thr Gly Pro Val Thr Ala Thr Gln Ser Ala Ala Gly
 325 330

<210> 123
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1462)
 <223> RXN03110

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ccgaggggta tctagttttt acgttgagaa ggagagctca gtg ctt att gaa cgc 115
 Val Leu Ile Glu Arg
 1 5

atc tac gac gaa gac ctt gcg cag gcc agc tat ttc att ggc tgc caa 163
 Ile Tyr Asp Glu Asp Leu Ala Gln Ala Ser Tyr Phe Ile Gly Cys Gln
 10 15 20

gcc cac aac acc gca gtc gtg gtt gat ccg cgt cgc gat att gcc gtc 211
 Ala His Asn Thr Ala Val Val Val Asp Pro Arg Arg Asp Ile Ala Val
 25 30 35

tat ctg gac atg gcc aag aaa aac gga atg gag att gtt gga gtt acc 259
 Tyr Leu Asp Met Ala Lys Lys Asn Gly Met Glu Ile Val Gly Val Thr
 40 45 50

gaa acc cat atc cat gcg gac tat ttg tca gga acc cgt gag tta gct 307
 Glu Thr His Ile His Ala Asp Tyr Leu Ser Gly Thr Arg Glu Leu Ala
 55 60 65

gct gca act aat gcc acc atg tac gtc tca ggg gag ggc ggc gcc gat 355
 Ala Ala Thr Asn Ala Thr Met Tyr Val Ser Gly Glu Gly Gly Ala Asp
 70 75 80 85

tgg cag tat gaa ttc gac gcc gag cga ata tgc gac ggc agc gag att 403
 Trp Gln Tyr Glu Phe Asp Ala Glu Arg Ile Cys Asp Gly Ser Glu Ile
 90 95 100

cgc ctg gga aat ctg gtg ctc aca gct gtt cac acc cca ggc cat acc 451
 Arg Leu Gly Asn Leu Val Leu Thr Ala Val His Thr Pro Gly His Thr
 105 110 115

ccg gaa cac tta tcg ttc ctg ctg aag gac ggc gcg ttc gca gat gag 499
 Pro Glu His Leu Ser Phe Leu Leu Lys Asp Gly Ala Phe Ala Asp Glu
 120 125 130

cca gga ttc atg ctc act ggc gat ttc gtt ttc gcg ggt gat ctt ggc 547
 Pro Gly Phe Met Leu Thr Gly Asp Phe Val Phe Ala Gly Asp Leu Gly
 135 140 145

cga cca gat ttg ctc gat gaa gca gct ggg gga gtg gac act cgt ttt	595
Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly Val Asp Thr Arg Phe	
150 155 160 165	
gag ggg gct cgc caa atg ttc aag agc ttg aag gaa aaa ttc ctg aca	643
Glu Gly Ala Arg Gln Met Phe Lys Ser Leu Lys Glu Lys Phe Leu Thr	
170 175 180	
ttg cct gat cac atc cag atc ttc cct ggt cat ggt tcc ggt tcc gcg	691
Leu Pro Asp His Ile Gln Ile Phe Pro Gly His Gly Ser Gly Ser Ala	
185 190 195	
tgt ggc aaa gcc ttg ggt tcg gtt cct tca aca aca ctt gga tat gaa	739
Cys Gly Lys Ala Leu Gly Ser Val Pro Ser Thr Thr Leu Gly Tyr Glu	
200 205 210	
cgt caa ttt gcg tgg tgg gga aag tat ctg gag gca gat gat gaa caa	787
Arg Gln Phe Ala Trp Trp Gly Lys Tyr Leu Glu Ala Asp Asp Glu Gln	
215 220 225	
gga ttc att gat gag ctt ctg gaa ggc caa cct gat gca cct gca tac	835
Gly Phe Ile Asp Glu Leu Leu Glu Gly Gln Pro Asp Ala Pro Ala Tyr	
230 235 240 245	
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Phe Gly Arg Met Lys Arg Gln Asn Arg Gln Gly Pro Ala Ile Met Gly	
250 255 260	
gct cgc gag ctg ttg cca cag ctg gaa gct tct gat ctg cac gac gtc	931
Ala Arg Glu Leu Leu Pro Gln Leu Glu Ala Ser Asp Leu His Asp Val	
265 270 275	
att gtt gtt gat acc cgc tca gcc gat gaa gtt cac cag ggc act gta	979
Ile Val Val Asp Thr Arg Ser Ala Asp Glu Val His Gln Gly Thr Val	
280 285 290	
gct ggt gca gtg aat att cct gcg ggc aat tcg atg gcg aaa ttt ggc	1027
Ala Gly Ala Val Asn Ile Pro Ala Gly Asn Ser Met Ala Lys Phe Gly	
295 300 305	
tcg tgg acc gtt gat ccc gag aag gat tcc cga gct ttg gtt ctg ctc	1075
Ser Trp Thr Val Asp Pro Glu Lys Asp Ser Arg Ala Leu Val Leu Leu	
310 315 320 325	
gcg gca agc caa att ggt gcc atg gag atg tgg gac cac atg gtt cgc	1123
Ala Ala Ser Gln Ile Gly Ala Met Glu Met Trp Asp His Met Val Arg	
330 335 340	
gtg gga atc gat aat gtt gct ggt ttt atc acc aac ttt gat ggg gtg	1171
Val Gly Ile Asp Asn Val Ala Gly Phe Ile Thr Asn Phe Asp Gly Val	
345 350 355	
gac cta gtt gca ccg caa act gtg tcc cca gat cag ctg gat gaa ttg	1219
Asp Leu Val Ala Pro Gln Thr Val Ser Pro Asp Gln Leu Asp Glu Leu	
360 365 370	
gaa tac gat cta ctt ctt gat gtc cgc aac cgc agt gaa gtc gaa gaa	1267
Glu Tyr Asp Leu Leu Leu Asp Val Arg Asn Arg Ser Glu Val Glu Glu	
375 380 385	

ggc tac atc cca gga gca ctc cat att aat ggt gca tcc gtg ctg tgg 1315
 Gly Tyr Ile Pro Gly Ala Leu His Ile Asn Gly Ala Ser Val Leu Trp
 390 395 400 405

aat ctg gag aaa ctg cca cgt gac gga aag atc gtg agc tac tgc aag 1363
 Asn Leu Glu Lys Leu Pro Arg Asp Gly Lys Ile Val Ser Tyr Cys Lys
 410 415 420

agt gga aca cgc agc tca atc gcc gca agc acc ctg cgt aat gct ggt 1411
 Ser Gly Thr Arg Ser Ser Ile Ala Ala Ser Thr Leu Arg Asn Ala Gly
 425 430 435

ttt gat gtg gtg gaa ctt caa gga tcc tat gac aac tgg gtc cgg cac 1459
 Phe Asp Val Val Glu Leu Gln Gly Ser Tyr Asp Asn Trp Val Arg His
 440 445 450

aac 1462
 Asn

<210> 124
 <211> 454
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 124
 Val Leu Ile Glu Arg Ile Tyr Asp Glu Asp Leu Ala Gln Ala Ser Tyr
 1 5 10 15

Phe Ile Gly Cys Gln Ala His Asn Thr Ala Val Val Val Asp Pro Arg
 20 25 30

Arg Asp Ile Ala Val Tyr Leu Asp Met Ala Lys Lys Asn Gly Met Glu
 35 40 45

Ile Val Gly Val Thr Glu Thr His Ile His Ala Asp Tyr Leu Ser Gly
 50 55 60

Thr Arg Glu Leu Ala Ala Ala Thr Asn Ala Thr Met Tyr Val Ser Gly
 65 70 75 80

Glu Gly Gly Ala Asp Trp Gln Tyr Glu Phe Asp Ala Glu Arg Ile Cys
 85 90 95

Asp Gly Ser Glu Ile Arg Leu Gly Asn Leu Val Leu Thr Ala Val His
 100 105 110

Thr Pro Gly His Thr Pro Glu His Leu Ser Phe Leu Leu Lys Asp Gly
 115 120 125

Ala Phe Ala Asp Glu Pro Gly Phe Met Leu Thr Gly Asp Phe Val Phe
 130 135 140

Ala Gly Asp Leu Gly Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly
 145 150 155 160

Val Asp Thr Arg Phe Glu Gly Ala Arg Gln Met Phe Lys Ser Leu Lys
 165 170 175

Glu Lys Phe Leu Thr Leu Pro Asp His Ile Gln Ile Phe Pro Gly His

180					185					190					
Gly	Ser	Gly	Ser	Ala	Cys	Gly	Lys	Ala	Leu	Gly	Ser	Val	Pro	Ser	Thr
		195					200					205			
Thr	Leu	Gly	Tyr	Glu	Arg	Gln	Phe	Ala	Trp	Trp	Gly	Lys	Tyr	Leu	Glu
	210					215					220				
Ala	Asp	Asp	Glu	Gln	Gly	Phe	Ile	Asp	Glu	Leu	Leu	Glu	Gly	Gln	Pro
225					230					235					240
Asp	Ala	Pro	Ala	Tyr	Phe	Gly	Arg	Met	Lys	Arg	Gln	Asn	Arg	Gln	Gly
				245					250					255	
Pro	Ala	Ile	Met	Gly	Ala	Arg	Glu	Leu	Leu	Pro	Gln	Leu	Glu	Ala	Ser
			260					265					270		
Asp	Leu	His	Asp	Val	Ile	Val	Val	Asp	Thr	Arg	Ser	Ala	Asp	Glu	Val
		275					280					285			
His	Gln	Gly	Thr	Val	Ala	Gly	Ala	Val	Asn	Ile	Pro	Ala	Gly	Asn	Ser
	290					295					300				
Met	Ala	Lys	Phe	Gly	Ser	Trp	Thr	Val	Asp	Pro	Glu	Lys	Asp	Ser	Arg
305					310					315					320
Ala	Leu	Val	Leu	Leu	Ala	Ala	Ser	Gln	Ile	Gly	Ala	Met	Glu	Met	Trp
				325					330					335	
Asp	His	Met	Val	Arg	Val	Gly	Ile	Asp	Asn	Val	Ala	Gly	Phe	Ile	Thr
			340					345					350		
Asn	Phe	Asp	Gly	Val	Asp	Leu	Val	Ala	Pro	Gln	Thr	Val	Ser	Pro	Asp
		355					360						365		
Gln	Leu	Asp	Glu	Leu	Glu	Tyr	Asp	Leu	Leu	Leu	Asp	Val	Arg	Asn	Arg
	370					375					380				
Ser	Glu	Val	Glu	Glu	Gly	Tyr	Ile	Pro	Gly	Ala	Leu	His	Ile	Asn	Gly
385					390					395					400
Ala	Ser	Val	Leu	Trp	Asn	Leu	Glu	Lys	Leu	Pro	Arg	Asp	Gly	Lys	Ile
				405					410					415	
Val	Ser	Tyr	Cys	Lys	Ser	Gly	Thr	Arg	Ser	Ser	Ile	Ala	Ala	Ser	Thr
			420					425					430		
Leu	Arg	Asn	Ala	Gly	Phe	Asp	Val	Val	Glu	Leu	Gln	Gly	Ser	Tyr	Asp
		435					440					445			
Asn	Trp	Val	Arg	His	Asn										
	450														

<210> 125

<211> 1023

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1023)

<223> FRXA00660

<400> 125

cca ggc cat acc ccg gaa cac tta tgc ttc ctg ctg aag gac ggc gcg	48
Pro Gly His Thr Pro Glu His Leu Ser Phe Leu Leu Lys Asp Gly Ala	
1 5 10 15	
ttc gca cat gag cca gga ttc atg ctc act ggc gat ttc gtt ttc gcg	96
Phe Ala His Glu Pro Gly Phe Met Leu Thr Gly Asp Phe Val Phe Ala	
20 25 30	
ggt gat ctt ggc cga cca gat ttg ctc gat gaa gca gct ggg gga gtg	144
Gly Asp Leu Gly Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly Val	
35 40 45	
gac act cgt ttt gag ggg gct cgc caa atg ttc aag agc ttg aag gaa	192
Asp Thr Arg Phe Glu Gly Ala Arg Gln Met Phe Lys Ser Leu Lys Glu	
50 55 60	
aaa ttc ctg aca ttg cct gat cac atc cag atc ttc cct ggt cat ggt	240
Lys Phe Leu Thr Leu Pro Asp His Ile Gln Ile Phe Pro Gly His Gly	
65 70 75 80	
tcc ggt tcc gcg tgt ggc aaa gcc ttg ggt tgc gtt cct tca aca aca	288
Ser Gly Ser Ala Cys Gly Lys Ala Leu Gly Ser Val Pro Ser Thr Thr	
85 90 95	
ctt gga tat gaa cgt caa ttt gcg tgg tgg gga aag tat ctg gag gca	336
Leu Gly Tyr Glu Arg Gln Phe Ala Trp Trp Gly Lys Tyr Leu Glu Ala	
100 105 110	
gat gat gaa caa gga ttc att gat gag ctt ctg gaa ggc caa cct gat	384
Asp Asp Glu Gln Gly Phe Ile Asp Glu Leu Leu Glu Gly Gln Pro Asp	
115 120 125	
gca cct gca tac ttc ggc agg atg aag agg caa aat agg caa ggg ccc	432
Ala Pro Ala Tyr Phe Gly Arg Met Lys Arg Gln Asn Arg Gln Gly Pro	
130 135 140	
gca att atg ggc gct cgc gag ctg ttg cca cag ctg gaa gct tct gat	480
Ala Ile Met Gly Ala Arg Glu Leu Leu Pro Gln Leu Glu Ala Ser Asp	
145 150 155 160	
ctg cac gac gtc att gtt gtt gat acc cgc tca gcc gat gaa gtt cac	528
Leu His Asp Val Ile Val Val Asp Thr Arg Ser Ala Asp Glu Val His	
165 170 175	
cag ggc act gta gct ggt gca gtg aat att cct gcg ggc aat tgc atg	576
Gln Gly Thr Val Ala Gly Ala Val Asn Ile Pro Ala Gly Asn Ser Met	
180 185 190	
gcg aaa ttt ggc tgc tgg acc gtt gat ccc gag aag gat tcc cga gct	624
Ala Lys Phe Gly Ser Trp Thr Val Asp Pro Glu Lys Asp Ser Arg Ala	
195 200 205	
ttg gtt ctg ctc gcg gca agc caa att ggt gcc atg gag atg tgg gac	672
Leu Val Leu Leu Ala Ala Ser Gln Ile Gly Ala Met Glu Met Trp Asp	
210 215 220	
cac atg gtt cgc gtg gga atc gat aat gtt gct ggt ttt atc acc aac	720

His Met Val Arg Val Gly Ile Asp Asn Val Ala Gly Phe Ile Thr Asn
 225 230 235 240
 ttt gat ggg gtg gac cta gtt gca ccg caa act gtg tcc cca gat cag 768
 Phe Asp Gly Val Asp Leu Val Ala Pro Gln Thr Val Ser Pro Asp Gln
 245 250 255
 ctg gat gaa ttg gaa tac gat cta ctt ctt gat gtc cgc aac cgc agt 816
 Leu Asp Glu Leu Glu Tyr Asp Leu Leu Leu Asp Val Arg Asn Arg Ser
 260 265 270
 gaa gtc gaa gaa ggc tac atc cca gga gca ctc cat att aat ggt gca 864
 Glu Val Glu Glu Gly Tyr Ile Pro Gly Ala Leu His Ile Asn Gly Ala
 275 280 285
 tcc gtg ctg tgg aat ctg gag aaa ctg cca cgt gac gga aag atc gtg 912
 Ser Val Leu Trp Asn Leu Glu Lys Leu Pro Arg Asp Gly Lys Ile Val
 290 295 300
 agc tac tgc aag agt gga aca cgc agc tca atc gcc gca agc acc ctg 960
 Ser Tyr Cys Lys Ser Gly Thr Arg Ser Ser Ile Ala Ala Ser Thr Leu
 305 310 315 320
 cgt aat gct ggt ttt gat gtg gtg gaa ctt caa gga tcc tat gac aac 1008
 Arg Asn Ala Gly Phe Asp Val Val Glu Leu Gln Gly Ser Tyr Asp Asn
 325 330 335
 tgg gtc cgg cac aac 1023
 Trp Val Arg His Asn
 340

<210> 126

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

Pro Gly His Thr Pro Glu His Leu Ser Phe Leu Leu Lys Asp Gly Ala
 1 5 10 15
 Phe Ala His Glu Pro Gly Phe Met Leu Thr Gly Asp Phe Val Phe Ala
 20 25 30
 Gly Asp Leu Gly Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly Val
 35 40 45
 Asp Thr Arg Phe Glu Gly Ala Arg Gln Met Phe Lys Ser Leu Lys Glu
 50 55 60
 Lys Phe Leu Thr Leu Pro Asp His Ile Gln Ile Phe Pro Gly His Gly
 65 70 75 80
 Ser Gly Ser Ala Cys Gly Lys Ala Leu Gly Ser Val Pro Ser Thr Thr
 85 90 95
 Leu Gly Tyr Glu Arg Gln Phe Ala Trp Trp Gly Lys Tyr Leu Glu Ala
 100 105 110
 Asp Asp Glu Gln Gly Phe Ile Asp Glu Leu Leu Glu Gly Gln Pro Asp
 115 120 125

Ala Pro Ala Tyr Phe Gly Arg Met Lys Arg Gln Asn Arg Gln Gly Pro
 130 135 140
 Ala Ile Met Gly Ala Arg Glu Leu Leu Pro Gln Leu Glu Ala Ser Asp
 145 150 155 160
 Leu His Asp Val Ile Val Val Asp Thr Arg Ser Ala Asp Glu Val His
 165 170 175
 Gln Gly Thr Val Ala Gly Ala Val Asn Ile Pro Ala Gly Asn Ser Met
 180 185 190
 Ala Lys Phe Gly Ser Trp Thr Val Asp Pro Glu Lys Asp Ser Arg Ala
 195 200 205
 Leu Val Leu Leu Ala Ala Ser Gln Ile Gly Ala Met Glu Met Trp Asp
 210 215 220
 His Met Val Arg Val Gly Ile Asp Asn Val Ala Gly Phe Ile Thr Asn
 225 230 235 240
 Phe Asp Gly Val Asp Leu Val Ala Pro Gln Thr Val Ser Pro Asp Gln
 245 250 255
 Leu Asp Glu Leu Glu Tyr Asp Leu Leu Leu Asp Val Arg Asn Arg Ser
 260 265 270
 Glu Val Glu Glu Gly Tyr Ile Pro Gly Ala Leu His Ile Asn Gly Ala
 275 280 285
 Ser Val Leu Trp Asn Leu Glu Lys Leu Pro Arg Asp Gly Lys Ile Val
 290 295 300
 Ser Tyr Cys Lys Ser Gly Thr Arg Ser Ser Ile Ala Ala Ser Thr Leu
 305 310 315 320
 Arg Asn Ala Gly Phe Asp Val Val Glu Leu Gln Gly Ser Tyr Asp Asn
 325 330 335
 Trp Val Arg His Asn
 340

<210> 127
 <211> 756
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(733)
 <223> RXA00801

<400> 127
 ggataagttt gtttctgagc gtattggtct tgatgatgtt gaagaggctt tcaacaccat 60
 gaaggctggc gacgtgctgc gttctgtggt ggagatctaa atg gct cac gac gga 115
 Met Ala His Asp Gly
 1 5

ttg cgc gta gaa aac att gtc acc tca ggc atc ttt gcc ctt gat ggt	163
Leu Arg Val Glu Asn Ile Val Thr Ser Gly Ile Phe Ala Leu Asp Gly	
10 15 20	
ggc gaa tgg gaa gtc gac aac aac atc tgg gtt gtg gga aat gat gat	211
Gly Glu Trp Glu Val Asp Asn Asn Ile Trp Val Val Gly Asn Asp Asp	
25 30 35	
gag gtt ttc atc atc gat gcg gca cac act gca gca ccc atc atc gag	259
Glu Val Phe Ile Ile Asp Ala Ala His Thr Ala Ala Pro Ile Ile Glu	
40 45 50	
gct gtc ggt gga cgt gct gtg aag ggc att ttg tgc acc cac gca cac	307
Ala Val Gly Gly Arg Ala Val Lys Gly Ile Leu Cys Thr His Ala His	
55 60 65	
aat gac cac atc act gtc gca cca gag cta tcc aag gaa ttt gat gca	355
Asn Asp His Ile Thr Val Ala Pro Glu Leu Ser Lys Glu Phe Asp Ala	
70 75 80 85	
cca atc ttc gtg cac cca ggt gac caa atg ctg tgg gag gaa acc cac	403
Pro Ile Phe Val His Pro Gly Asp Gln Met Leu Trp Glu Glu Thr His	
90 95 100	
gga aac ctg acc cac gag gat ttg gca gat cag cag aag ttc caa atc	451
Gly Asn Leu Thr His Glu Asp Leu Ala Asp Gln Gln Lys Phe Gln Ile	
105 110 115	
gct gga act gaa ctg atc gtg ctt aat acc cct gga cac tca cct gga	499
Ala Gly Thr Glu Leu Ile Val Leu Asn Thr Pro Gly His Ser Pro Gly	
120 125 130	
tcc agc tgc ttc tac ctc cct gaa gca aac gag ctc ttc tct gga gac	547
Ser Ser Cys Phe Tyr Leu Pro Glu Ala Asn Glu Leu Phe Ser Gly Asp	
135 140 145	
act ttg ttc cag ggt ggg ccg gga gca act ggc cgt aag tac agc tcc	595
Thr Leu Phe Gln Gly Gly Pro Gly Ala Thr Gly Arg Lys Tyr Ser Ser	
150 155 160 165	
ttt gac acc atc att gag tcc ctc aag acc tca att ttg gat cta cca	643
Phe Asp Thr Ile Ile Glu Ser Leu Lys Thr Ser Ile Leu Asp Leu Pro	
170 175 180	
gcg gaa acc acc gtg cgc act ggc cat ggt gat cac acc agt gtg ggg	691
Ala Glu Thr Thr Val Arg Thr Gly His Gly Asp His Thr Ser Val Gly	
185 190 195	
gct gag gct cca cac ttg gag gaa tgg att aaa cgc ggg cac	733
Ala Glu Ala Pro His Leu Glu Glu Trp Ile Lys Arg Gly His	
200 205 210	
taagccccga acgattagta ggc	756

<210> 128

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Met Ala His Asp Gly Leu Arg Val Glu Asn Ile Val Thr Ser Gly Ile
 1 5 10 15
 Phe Ala Leu Asp Gly Gly Glu Trp Glu Val Asp Asn Asn Ile Trp Val
 20 25 30
 Val Gly Asn Asp Asp Glu Val Phe Ile Ile Asp Ala Ala His Thr Ala
 35 40 45
 Ala Pro Ile Ile Glu Ala Val Gly Gly Arg Ala Val Lys Gly Ile Leu
 50 55 60
 Cys Thr His Ala His Asn Asp His Ile Thr Val Ala Pro Glu Leu Ser
 65 70 75 80
 Lys Glu Phe Asp Ala Pro Ile Phe Val His Pro Gly Asp Gln Met Leu
 85 90 95
 Trp Glu Glu Thr His Gly Asn Leu Thr His Glu Asp Leu Ala Asp Gln
 100 105 110
 Gln Lys Phe Gln Ile Ala Gly Thr Glu Leu Ile Val Leu Asn Thr Pro
 115 120 125
 Gly His Ser Pro Gly Ser Ser Cys Phe Tyr Leu Pro Glu Ala Asn Glu
 130 135 140
 Leu Phe Ser Gly Asp Thr Leu Phe Gln Gly Gly Pro Gly Ala Thr Gly
 145 150 155 160
 Arg Lys Tyr Ser Ser Phe Asp Thr Ile Ile Glu Ser Leu Lys Thr Ser
 165 170 175
 Ile Leu Asp Leu Pro Ala Glu Thr Thr Val Arg Thr Gly His Gly Asp
 180 185 190
 His Thr Ser Val Gly Ala Glu Ala Pro His Leu Glu Glu Trp Ile Lys
 195 200 205
 Arg Gly His
 210

<210> 129
 <211> 966
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(943)
 <223> RXA00821

<400> 129
 ttaaaagctt gcttctcgac gcaaaaaccc atccggcgca tcccttcaat gttaggggtg 60
 cgctgctatt tttctcccca gttctacgaa atgacttatt gtg act aag ctt gag 115
 Val Thr Lys Leu Glu
 1 5
 cgc atg gag cat cct gct tac agc caa ttg cgg ccg gtt acc ccg tcc 163

Arg Met Glu His Pro Ala Tyr Ser Gln Leu Arg Pro Val Thr Pro Ser	
10 15 20	
gca tct gtt gtt ttg tgc cct aat ccc ggt tac agc tcg ctg gaa ggc	211
Ala Ser Val Val Leu Cys Pro Asn Pro Gly Tyr Ser Ser Leu Glu Gly	
25 30 35	
act aat tct tgg gtt atc cgg gca cca gaa gac ccc cgg agc att gtc	259
Thr Asn Ser Trp Val Ile Arg Ala Pro Glu Asp Pro Arg Ser Ile Val	
40 45 50	
atc gat cca ggt cct gaa gat gag ggc cac ctt aac gtc ttg cat tcc	307
Ile Asp Pro Gly Pro Glu Asp Glu Gly His Leu Asn Val Leu His Ser	
55 60 65	
aag gct gag gag gtg ggt ttg att ctt ctg acc cac cgt cac tat gat	355
Lys Ala Glu Glu Val Gly Leu Ile Leu Leu Thr His Arg His Tyr Asp	
70 75 80 85	
cat gct gac ggc gca cag cgt ttc cgt cag ctg acc aat gca cct gtg	403
His Ala Asp Gly Ala Gln Arg Phe Arg Gln Leu Thr Asn Ala Pro Val	
90 95 100	
cgt gcg atg gac cct tcg tac tgt gct ggt gcg gag gag att cat gat	451
Arg Ala Met Asp Pro Ser Tyr Cys Ala Gly Ala Glu Glu Ile His Asp	
105 110 115	
ggt gag atc atc acg atc gac ggt gtc acc cca cag att gag gtg gtg	499
Gly Glu Ile Ile Thr Ile Asp Gly Val Thr Pro Gln Ile Glu Val Val	
120 125 130	
gcc aca cct ggt cat acc cgt gat tct gtg tct tat ttc atc tgg agt	547
Ala Thr Pro Gly His Thr Arg Asp Ser Val Ser Tyr Phe Ile Trp Ser	
135 140 145	
gga gtc cct cat gag tcc act ttg gag ggc atc gtt tct ggc gac acc	595
Gly Val Pro His Glu Ser Thr Leu Glu Gly Ile Val Ser Gly Asp Thr	
150 155 160 165	
att gcg ggt cgt cac acc acg atg att tca gag acc gac ggc gat ttg	643
Ile Ala Gly Arg His Thr Thr Met Ile Ser Glu Thr Asp Gly Asp Leu	
170 175 180	
ggt gag tac ctg aat tct ttg gcc att ttg gag gag cgc ggc aag gat	691
Gly Glu Tyr Leu Asn Ser Leu Ala Ile Leu Glu Glu Arg Gly Lys Asp	
185 190 195	
att ccg ctg ctt cca gga cat ggt cca gat gga cag gac gtg tcc tcc	739
Ile Pro Leu Leu Pro Gly His Gly Pro Asp Gly Gln Asp Val Ser Ser	
200 205 210	
ttc gcg cgt aag tac att gag cgt cgt gag ctg cgt ctg aac cag atc	787
Phe Ala Arg Lys Tyr Ile Glu Arg Arg Glu Leu Arg Leu Asn Gln Ile	
215 220 225	
cgt gag gta tgg gag acc cgt ggc cgt gac gtg tcc atg aag gat ctc	835
Arg Glu Val Trp Glu Thr Arg Gly Arg Asp Val Ser Met Lys Asp Leu	
230 235 240 245	
atc gac gcc atc tac gat gat gtt gat cca gtt ctg cgt ggt gca gcc	883
Ile Asp Ala Ile Tyr Asp Asp Val Asp Pro Val Leu Arg Gly Ala Ala	

250 255 260
 gag cag tcc act cat gtg gct att cgt tac ctg cag gct cag gaa gct 931
 Glu Gln Ser Thr His Val Ala Ile Arg Tyr Leu Gln Ala Gln Glu Ala
 265 270 275

tcc gcc tca aac taaacacttt taactaaaca aca 966
 Ser Ala Ser Asn
 280

<210> 130
 <211> 281
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 130
 Val Thr Lys Leu Glu Arg Met Glu His Pro Ala Tyr Ser Gln Leu Arg
 1 5 10 15

Pro Val Thr Pro Ser Ala Ser Val Val Leu Cys Pro Asn Pro Gly Tyr
 20 25 30

Ser Ser Leu Glu Gly Thr Asn Ser Trp Val Ile Arg Ala Pro Glu Asp
 35 40 45

Pro Arg Ser Ile Val Ile Asp Pro Gly Pro Glu Asp Glu Gly His Leu
 50 55 60

Asn Val Leu His Ser Lys Ala Glu Glu Val Gly Leu Ile Leu Leu Thr
 65 70 75 80

His Arg His Tyr Asp His Ala Asp Gly Ala Gln Arg Phe Arg Gln Leu
 85 90 95

Thr Asn Ala Pro Val Arg Ala Met Asp Pro Ser Tyr Cys Ala Gly Ala
 100 105 110

Glu Glu Ile His Asp Gly Glu Ile Ile Thr Ile Asp Gly Val Thr Pro
 115 120 125

Gln Ile Glu Val Val Ala Thr Pro Gly His Thr Arg Asp Ser Val Ser
 130 135 140

Tyr Phe Ile Trp Ser Gly Val Pro His Glu Ser Thr Leu Glu Gly Ile
 145 150 155 160

Val Ser Gly Asp Thr Ile Ala Gly Arg His Thr Thr Met Ile Ser Glu
 165 170 175

Thr Asp Gly Asp Leu Gly Glu Tyr Leu Asn Ser Leu Ala Ile Leu Glu
 180 185 190

Glu Arg Gly Lys Asp Ile Pro Leu Leu Pro Gly His Gly Pro Asp Gly
 195 200 205

Gln Asp Val Ser Ser Phe Ala Arg Lys Tyr Ile Glu Arg Arg Glu Leu
 210 215 220

Arg Leu Asn Gln Ile Arg Glu Val Trp Glu Thr Arg Gly Arg Asp Val
 225 230 235 240

Ser Met Lys Asp Leu Ile Asp Ala Ile Tyr Asp Asp Val Asp Pro Val
 245 250 255

Leu Arg Gly Ala Ala Glu Gln Ser Thr His Val Ala Ile Arg Tyr Leu
 260 265 270

Gln Ala Gln Glu Ala Ser Ala Ser Asn
 275 280

<210> 131
 <211> 1530
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1507)
 <223> RXN02966

<400> 131
 aaatataccc cccaggggtat cttgacagat taaagctcga tgttttaggc tctacatata 60

ccccacggg tatccctca actttgatct aaggtgtcac atg ctt ttt gaa cgc 115
 Met Leu Phe Glu Arg
 1 5

atc tac gaa gaa ggc ctc gcc caa gcc agc tat ttc att ggc tgc caa 163
 Ile Tyr Glu Glu Gly Leu Ala Gln Ala Ser Tyr Phe Ile Gly Cys Gln
 10 15 20

cgc gaa ggc aaa gcg att gtt gtt gat gct cgc cga gat atc cag acc 211
 Arg Glu Gly Lys Ala Ile Val Val Asp Ala Arg Arg Asp Ile Gln Thr
 25 30 35

tat ctg gac ctt gca gca aaa aac aac atg gtc att agc gcc gta acc 259
 Tyr Leu Asp Leu Ala Ala Lys Asn Asn Met Val Ile Ser Ala Val Thr
 40 45 50

gaa acc cat att cat gcc gat tat ctc tcc ggt act cgc gaa ctt gca 307
 Glu Thr His Ile His Ala Asp Tyr Leu Ser Gly Thr Arg Glu Leu Ala
 55 60 65

gct gcc acc ggc gcc gag att ttc ctc tct ggc gaa ggc gga gct gat 355
 Ala Ala Thr Gly Ala Glu Ile Phe Leu Ser Gly Glu Gly Gly Ala Asp
 70 75 80 85

tgg caa tat ggc ttt aca ggc acc acc ttg atg cac aat tcc acc atc 403
 Trp Gln Tyr Gly Phe Thr Gly Thr Thr Leu Met His Asn Ser Thr Ile
 90 95 100

aag ctg gga aat atc acc atc aca gcc aag cac act ccc gga cac act 451
 Lys Leu Gly Asn Ile Thr Ile Thr Ala Lys His Thr Pro Gly His Thr
 105 110 115

cca gag cac ctg tca ttt ttg att act gat ggt gcg gtc tca aag gat 499
 Pro Glu His Leu Ser Phe Leu Ile Thr Asp Gly Ala Val Ser Lys Asp
 120 125 130

ccc ggt ttt atg ctc agc ggt gac ttc gtc ttc gta ggt gac gtg gga 547

Pro Gly Phe Met Leu Ser Gly Asp Phe Val Phe Val Gly Asp Val Gly	
135 140 145	
cgt cca gat tta ctt gat gag gca gct ggc ggc gtg gac acc cgc ttc	595
Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly Val Asp Thr Arg Phe	
150 155 160 165	
gcc gga gca cag caa ctc ttc cat agc cta aaa gag cag ttc ctt gca	643
Ala Gly Ala Gln Gln Leu Phe His Ser Leu Lys Glu Gln Phe Leu Ala	
170 175 180	
ctc ccc gac cac att cag gtt tat cca ggt cat ggt gct ggc agc cct	691
Leu Pro Asp His Ile Gln Val Tyr Pro Gly His Gly Ala Gly Ser Pro	
185 190 195	
tgt ggc aag gca ttg ggc gcg atc cct agc acc acc gtg gga tat gaa	739
Cys Gly Lys Ala Leu Gly Ala Ile Pro Ser Thr Thr Val Gly Tyr Glu	
200 205 210	
aag gct aat gcg tgg tgg gct cca tat ctg cgc agt gat gat gaa gcc	787
Lys Ala Asn Ala Trp Trp Ala Pro Tyr Leu Arg Ser Asp Asp Glu Ala	
215 220 225	
ggc ttt gtg gaa gag ctt ctc gac ggc cag cca gat gcc cac gct tac	835
Gly Phe Val Glu Glu Leu Leu Asp Gly Gln Pro Asp Ala His Ala Tyr	
230 235 240 245	
ttt gct cgc atg aaa aag cag aac aag cag gga cct gca gta ctt agt	883
Phe Ala Arg Met Lys Lys Gln Asn Lys Gln Gly Pro Ala Val Leu Ser	
250 255 260	
aca tta tcc ccg ctt gtg aag cta gaa gcc gag gaa gtc gtc gaa aag	931
Thr Leu Ser Pro Leu Val Lys Leu Glu Ala Glu Glu Val Val Glu Lys	
265 270 275	
ctt ggt tct gaa gca gta ttt gtg gat acc cgc gag caa aac caa gtc	979
Leu Gly Ser Glu Ala Val Phe Val Asp Thr Arg Glu Gln Asn Gln Val	
280 285 290	
cat ctc gga acc gtt gtt ggg gca ttg aat att ccg cgc ggc gcc aag	1027
His Leu Gly Thr Val Val Gly Ala Leu Asn Ile Pro Arg Gly Ala Lys	
295 300 305	
gcg tcc aat ttt gcg gcg tgg gtt att gat cct caa aag gat gct cag	1075
Ala Ser Asn Phe Ala Ala Trp Val Ile Asp Pro Gln Lys Asp Ala Gln	
310 315 320 325	
gac ctt att gtt ttg gct ccg gac gcc aat acc gct gcg gat ttc cgc	1123
Asp Leu Ile Val Leu Ala Pro Asp Ala Asn Thr Ala Ala Asp Phe Arg	
330 335 340	
gac gct ttg ctg ccg gtt ggc atc gac act gtg cgt tat ttc acc aac	1171
Asp Ala Leu Leu Arg Val Gly Ile Asp Thr Val Arg Tyr Phe Thr Asn	
345 350 355	
agt atc gat gga ttg cct acc ttt gtg cca gaa ctc atc tcc ccc gct	1219
Ser Ile Asp Gly Leu Pro Thr Phe Val Pro Glu Leu Ile Ser Pro Ala	
360 365 370	
gag cta gct gag acc aac tat gac gca ctg att gat atc cgt gca aag	1267
Glu Leu Ala Glu Thr Asn Tyr Asp Ala Leu Ile Asp Ile Arg Ala Lys	

375	380	385	
tcc gaa ttt gcc gct ggc agc att ccc ggc gcg cag cag ctt tct gga			1315
Ser Glu Phe Ala Ala Gly Ser Ile Pro Gly Ala Gln Gln Leu Ser Gly			
390	395	400	405
ggg tcg gcc atg tgg cgc ctc aat gag ctg cct gcg ggt ggc act ttg			1363
Gly Ser Ala Met Trp Arg Leu Asn Glu Leu Pro Ala Gly Gly Thr Leu			
	410	415	420
gta acc ttc tgc caa tca gga gcg cga aat acc gtg gta gcc aat gct			1411
Val Thr Phe Cys Gln Ser Gly Ala Arg Asn Thr Val Val Ala Asn Ala			
	425	430	435
ttg cga cgc gcc gga ttc acc gtt atc gag ctc gag ggc agc tac gcc			1459
Leu Arg Arg Ala Gly Phe Thr Val Ile Glu Leu Glu Gly Ser Tyr Ala			
	440	445	450
gcg tgg gaa aaa tca gct gcc aat cct aaa aac ttg cag act gcc gtc			1507
Ala Trp Glu Lys Ser Ala Ala Asn Pro Lys Asn Leu Gln Thr Ala Val			
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tagttttaga tccggcgctg tat			1530

<210> 132

<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

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			20					25					30		

Arg	Asp	Ile	Gln	Thr	Tyr	Leu	Asp	Leu	Ala	Ala	Lys	Asn	Asn	Met	Val
		35					40					45			

Ile	Ser	Ala	Val	Thr	Glu	Thr	His	Ile	His	Ala	Asp	Tyr	Leu	Ser	Gly
	50					55					60				

Thr	Arg	Glu	Leu	Ala	Ala	Ala	Thr	Gly	Ala	Glu	Ile	Phe	Leu	Ser	Gly
65					70					75				80	

Glu	Gly	Gly	Ala	Asp	Trp	Gln	Tyr	Gly	Phe	Thr	Gly	Thr	Thr	Leu	Met
				85					90					95	

His	Asn	Ser	Thr	Ile	Lys	Leu	Gly	Asn	Ile	Thr	Ile	Thr	Ala	Lys	His
			100					105					110		

Thr	Pro	Gly	His	Thr	Pro	Glu	His	Leu	Ser	Phe	Leu	Ile	Thr	Asp	Gly
		115				120						125			

Ala	Val	Ser	Lys	Asp	Pro	Gly	Phe	Met	Leu	Ser	Gly	Asp	Phe	Val	Phe
	130					135					140				

Val	Gly	Asp	Val	Gly	Arg	Pro	Asp	Leu	Leu	Asp	Glu	Ala	Ala	Gly	Gly
145					150					155				160	

Val Asp Thr Arg Phe Ala Gly Ala Gln Gln Leu Phe His Ser Leu Lys
 165 170 175
 Glu Gln Phe Leu Ala Leu Pro Asp His Ile Gln Val Tyr Pro Gly His
 180 185 190
 Gly Ala Gly Ser Pro Cys Gly Lys Ala Leu Gly Ala Ile Pro Ser Thr
 195 200 205
 Thr Val Gly Tyr Glu Lys Ala Asn Ala Trp Trp Ala Pro Tyr Leu Arg
 210 215 220
 Ser Asp Asp Glu Ala Gly Phe Val Glu Glu Leu Leu Asp Gly Gln Pro
 225 230 235 240
 Asp Ala His Ala Tyr Phe Ala Arg Met Lys Lys Gln Asn Lys Gln Gly
 245 250 255
 Pro Ala Val Leu Ser Thr Leu Ser Pro Leu Val Lys Leu Glu Ala Glu
 260 265 270
 Glu Val Val Glu Lys Leu Gly Ser Glu Ala Val Phe Val Asp Thr Arg
 275 280 285
 Glu Gln Asn Gln Val His Leu Gly Thr Val Val Gly Ala Leu Asn Ile
 290 295 300
 Pro Arg Gly Ala Lys Ala Ser Asn Phe Ala Ala Trp Val Ile Asp Pro
 305 310 315 320
 Gln Lys Asp Ala Gln Asp Leu Ile Val Leu Ala Pro Asp Ala Asn Thr
 325 330 335
 Ala Ala Asp Phe Arg Asp Ala Leu Leu Arg Val Gly Ile Asp Thr Val
 340 345 350
 Arg Tyr Phe Thr Asn Ser Ile Asp Gly Leu Pro Thr Phe Val Pro Glu
 355 360 365
 Leu Ile Ser Pro Ala Glu Leu Ala Glu Thr Asn Tyr Asp Ala Leu Ile
 370 375 380
 Asp Ile Arg Ala Lys Ser Glu Phe Ala Ala Gly Ser Ile Pro Gly Ala
 385 390 395 400
 Gln Gln Leu Ser Gly Gly Ser Ala Met Trp Arg Leu Asn Glu Leu Pro
 405 410 415
 Ala Gly Gly Thr Leu Val Thr Phe Cys Gln Ser Gly Ala Arg Asn Thr
 420 425 430
 Val Val Ala Asn Ala Leu Arg Arg Ala Gly Phe Thr Val Ile Glu Leu
 435 440 445
 Glu Gly Ser Tyr Ala Ala Trp Glu Lys Ser Ala Ala Asn Pro Lys Asn
 450 455 460
 Leu Gln Thr Ala Val
 465

gcc gga gca cag caa ctc ttc cat agc cta aaa gag cag ttc ctt gca 643
Ala Gly Ala Gln Gln Leu Phe His Ser Leu Lys Glu Gln Phe Leu Ala
170 175 180

ctc ccc gac cac att cag gtt tat cca ggt cat ggt gct ggc agc cct	691
Leu Pro Asp His Ile Gln Val Tyr Pro Gly His Gly Ala Gly Ser Pro	
185 190 195	
tgt ggc aag gca ttg ggc gcg atc cct agc acc acc gtg gga tat gaa	739
Cys Gly Lys Ala Leu Gly Ala Ile Pro Ser Thr Thr Val Gly Tyr Glu	
200 205 210	
aag gct aat gcg tgg tgg gct cca tat ctg cgc agt gat gat gaa gcc	787
Lys Ala Asn Ala Trp Trp Ala Pro Tyr Leu Arg Ser Asp Asp Glu Ala	
215 220 225	
ggc ttt gtg gaa gag ctt ctc gac ggc cag cca gat gcc cac gct tac	835
Gly Phe Val Glu Glu Leu Leu Asp Gly Gln Pro Asp Ala His Ala Tyr	
230 235 240 245	
ttt gct cgc atg aaa aag cag aac aag cag gga cct gca gta ctt agt	883
Phe Ala Arg Met Lys Lys Gln Asn Lys Gln Gly Pro Ala Val Leu Ser	
250 255 260	
aca tta tcc ccg ctt gtg aag cta gaa gcc gag gaa gtc gtc gaa aag	931
Thr Leu Ser Pro Leu Val Lys Leu Glu Ala Glu Glu Val Val Glu Lys	
265 270 275	
ctt ggt tct gaa gca gta ttt gtg gat acc cgc gag caa aac caa gtc	979
Leu Gly Ser Glu Ala Val Phe Val Asp Thr Arg Glu Gln Asn Gln Val	
280 285 290	
cat ctc gga acc gtt gtt ggg gca ttg aat att ccg cgc ggc gcc aag	1027
His Leu Gly Thr Val Val Gly Ala Leu Asn Ile Pro Arg Gly Ala Lys	
295 300 305	
gcg tcc aat ttt gcg gcg tgg gtt att gat cct caa aag gat gct cag	1075
Ala Ser Asn Phe Ala Ala Trp Val Ile Asp Pro Gln Lys Asp Ala Gln	
310 315 320 325	
gac ctt att gtt ttg gct ccg gac gcc aat acc gct gcg gat ttc cgc	1123
Asp Leu Ile Val Leu Ala Pro Asp Ala Asn Thr Ala Ala Asp Phe Arg	
330 335 340	
gac gct ttg ctg cgg gtt ggc atc gac act gtg cgt tat ttc acc aac	1171
Asp Ala Leu Leu Arg Val Gly Ile Asp Thr Val Arg Tyr Phe Thr Asn	
345 350 355	
agt atc gat gga ttg cct acc ttt gtg cca gaa ctc atc tcc ccc gct	1219
Ser Ile Asp Gly Leu Pro Thr Phe Val Pro Glu Leu Ile Ser Pro Ala	
360 365 370	
gag cta gct gag acc aac tat gac gca ctg att gat atc cgt gca aag	1267
Glu Leu Ala Glu Thr Asn Tyr Asp Ala Leu Ile Asp Ile Arg Ala Lys	
375 380 385	
tcc gaa ttt gcc gct ggc agc att ccc ggc gcg cag cag ctt tct gga	1315
Ser Glu Phe Ala Ala Gly Ser Ile Pro Gly Ala Gln Gln Leu Ser Gly	
390 395 400 405	
ggg tgc gcc atg tgg cgc ctc aat gag ctg cct gcg ggt ggc act ttg	1363
Gly Ser Ala Met Trp Arg Leu Asn Glu Leu Pro Ala Gly Gly Thr Leu	
410 415 420	
gta acc ttc tgc caa tca gga gcg cga aat acc gtg gta gcc aat gct	1411

Val Thr Phe Cys Gln Ser Gly Ala Arg Asn Thr Val Val Ala Asn Ala
 425 430 435

ttg cga cgc gcc gga ttc acc gtt atc gag ctc gag ggc agc tac gcc 1459
 Leu Arg Arg Ala Gly Phe Thr Val Ile Glu Leu Glu Gly Ser Tyr Ala
 440 445 450

gcg tgg gaa aaa tca gct gcc aat cct aaa aac ttg cag act gcc gtc 1507
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 455 460 465

tagttttaga tccggcgctg tat 1530

<210> 134
 <211> 469
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 134
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Arg Asp Ile Gln Thr Tyr Leu Asp Leu Ala Ala Lys Asn Asn Met Val
 35 40 45

Ile Ser Ala Val Thr Glu Thr His Ile His Ala Asp Tyr Leu Ser Gly
 50 55 60

Thr Arg Glu Leu Ala Ala Ala Thr Gly Ala Glu Ile Phe Leu Ser Gly
 65 70 75 80

Glu Gly Gly Ala Asp Trp Gln Tyr Gly Phe Thr Gly Thr Thr Leu Met
 85 90 95

His Asn Ser Thr Ile Lys Leu Glu Asn Ile Thr Ile Thr Ala Lys His
 100 105 110

Thr Pro Gly His Thr Pro Glu His Leu Ser Phe Leu Ile Thr Asp Gly
 115 120 125

Ala Val Ser Lys Asp Pro Gly Phe Met Leu Ser Gly Asp Phe Val Phe
 130 135 140

Val Gly Asp Val Gly Arg Pro Asp Leu Leu Asp Glu Ala Ala Gly Gly
 145 150 155 160

Val Asp Thr Arg Phe Ala Gly Ala Gln Gln Leu Phe His Ser Leu Lys
 165 170 175

Glu Gln Phe Leu Ala Leu Pro Asp His Ile Gln Val Tyr Pro Gly His
 180 185 190

Gly Ala Gly Ser Pro Cys Gly Lys Ala Leu Gly Ala Ile Pro Ser Thr
 195 200 205

Thr Val Gly Tyr Glu Lys Ala Asn Ala Trp Trp Ala Pro Tyr Leu Arg
 210 215 220

Ser Asp Asp Glu Ala Gly Phe Val Glu Glu Leu Leu Asp Gly Gln Pro
 225 230 235 240
 Asp Ala His Ala Tyr Phe Ala Arg Met Lys Lys Gln Asn Lys Gln Gly
 245 250 255
 Pro Ala Val Leu Ser Thr Leu Ser Pro Leu Val Lys Leu Glu Ala Glu
 260 265 270
 Glu Val Val Glu Lys Leu Gly Ser Glu Ala Val Phe Val Asp Thr Arg
 275 280 285
 Glu Gln Asn Gln Val His Leu Gly Thr Val Val Gly Ala Leu Asn Ile
 290 295 300
 Pro Arg Gly Ala Lys Ala Ser Asn Phe Ala Ala Trp Val Ile Asp Pro
 305 310 315 320
 Gln Lys Asp Ala Gln Asp Leu Ile Val Leu Ala Pro Asp Ala Asn Thr
 325 330 335
 Ala Ala Asp Phe Arg Asp Ala Leu Leu Arg Val Gly Ile Asp Thr Val
 340 345 350
 Arg Tyr Phe Thr Asn Ser Ile Asp Gly Leu Pro Thr Phe Val Pro Glu
 355 360 365
 Leu Ile Ser Pro Ala Glu Leu Ala Glu Thr Asn Tyr Asp Ala Leu Ile
 370 375 380
 Asp Ile Arg Ala Lys Ser Glu Phe Ala Ala Gly Ser Ile Pro Gly Ala
 385 390 395 400
 Gln Gln Leu Ser Gly Gly Ser Ala Met Trp Arg Leu Asn Glu Leu Pro
 405 410 415
 Ala Gly Gly Thr Leu Val Thr Phe Cys Gln Ser Gly Ala Arg Asn Thr
 420 425 430
 Val Val Ala Asn Ala Leu Arg Arg Ala Gly Phe Thr Val Ile Glu Leu
 435 440 445
 Glu Gly Ser Tyr Ala Ala Trp Glu Lys Ser Ala Ala Asn Pro Lys Asn
 450 455 460
 Leu Gln Thr Ala Val
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<210> 135
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(652)
 <223> RXA01853

<400> 135

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                      Met Glu Ile Leu Gly
                      1 5

ttc gcg gct ggt ccg tat aaa aca aat tgc tat gtg gtg cgc ggg gag 163
Phe Ala Ala Gly Pro Tyr Lys Thr Asn Cys Tyr Val Val Arg Gly Glu
                      10 15 20

aat gag gtc gcg atc att gat cct ggc atg cat gcc cac gat gat ttg 211
Asn Glu Val Ala Ile Ile Asp Pro Gly Met His Ala His Asp Asp Leu
                      25 30 35

gtg gaa tac atc acc acg aat aat ttg agc gtg gac aag att gtg ctc 259
Val Glu Tyr Ile Thr Thr Asn Asn Leu Ser Val Asp Lys Ile Val Leu
                      40 45 50

acc cac gga cac att gat cac acc cgt gat gct ggt gtt gtg gca aag 307
Thr His Gly His Ile Asp His Thr Arg Asp Ala Gly Val Val Ala Lys
                      55 60 65

cgt ttc aat gcg ccg gtc tat atc cat cct gat gat gcg ttt ttc ctt 355
Arg Phe Asn Ala Pro Val Tyr Ile His Pro Asp Asp Ala Phe Phe Leu
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gag gtc tac aag gga tct gga aca aag acg gcc atg ctt ttc gac gcc 403
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Asp Asn Met Val Ser Pro Asp Pro Glu Ser Leu Arg Asp Leu Val Asp
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ggt gag aca atc act ttg gct ggc gaa gaa ttc acg ttg aag cat gca 499
Gly Glu Thr Ile Thr Leu Ala Gly Glu Glu Phe Thr Leu Lys His Ala
                      120 125 130

cca ggg cat tca cct ggt tgt acg ctg atc gtc ggc aag gaa tac tgc 547
Pro Gly His Ser Pro Gly Cys Thr Leu Ile Val Gly Lys Glu Tyr Cys
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Phe Ser Gly Asp Val Leu Phe Lys Gly Ser Ile Gly Arg Thr Asp Phe
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<210> 136

<211> 184

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

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 20 25 30
 Ala His Asp Asp Leu Val Glu Tyr Ile Thr Thr Asn Asn Leu Ser Val
 35 40 45
 Asp Lys Ile Val Leu Thr His Gly His Ile Asp His Thr Arg Asp Ala
 50 55 60
 Gly Val Val Ala Lys Arg Phe Asn Ala Pro Val Tyr Ile His Pro Asp
 65 70 75 80
 Asp Ala Phe Phe Leu Glu Val Tyr Lys Gly Ser Gly Thr Lys Thr Ala
 85 90 95
 Met Leu Phe Asp Ala Asp Asn Met Val Ser Pro Asp Pro Glu Ser Leu
 100 105 110
 Arg Asp Leu Val Asp Gly Glu Thr Ile Thr Leu Ala Gly Glu Glu Phe
 115 120 125
 Thr Leu Lys His Ala Pro Gly His Ser Pro Gly Cys Thr Leu Ile Val
 130 135 140
 Gly Lys Glu Tyr Cys Phe Ser Gly Asp Val Leu Phe Lys Gly Ser Ile
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 Gly Arg Thr Asp Phe Glu Trp Ser Asp Ala Asp Ala Met Asn Glu Ser
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 Leu Arg Thr Ala Val Leu Pro Leu
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 <213> Corynebacterium glutamicum

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 Met Thr Asn Glu Leu
 1 5

act ctt cac cat att tcc gtg tcc caa atg gac aac aat tgc tac ctt 163
 Thr Leu His His Ile Ser Val Ser Gln Met Asp Asn Asn Cys Tyr Leu
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ttg gcc gca aat ggc aac ggt tta ctc att gat gct gca gat gac gca 211
 Leu Ala Ala Asn Gly Asn Gly Leu Leu Ile Asp Ala Ala Asp Asp Ala
 25 30 35

gct gca cta ctt aaa tta gcc gaa gat gcc ggt gtg acc atc acc aaa 259
 Ala Ala Leu Leu Lys Leu Ala Glu Asp Ala Gly Val Thr Ile Thr Lys
 40 45 50

gtg ttg acc acc cac cgc cac gca gac cac gtc cgt gca ttg ccg gag 307
 Val Leu Thr Thr His Arg His Ala Asp His Val Arg Ala Leu Pro Glu
 55 60 65

gtt ctc cag aag acc gga gca act cac tac gcg cct ttc ctt gag gtg 355
 Val Leu Gln Lys Thr Gly Ala Thr His Tyr Ala Pro Phe Leu Glu Val
 70 75 80 85

cca gct ttg ccc tcc gct gtt gat gtg gaa ctg cat cat ggt gat tca 403
 Pro Ala Leu Pro Ser Ala Val Asp Val Glu Leu His His Gly Asp Ser
 90 95 100

att gaa ttt gag ggt cat gta ttc cct atc agc att ctg cgc ggc cac 451
 Ile Glu Phe Glu Gly His Val Phe Pro Ile Ser Ile Leu Arg Gly His
 105 110 115

acc cca ggc ggt gca gta ctc acc gct gag atc gac ggt aaa act cac 499
 Thr Pro Gly Gly Ala Val Leu Thr Ala Glu Ile Asp Gly Lys Thr His
 120 125 130

ctt ttc gtg ggt gac agc ctc ttc ccc ggc ggt ttg ggc aaa acc agc 547
 Leu Phe Val Gly Asp Ser Leu Phe Pro Gly Gly Leu Gly Lys Thr Ser
 135 140 145

agc gaa ggc gac ttc gtc cga ctg ttc aac gat gtc aaa gag cgc atc 595
 Ser Glu Gly Asp Phe Val Arg Leu Phe Asn Asp Val Lys Glu Arg Ile
 150 155 160 165

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 Phe Asp Thr Tyr Asp Asp Asp Ser Ile Val Trp Pro Gly His Gly Lys
 170 175 180

gaa acc acc ctt gga gcc gag cgt cca cag ctg gaa atc tgg tgg gag 691
 Glu Thr Thr Leu Gly Ala Glu Arg Pro Gln Leu Glu Ile Trp Trp Glu
 185 190 195

cgt cgc tgg taagcgcttt tctcaaccag gca 723
 Arg Arg Trp
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<210> 138

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

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 20 25 30

Ala Ala Asp Asp Ala Ala Ala Leu Leu Lys Leu Ala Glu Asp Ala Gly
 35 40 45

Val Thr Ile Thr Lys Val Leu Thr Thr His Arg His Ala Asp His Val
 50 55 60

Arg Ala Leu Pro Glu Val Leu Gln Lys Thr Gly Ala Thr His Tyr Ala
 65 70 75 80

Pro Phe Leu Glu Val Pro Ala Leu Pro Ser Ala Val Asp Val Glu Leu
 85 90 95

His His Gly Asp Ser Ile Glu Phe Glu Gly His Val Phe Pro Ile Ser
 100 105 110

Ile Leu Arg Gly His Thr Pro Gly Gly Ala Val Leu Thr Ala Glu Ile
 115 120 125

Asp Gly Lys Thr His Leu Phe Val Gly Asp Ser Leu Phe Pro Gly Gly
 130 135 140

Leu Gly Lys Thr Ser Ser Glu Gly Asp Phe Val Arg Leu Phe Asn Asp
 145 150 155 160

Val Lys Glu Arg Ile Phe Asp Thr Tyr Asp Asp Asp Ser Ile Val Trp
 165 170 175

Pro Gly His Gly Lys Glu Thr Thr Leu Gly Ala Glu Arg Pro Gln Leu
 180 185 190

Glu Ile Trp Trp Glu Arg Arg Trp
 195 200

<210> 139

<211> 404

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(381)

<223> FRXA02424

<400> 139

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 Thr Gly Ala Thr His Tyr Ala Pro Phe Leu Glu Val Pro Ala Leu Pro
 1 5 10 15

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 Ser Ala Val Asp Val Glu Leu His His Gly Asp Ser Ile Glu Phe Glu
 20 25 30

ggt cat gta ttc cct atc agc att ctg cgc ggc cac acc cca ggc ggt 144
 Gly His Val Phe Pro Ile Ser Ile Leu Arg Gly His Thr Pro Gly Gly
 35 40 45

gca gta ctc acc gct gag atc gac ggt aaa act cac ctt ttc gtg ggt 192
 Ala Val Leu Thr Ala Glu Ile Asp Gly Lys Thr His Leu Phe Val Gly
 50 55 60

gac agc ctc ttc ccc ggc ggt ttg ggc aaa acc agc agc gaa ggc gac 240
 Asp Ser Leu Phe Pro Gly Gly Leu Gly Lys Thr Ser Ser Glu Gly Asp
 65 70 75 80

ttc gtc cga ctg ttc aac gat gtc aaa gag cgc atc ttt gac acc tac 288
 Phe Val Arg Leu Phe Asn Asp Val Lys Glu Arg Ile Phe Asp Thr Tyr
 85 90 95

 gac gat gac agc atc gtg tgg cca ggt cac ggc aag gaa acc acc ctt 336
 Asp Asp Asp Ser Ile Val Trp Pro Gly His Gly Lys Glu Thr Thr Leu
 100 105 110

 gga gcc gag cgt cca cag ctg gaa atc tgg tgg gag cgt cgc tgg 381
 Gly Ala Glu Arg Pro Gln Leu Glu Ile Trp Trp Glu Arg Arg Trp
 115 120 125

 taagcgcttt tctcaaccag gca 404

<210> 140
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 140
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 20 25 30

 Gly His Val Phe Pro Ile Ser Ile Leu Arg Gly His Thr Pro Gly Gly
 35 40 45

 Ala Val Leu Thr Ala Glu Ile Asp Gly Lys Thr His Leu Phe Val Gly
 50 55 60

 Asp Ser Leu Phe Pro Gly Gly Leu Gly Lys Thr Ser Ser Glu Gly Asp
 65 70 75 80

 Phe Val Arg Leu Phe Asn Asp Val Lys Glu Arg Ile Phe Asp Thr Tyr
 85 90 95

 Asp Asp Asp Ser Ile Val Trp Pro Gly His Gly Lys Glu Thr Thr Leu
 100 105 110

 Gly Ala Glu Arg Pro Gln Leu Glu Ile Trp Trp Glu Arg Arg Trp
 115 120 125

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(859)
 <223> RXN00419

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	Met	Leu	Asn	Ala	Val	
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Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly Thr Ser Glu Ile Gly						
	10				20	
att tcc att gtc tcc cgc ttc ctc aag cag ggt cca tcc cat gtg acc						211
Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly Pro Ser His Val Thr						
	25				35	
ttg gca gcg cgt aaa gat tcc cca cgc gtg gac gca gca gtc gca gag						259
Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp Ala Ala Val Ala Glu						
	40				50	
atc aaa gca gct ggc gct gct tcc gtt gct gtt gtt gat ttc gat gcg						307
Ile Lys Ala Ala Gly Ala Ala Ser Val Ala Val Val Asp Phe Asp Ala						
	55				65	
ctc gac acc gaa tcc cac cct gca gcc atc gac gca gcc ttt gaa aac						355
Leu Asp Thr Glu Ser His Pro Ala Ala Ile Asp Ala Ala Phe Glu Asn						
	70				80	85
ggc gac gtt gac gta gca atc gtg gct ttc ggc atc ctc ggc gac aac						403
Gly Asp Val Asp Val Ala Ile Val Ala Phe Gly Ile Leu Gly Asp Asn						
	90				95	100
gaa gca cag tgg cgc gac caa gca cta gca gtg gaa gca acc acc gtg						451
Glu Ala Gln Trp Arg Asp Gln Ala Leu Ala Val Glu Ala Thr Thr Val						
	105				110	115
aac tac acc gcc ggc gtt tcc gta ggt gta ctg ctg ggc cag aaa ttt						499
Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln Lys Phe						
	120				125	130
gag cag cag ggc cac ggc acc atc gtg gca ttg tcc tct gtg gca ggc						547
Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val Ala Gly						
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cag cga gtc cgc cgc tcc aac ttt gtc tac ggc tcc gcc aag gca ggt						595
Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys Ala Gly						
	150				155	160
ttc gac ggt ttc tac acc cag ctc ggc gaa gcc ctg cgt gga tcc ggt						643
Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly Ser Gly						
	170				175	180
gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag atg tcc						691
Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys Met Ser						
	185				190	195
gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac gtg gca						739
Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp Val Ala						
	200				205	210
gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc ttt gtc						787
Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile Phe Val						
	215				220	225
cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att ccg cga						835
His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile Pro Arg						

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<211> 253
<212> PRT
<213> *Corynebacterium glutamicum*

243

<210> 143
 <211> 485
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(462)
 <223> FRXA00419

<400> 143
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 acc gtg aac tac acc gcc ggc ggt tcc gta ggt gta ctg ctg ggc cag 96
 Thr Val Asn Tyr Thr Ala Gly Val Ser Val Gly Val Leu Leu Gly Gln
 20 25 30
 aaa ttt gag cag cag ggc cac ggc acc atc gtg gca ttg tcc tct gtg 144
 Lys Phe Glu Gln Gln Gly His Gly Thr Ile Val Ala Leu Ser Ser Val
 35 40 45
 gca ggc cag cga gtc cgc cgc tcc aac ttt gtc tac ggc tcc gcc aag 192
 Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys
 50 55 60
 gca ggt ttc gac ggt ttc tac acc cag ctc ggc gaa gcc ctg cgt gga 240
 Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly
 65 70 75 80
 tcc ggt gcc aac gta ttg gtg gtt cgc cca ggc cag gta cgc acc aag 288
 Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys
 85 90 95
 atg tcc gca gat ggt ggc gaa gcc cca ctg acc gtc aac cgc gaa gac 336
 Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp
 100 105 110
 gtg gca gat gct gtt tat gat gca gtg gtg aac aag aag gac atc atc 384
 Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile
 115 120 125
 ttt gtc cac cca ctg ttc cag tac gtc tct ttt gcg ttc caa ttc att 432
 Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile
 130 135 140
 ccg cga gca atc ttc cgc aag ctg ccg ttc taacggaagt tacggaagtt 482
 Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe
 145 150
 acg 485

<210> 144
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 144

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 35 40 45
 Ala Gly Gln Arg Val Arg Arg Ser Asn Phe Val Tyr Gly Ser Ala Lys
 50 55 60
 Ala Gly Phe Asp Gly Phe Tyr Thr Gln Leu Gly Glu Ala Leu Arg Gly
 65 70 75 80
 Ser Gly Ala Asn Val Leu Val Val Arg Pro Gly Gln Val Arg Thr Lys
 85 90 95
 Met Ser Ala Asp Gly Gly Glu Ala Pro Leu Thr Val Asn Arg Glu Asp
 100 105 110
 Val Ala Asp Ala Val Tyr Asp Ala Val Val Asn Lys Lys Asp Ile Ile
 115 120 125
 Phe Val His Pro Leu Phe Gln Tyr Val Ser Phe Ala Phe Gln Phe Ile
 130 135 140
 Pro Arg Ala Ile Phe Arg Lys Leu Pro Phe
 145 150

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<211> 259

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(259)

<223> FRXA00421

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gccgacttga gctttcttaa gaaagggtt gaactaaaca atg ctt aac gca gtg 115
 Met Leu Asn Ala Val
 1 5

ggc aaa gcc caa aac att ctc ctt ctt ggt gga acc tct gag atc ggt 163
 Gly Lys Ala Gln Asn Ile Leu Leu Leu Gly Gly Thr Ser Glu Ile Gly
 10 15 20

att tcc att gtc tcc cgc ttc ctc aag cag ggt cca tcc cat gtg acc 211
 Ile Ser Ile Val Ser Arg Phe Leu Lys Gln Gly Pro Ser His Val Thr
 25 30 35

ttg gca gcg cgt aaa gat tcc cca cgc gtg gac gca gca gtc gca gag 259
 Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp Ala Ala Val Ala Glu
 40 45 50

<210> 146
 <211> 53
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 146
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 Pro Ser His Val Thr Leu Ala Ala Arg Lys Asp Ser Pro Arg Val Asp
 35 40 45
 Ala Ala Val Ala Glu
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<220>
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 <222> (101)..(838)
 <223> RXN02923

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 Leu Ser Ile Leu Leu
 1 5
 cta ggc gga acc tct gac att gcc ggt gag att gcc acg ttg acg tgt 163
 Leu Gly Gly Thr Ser Asp Ile Ala Gly Glu Ile Ala Thr Leu Thr Cys
 10 15 20
 cac ggc gaa gac gtt gtt ttg gct gct cgt cga cca gag gct gca cag 211
 His Gly Glu Asp Val Val Leu Ala Ala Arg Arg Pro Glu Ala Ala Gln
 25 30 35
 ggc tta gcg gaa gat ctt cga cag cgc ggt gcc aca tct gtt cat gtt 259
 Gly Leu Ala Glu Asp Leu Arg Gln Arg Gly Ala Thr Ser Val His Val
 40 45 50
 ttg agc ttt gac gcc caa gta cta gac acg cac cga gaa ctt gtg aag 307
 Leu Ser Phe Asp Ala Gln Val Leu Asp Thr His Arg Glu Leu Val Lys
 55 60 65
 aaa aca caa gag cta gct ggc gag att tcc ctt gcc gtg gtt gct ttt 355
 Lys Thr Gln Glu Leu Ala Gly Glu Ile Ser Leu Ala Val Val Ala Phe
 70 75 80 85
 ggc atc ttg gga gac caa gaa cgc gca gaa acc gat gag acc cat gcg 403
 Gly Ile Leu Gly Asp Gln Glu Arg Ala Glu Thr Asp Glu Thr His Ala
 90 95 100
 gta gag atc gcc acc gtg gat tac acc gct cag gtc tcc atg ctc act 451

Val Glu Ile Ala Thr Val Asp Tyr Thr Ala Gln Val Ser Met Leu Thr
 105 110 115

gtg ctt gct gat gag ctc cgc gca caa act act cca gca gcg atc gtg 499
 Val Leu Ala Asp Glu Leu Arg Ala Gln Thr Thr Pro Ala Ala Ile Val
 120 125 130

gcg ttt tcc tcg att gct ggg tgg cgg gcg cgc cgg cct aac tat gtc 547
 Ala Phe Ser Ser Ile Ala Gly Trp Arg Ala Arg Arg Pro Asn Tyr Val
 135 140 145

tat gga tcc acc aag gct ggt ctc gat gca ttt tgc caa ggg ctt gca 595
 Tyr Gly Ser Thr Lys Ala Gly Leu Asp Ala Phe Cys Gln Gly Leu Ala
 150 155 160 165

gat agc ctg cat ggg aca cac gtg cga ttg att att gcg cgt cct ggc 643
 Asp Ser Leu His Gly Thr His Val Arg Leu Ile Ile Ala Arg Pro Gly
 170 175 180

ttt gtt att ggt tct atg acc acg ggg atg aag cct gct ccg atg tcg 691
 Phe Val Ile Gly Ser Met Thr Thr Gly Met Lys Pro Ala Pro Met Ser
 185 190 195

gtg tat cca cga gat gtt gcc gca gct gtt gtt agt gct tat acc tct 739
 Val Tyr Pro Arg Asp Val Ala Ala Val Val Ser Ala Tyr Thr Ser
 200 205 210

aag aag agg agc acg acc ttg tgg att ccg gga cgt ctg cgg gtt ctc 787
 Lys Lys Arg Ser Thr Thr Leu Trp Ile Pro Gly Arg Leu Arg Val Leu
 215 220 225

gcc tgg att atg cgg atg gtt cct cgt ccg gtg tgg cgg aag atg cca 835
 Ala Trp Ile Met Arg Met Val Pro Arg Pro Val Trp Arg Lys Met Pro
 230 235 240 245

cgc tagatacccg ttcagccctc aca 861
 Arg

<210> 148

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

Leu Ser Ile Leu Leu Leu Gly Gly Thr Ser Asp Ile Ala Gly Glu Ile
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Ala Thr Leu Thr Cys His Gly Glu Asp Val Val Leu Ala Ala Arg Arg
 20 25 30

Pro Glu Ala Ala Gln Gly Leu Ala Glu Asp Leu Arg Gln Arg Gly Ala
 35 40 45

Thr Ser Val His Val Leu Ser Phe Asp Ala Gln Val Leu Asp Thr His
 50 55 60

Arg Glu Leu Val Lys Lys Thr Gln Glu Leu Ala Gly Glu Ile Ser Leu
 65 70 75 80

<210> 149
<211> 1203
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(1180)
<223> RXN02922
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Gly Gly Leu Gly Phe Ser Leu Pro Glu Ala Phe Glu Val Leu Val Ala															
55 60 65															
gcg gcc gct gca gat tca aat atc gcg cag gga ttg cgg cct cac ttc	355														
Ala Ala Ala Ala Asp Ser Asn Ile Ala Gln Gly Leu Arg Pro His Phe															
70 75 80 85															
ttg gca gtg gag agc tta ttg atc gct cct tat tca gag cac cgc acc	403														
Leu Ala Val Glu Ser Leu Leu Ile Ala Pro Tyr Ser Glu His Arg Thr															
90 95 100															
aag tgg ctg cga aaa atc gct gag aaa ggc gtg gtc att ggc aat gcg	451														
Lys Trp Leu Arg Lys Ile Ala Glu Lys Gly Val Val Ile Gly Asn Ala															
105 110 115															
ttg act gaa gtg gga aac aag cca ggt gag ctg aaa acc aag atc cga	499														
Leu Thr Glu Val Gly Asn Lys Pro Gly Glu Leu Lys Thr Lys Ile Arg															
120 125 130															
aag gaa ggc gag tct tac gtt ctc agc gac acc aag ttc tat tcc acg	547														
Lys Glu Gly Glu Ser Tyr Val Leu Ser Asp Thr Lys Phe Tyr Ser Thr															
135 140 145															
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Gly Ser Leu Tyr Ala Asp Trp Ile Gln Val His Ala Lys Asp Glu Glu															
150 155 160 165															
gat caa gat gtt ttc gcc ttt gtt gat cgc gac gca tca ggc gtt gtt	643														
Asp Gln Asp Val Phe Ala Phe Val Asp Arg Asp Ala Ser Gly Val Val															
170 175 180															
ttg gtg gat tac tgg gac gaa ttt ggg caa caa cta ttt gcc tcc gga	691														
Leu Val Asp Tyr Trp Asp Glu Phe Gly Gln Gln Leu Phe Ala Ser Gly															
185 190 195															
acc agc ttc ttt gaa aaa gtc gtg gta gat cca ctg gac att gtc acc	739														
Thr Ser Phe Phe Glu Lys Val Val Val Asp Pro Leu Asp Ile Val Thr															
200 205 210															
cgt gat tac acc gca ccc agc gct ttc cag gcg ctg gcg cag tca cat	787														
Arg Asp Tyr Thr Ala Pro Ser Ala Phe Gln Ala Leu Ala Gln Ser His															
215 220 225															
cat ttg tct acg ttg act ggt att tcg cag gca atc acc cgt gac att	835														
His Leu Ser Thr Leu Thr Gly Ile Ser Gln Ala Ile Thr Arg Asp Ile															
230 235 240 245															
gtt acc tat gta caa aac cgc acc cgt att ttc agc cac gga agt ggt	883														
Val Thr Tyr Val Gln Asn Arg Thr Arg Ile Phe Ser His Gly Ser Gly															
250 255 260															
gac ctt cca cgc ttt gat ccg cag gtg caa cag gtg gtg ggt gag gtg	931														
Asp Leu Pro Arg Phe Asp Pro Gln Val Gln Gln Val Val Gly Glu Val															
265 270 275															
aaa gcc aag tcg tat gca gtc gag aaa atc ttt cag ggt ttc gca caa	979														
Lys Ala Lys Ser Tyr Ala Val Glu Lys Ile Phe Gln Gly Phe Ala Gln															
280 285 290															

gaa ctg gat ctt gtc gtc gat aag gca aaa gcc ggc act gct acg gag 1027
 Glu Leu Asp Leu Val Val Asp Lys Ala Lys Ala Gly Thr Ala Thr Glu
 295 300 305

gtc gat ctg gcc gct gtc gac ctg agc gcc tac caa gcc cag tta gcg 1075
 Val Asp Leu Ala Ala Val Asp Leu Ser Ala Tyr Gln Ala Gln Leu Ala
 310 315 320 325

gtg gca cct ttg gtg ctg agc cag gcc acc cag gcc ttt gag gtt ggc 1123
 Val Ala Pro Leu Val Leu Ser Gln Ala Thr Gln Ala Phe Glu Val Gly
 330 335 340

gca gat gcc tta aac ggc ggc cac gtg gct gcc caa tac acg atc gga 1171
 Ala Asp Ala Leu Asn Gly Gly His Val Ala Ala Gln Tyr Thr Ile Gly
 345 350 355

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 Ser Leu Ser
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<210> 150

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

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Arg Asp Leu Ala Lys Gln Leu Ser Ala Gly Gly Phe Thr Lys Leu Arg
 35 40 45

Ile Pro Val Glu Phe Gly Gly Leu Gly Phe Ser Leu Pro Glu Ala Phe
 50 55 60

Glu Val Leu Val Ala Ala Ala Ala Asp Ser Asn Ile Ala Gln Gly
 65 70 75 80

Leu Arg Pro His Phe Leu Ala Val Glu Ser Leu Leu Ile Ala Pro Tyr
 85 90 95

Ser Glu His Arg Thr Lys Trp Leu Arg Lys Ile Ala Glu Lys Gly Val
 100 105 110

Val Ile Gly Asn Ala Leu Thr Glu Val Gly Asn Lys Pro Gly Glu Leu
 115 120 125

Lys Thr Lys Ile Arg Lys Glu Gly Glu Ser Tyr Val Leu Ser Asp Thr
 130 135 140

Lys Phe Tyr Ser Thr Gly Ser Leu Tyr Ala Asp Trp Ile Gln Val His
 145 150 155 160

Ala Lys Asp Glu Glu Asp Gln Asp Val Phe Ala Phe Val Asp Arg Asp
 165 170 175

Ala Ser Gly Val Val Leu Val Asp Tyr Trp Asp Glu Phe Gly Gln Gln
 180 185 190

Leu Phe Ala Ser Gly Thr Ser Phe Phe Glu Lys Val Val Val Asp Pro
 195 200 205

Leu Asp Ile Val Thr Arg Asp Tyr Thr Ala Pro Ser Ala Phe Gln Ala
 210 215 220

Leu Ala Gln Ser His His Leu Ser Thr Leu Thr Gly Ile Ser Gln Ala
 225 230 235 240

Ile Thr Arg Asp Ile Val Thr Tyr Val Gln Asn Arg Thr Arg Ile Phe
 245 250 255

Ser His Gly Ser Gly Asp Leu Pro Arg Phe Asp Pro Gln Val Gln Gln
 260 265 270

Val Val Gly Glu Val Lys Ala Lys Ser Tyr Ala Val Glu Lys Ile Phe
 275 280 285

Gln Gly Phe Ala Gln Glu Leu Asp Leu Val Val Asp Lys Ala Lys Ala
 290 295 300

Gly Thr Ala Thr Glu Val Asp Leu Ala Ala Val Asp Leu Ser Ala Tyr
 305 310 315 320

Gln Ala Gln Leu Ala Val Ala Pro Leu Val Leu Ser Gln Ala Thr Gln
 325 330 335

Ala Phe Glu Val Gly Ala Asp Ala Leu Asn Gly Gly His Val Ala Ala
 340 345 350

Gln Tyr Thr Ile Gly Ser Leu Ser
 355 360

<210> 151
 <211> 516
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(493)
 <223> RXN03065

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 ggcttctttg taaagaggcc agcccgctaa gctaggtcgc atg atc agc att gga 115
 Met Ile Ser Ile Gly
 1 5

acc gac ctc gtt cac att tcg gcg ttc gca gag cag ctt gca cag ccg 163
 Thr Asp Leu Val His Ile Ser Ala Phe Ala Glu Gln Leu Ala Gln Pro
 10 15 20

gga agt tcc ttc atg gag gtg ttt tcc gca ggg gag cgt cgt aaa gca 211
 Gly Ser Ser Phe Met Glu Val Phe Ser Ala Gly Glu Arg Arg Lys Ala
 25 30 35

aat gaa cgc cag gca agc cgc tac gcc gag cat ttg gcg ggg cgg tgg 259
 Asn Glu Arg Gln Ala Ser Arg Tyr Ala Glu His Leu Ala Gly Arg Trp
 40 45 50
 gcg gca aaa gaa tcc ttt att aag gcc tgg tca cag gcc att tat ggc 307
 Ala Ala Lys Glu Ser Phe Ile Lys Ala Trp Ser Gln Ala Ile Tyr Gly
 55 60 65
 cag cca ccc gtg atc gcc gaa gaa gcc gtg gtg tgg cgg gac atc gaa 355
 Gln Pro Pro Val Ile Ala Glu Glu Ala Val Val Trp Arg Asp Ile Glu
 70 75 80 85
 gtt cgc gca gac gcg tgg ggg cgc gtc gcg atc gaa ttg gcg ccc gaa 403
 Val Arg Ala Asp Ala Trp Gly Arg Val Ala Ile Glu Leu Ala Pro Glu
 90 95 100
 ttg gcc gca gtg gtc cgg gaa tcc atc ggg gag ttt tcc agc agc ttg 451
 Leu Ala Ala Val Val Arg Glu Ser Ile Gly Glu Phe Ser Ser Ser Leu
 105 110 115
 agc atc agc cac gac ggc gac tac gcg gtg gaa cgt gcg tgt 493
 Ser Ile Ser His Asp Gly Asp Tyr Ala Val Glu Arg Ala Cys
 120 125 130
 tgactatcca gtagccacgg aga 516

<210> 152
 <211> 131
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 152
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 Gln Leu Ala Gln Pro Gly Ser Ser Phe Met Glu Val Phe Ser Ala Gly
 20 25 30
 Glu Arg Arg Lys Ala Asn Glu Arg Gln Ala Ser Arg Tyr Ala Glu His
 35 40 45
 Leu Ala Gly Arg Trp Ala Ala Lys Glu Ser Phe Ile Lys Ala Trp Ser
 50 55 60
 Gln Ala Ile Tyr Gly Gln Pro Pro Val Ile Ala Glu Glu Ala Val Val
 65 70 75 80
 Trp Arg Asp Ile Glu Val Arg Ala Asp Ala Trp Gly Arg Val Ala Ile
 85 90 95
 Glu Leu Ala Pro Glu Leu Ala Ala Val Val Arg Glu Ser Ile Gly Glu
 100 105 110
 Phe Ser Ser Ser Leu Ser Ile Ser His Asp Gly Asp Tyr Ala Val Glu
 115 120 125
 Arg Ala Cys
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<210> 153
<211> 543
<212> DNA
<213> *Corynebacterium glutamicum*

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<223> RXN03132
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Met Asn Val Asn Gln																	
1 5																	
cag ttg gga gcc cgc acc gcc atg aac cac cct gag acc gca acc gtc 163																	
Gln Leu Gly Ala Arg Thr Ala Met Asn His Pro Glu Thr Ala Thr Val																	
10 15 20																	
ctt cgc tcc atc tct gac atg gtt agc acc gaa acc aat ccg cgc cgt 211																	
Leu Arg Ser Ile Ser Asp Met Val Ser Thr Glu Thr Asn Pro Arg Arg																	
25 30 35																	
aaa agc cgc ctc gag cag ctc att tac gcc acc gcc agc gcc tgg ccc 259																	
Lys Ser Arg Leu Glu Gln Leu Ile Tyr Ala Thr Ala Ser Ala Trp Pro																	
40 45 50																	
cac tac ccc att gcc cac gca gcc cag gcc gcg gtg caa tta gcc agg 307																	
His Tyr Pro Ile Ala His Ala Ala Gln Ala Ala Val Gln Leu Ala Arg																	
55 60 65																	
cca atg cgg gtt ttt gag ctc cag agc ttt gaa ggc gtc aag cac gca 355																	
Pro Met Arg Val Phe Glu Leu Gln Ser Phe Glu Gly Val Lys His Ala																	
70 75 80 85																	
ctc cac cac atc gat ctt cgc ccc gcc ctc gaa tgg gac atc atg gga 403																	
Leu His His Ile Asp Leu Arg Pro Ala Leu Glu Trp Asp Ile Met Gly																	
90 95 100																	
ttt ccc gaa tcc ccc gac acg ctg ccc att ttg ctc agt gac ctg cgc 451																	
Phe Pro Glu Ser Pro Asp Thr Leu Pro Ile Leu Leu Ser Asp Leu Arg																	
105 110 115																	
gac ccc cct tac gcc acc act gct gtg cca cct caa tcc acg cca cgc 499																	
Asp Pro Pro Tyr Ala Thr Thr Ala Val Pro Pro Gln Ser Thr Pro Arg																	
120 125 130																	
tcc gct cac cga tcc aca cat tgacgcttcc aggcgccacc gcg 543																	
Ser Ala His Arg Ser Thr His																	
135 140																	

<210> 154
<211> 140
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 154

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 20 25 30
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 35 40 45
 Ala Ser Ala Trp Pro His Tyr Pro Ile Ala His Ala Ala Gln Ala Ala
 50 55 60
 Val Gln Leu Ala Arg Pro Met Arg Val Phe Glu Leu Gln Ser Phe Glu
 65 70 75 80
 Gly Val Lys His Ala Leu His His Ile Asp Leu Arg Pro Ala Leu Glu
 85 90 95
 Trp Asp Ile Met Gly Phe Pro Glu Ser Pro Asp Thr Leu Pro Ile Leu
 100 105 110
 Leu Ser Asp Leu Arg Asp Pro Pro Tyr Ala Thr Thr Ala Val Pro Pro
 115 120 125
 Gln Ser Thr Pro Arg Ser Ala His Arg Ser Thr His
 130 135 140

<210> 155

<211> 461

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(438)

<223> RXN03157

<400> 155

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 acc atc ttg gtc acc gcc aac ccc aac aaa aac tca gga ctg ttc acc 96
 Thr Ile Leu Val Thr Ala Asn Pro Asn Lys Asn Ser Gly Leu Phe Thr
 20 25 30
 gtc gca gaa cgc atg gat ctc atc cgc gaa tcc acc gca cac ctg gac 144
 Val Ala Glu Arg Met Asp Leu Ile Arg Glu Ser Thr Ala His Leu Asp
 35 40 45
 aac gta aaa gta gac act tgg gcc tca ctg ctc gtg gat tac acc acc 192
 Asn Val Lys Val Asp Thr Trp Ala Ser Leu Leu Val Asp Tyr Thr Thr
 50 55 60
 gaa cat ggc atc ggc gcc cta gtc aaa ggc ctg cga agc tcc ctc gac 240
 Glu His Gly Ile Gly Ala Leu Val Lys Gly Leu Arg Ser Ser Leu Asp
 65 70 75 80
 tac gaa tac gag ctc ccc atg gca cag atg aac agg cga ctc acg ggc 288
 Tyr Glu Tyr Glu Leu Pro Met Ala Gln Met Asn Arg Arg Leu Thr Gly

85										90					95					
gta	gac	acc	ttc	ttc	ctc	ctc	acc	gac	gag	aaa	tac	ggc	tac	gtc	agc	336				
Val	Asp	Thr	Phe	Phe	Leu	Leu	Thr	Asp	Glu	Lys	Tyr	Gly	Tyr	Val	Ser					
100					105					110										
tcc	aca	ctg	tgc	aaa	gaa	gtt	gcc	cgc	ttc	ggg	ggc	gat	gtc	tcc	ggc	384				
Ser	Thr	Leu	Cys	Lys	Glu	Val	Ala	Arg	Phe	Gly	Gly	Asp	Val	Ser	Gly					
115					120					125										
ctc	cta	cct	gag	gta	gtg	gca	aaa	gcc	gtg	aca	gaa	aaa	tac	agc	aac	432				
Leu	Leu	Pro	Glu	Val	Val	Ala	Lys	Ala	Val	Thr	Glu	Lys	Tyr	Ser	Asn					
130					135					140										
cag	cac	tagtttcttt	tgcatcaagc	gtc												461				
Gln	His																			
145																				

<210> 156

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

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Thr	Ile	Leu	Val	Thr	Ala	Asn	Pro	Asn	Lys	Asn	Ser	Gly	Leu	Phe	Thr
			20					25					30		

Val	Ala	Glu	Arg	Met	Asp	Leu	Ile	Arg	Glu	Ser	Thr	Ala	His	Leu	Asp
		35					40					45			

Asn	Val	Lys	Val	Asp	Thr	Trp	Ala	Ser	Leu	Leu	Val	Asp	Tyr	Thr	Thr
	50					55					60				

Glu	His	Gly	Ile	Gly	Ala	Leu	Val	Lys	Gly	Leu	Arg	Ser	Ser	Leu	Asp
65					70					75					80

Tyr	Glu	Tyr	Glu	Leu	Pro	Met	Ala	Gln	Met	Asn	Arg	Arg	Leu	Thr	Gly
				85					90					95	

Val	Asp	Thr	Phe	Phe	Leu	Leu	Thr	Asp	Glu	Lys	Tyr	Gly	Tyr	Val	Ser
			100					105					110		

Ser	Thr	Leu	Cys	Lys	Glu	Val	Ala	Arg	Phe	Gly	Gly	Asp	Val	Ser	Gly
		115					120					125			

Leu	Leu	Pro	Glu	Val	Val	Ala	Lys	Ala	Val	Thr	Glu	Lys	Tyr	Ser	Asn
	130					135					140				

Gln His
145

<210> 157

<211> 1206

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1183)

<223> RXN00934

<400> 157

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                                         Val Arg Ile Gly Met
                                         1 5

gtc tgc ccg tac tcc ttc gat gag ccg ggc ggt gtt caa gcg cat atc 163
Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly Val Gln Ala His Ile
              10              15              20

ctt gac tta gcg cga acc ttc att gcc caa ggc cat gag gtt cag gtg 211
Leu Asp Leu Ala Arg Thr Phe Ile Ala Gln Gly His Glu Val Gln Val
              25              30              35

ctt ggt ccg tgt agt gcg gat acg cag gtg ccc gat ttc gtg gtg cgc 259
Leu Gly Pro Cys Ser Ala Asp Thr Gln Val Pro Asp Phe Val Val Arg
              40              45              50

ggg ggt ggc agc atc ccg att ccg tac aat ggc tcg gtt gcc cgc ttg 307
Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly Ser Val Ala Arg Leu
              55              60              65

agc ttt ggg ccg aaa atg ttc aag gcc gtg cgc acg ttc ctc cgc gaa 355
Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg Thr Phe Leu Arg Glu
              70              75              80              85

ggc aac ttc gat gtg ctg cat atc cat gaa ccg aat tca cca agt ttt 403
Gly Asn Phe Asp Val Leu His Ile His Glu Pro Asn Ser Pro Ser Phe
              90              95              100

tcc atg gcg gcg cta cgc ttt gcg gaa ggc ccc atc gtt gct act tac 451
Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro Ile Val Ala Thr Tyr
              105              110              115

cac gcc tcc agt agc gga tcg aag ctg ctc aag gct ttc tta cca gtg 499
His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys Ala Phe Leu Pro Val
              120              125              130

ctt tcg ccc atg ctg gag aaa gtg cgc gca ggc atc gcc gtg tct gaa 547
Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly Ile Ala Val Ser Glu
              135              140              145

atg gct cgg cgc tgg cag gtg gag caa gtc ggc ggc gat ccc gtg ctg 595
Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly Gly Asp Pro Val Leu
              150              155              160              165

atc ccc aac ggg gta gag acc tcc atg ttc aaa gcc gcg cgc caa atc 643
Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys Ala Ala Arg Gln Ile
              170              175              180

gaa ccg aat gat cct gta gag atc gtc ttt ttg ggt cgc ctc gat gag 691
Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu Gly Arg Leu Asp Glu
              185              190              195

tcc cgc aaa ggc ctc gac atc ctc ctg cgc gct ctg acc agg ctg gat 739

```

Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala Leu Thr Arg Leu Asp
 200 205 210

cgc ccg ttt acc tgc acc gtc att ggc ggc ggc acc ccg cga gaa gtc 787
 Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly Thr Pro Arg Glu Val
 215 220 225

gcc ggc atc aac ttt gtg ggc cgc gtc agc gat gag gaa aag gca gca 835
 Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp Glu Glu Lys Ala Ala
 230 235 240 245

atc tta ggt cgc gca gac atc tat gtc gca ccc aac acc ggc ggc gaa 883
 Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro Asn Thr Gly Gly Glu
 250 255 260

agc ttc ggc atc gtg cta gtt gaa gcg atg gcc gcg gga tgc gct gtc 931
 Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala Ala Gly Cys Ala Val
 265 270 275

gtc gcc agc gac cta gaa gcg ttc tcc ctg gtc acc gat tct gaa gcc 979
 Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val Thr Asp Ser Glu Ala
 280 285 290

gca cag cca gcg ggc gtg cta ttt aaa acc ggc tca gac gcc gac cta 1027
 Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly Ser Asp Ala Asp Leu
 295 300 305

gcc aaa aaa ctt caa gcg ctt atc gac gac ccc tcc tcc cgt tcc acg 1075
 Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro Ser Ser Arg Ser Thr
 310 315 320 325

ctt atc gcc gcg ggc cta aag cgc gca aac gcc tac gac tgg tcg aca 1123
 Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala Tyr Asp Trp Ser Thr
 330 335 340

gta tcc acc cag gtc atg gca gtc tat gaa acc att gcg atc gac aaa 1171
 Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr Ile Ala Ile Asp Lys
 345 350 355

gtg agg ctt gga tgacccttgt ttacctcctc atc 1206
 Val Arg Leu Gly
 360

<210> 158

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 158

Val Arg Ile Gly Met Val Cys Pro Tyr Ser Phe Asp Glu Pro Gly Gly
 1 5 10 15

Val Gln Ala His Ile Leu Asp Leu Ala Arg Thr Phe Ile Ala Gln Gly
 20 25 30

His Glu Val Gln Val Leu Gly Pro Cys Ser Ala Asp Thr Gln Val Pro
 35 40 45

Asp Phe Val Val Arg Gly Gly Gly Ser Ile Pro Ile Pro Tyr Asn Gly
 50 55 60

Ser Val Ala Arg Leu Ser Phe Gly Pro Lys Met Phe Lys Ala Val Arg
 65 70 75 80
 Thr Phe Leu Arg Glu Gly Asn Phe Asp Val Leu His Ile His Glu Pro
 85 90 95
 Asn Ser Pro Ser Phe Ser Met Ala Ala Leu Arg Phe Ala Glu Gly Pro
 100 105 110
 Ile Val Ala Thr Tyr His Ala Ser Ser Ser Gly Ser Lys Leu Leu Lys
 115 120 125
 Ala Phe Leu Pro Val Leu Ser Pro Met Leu Glu Lys Val Arg Ala Gly
 130 135 140
 Ile Ala Val Ser Glu Met Ala Arg Arg Trp Gln Val Glu Gln Val Gly
 145 150 155 160
 Gly Asp Pro Val Leu Ile Pro Asn Gly Val Glu Thr Ser Met Phe Lys
 165 170 175
 Ala Ala Arg Gln Ile Glu Pro Asn Asp Pro Val Glu Ile Val Phe Leu
 180 185 190
 Gly Arg Leu Asp Glu Ser Arg Lys Gly Leu Asp Ile Leu Leu Arg Ala
 195 200 205
 Leu Thr Arg Leu Asp Arg Pro Phe Thr Cys Thr Val Ile Gly Gly Gly
 210 215 220
 Thr Pro Arg Glu Val Ala Gly Ile Asn Phe Val Gly Arg Val Ser Asp
 225 230 235 240
 Glu Glu Lys Ala Ala Ile Leu Gly Arg Ala Asp Ile Tyr Val Ala Pro
 245 250 255
 Asn Thr Gly Gly Glu Ser Phe Gly Ile Val Leu Val Glu Ala Met Ala
 260 265 270
 Ala Gly Cys Ala Val Val Ala Ser Asp Leu Glu Ala Phe Ser Leu Val
 275 280 285
 Thr Asp Ser Glu Ala Ala Gln Pro Ala Gly Val Leu Phe Lys Thr Gly
 290 295 300
 Ser Asp Ala Asp Leu Ala Lys Lys Leu Gln Ala Leu Ile Asp Asp Pro
 305 310 315 320
 Ser Ser Arg Ser Thr Leu Ile Ala Ala Gly Leu Lys Arg Ala Asn Ala
 325 330 335
 Tyr Asp Trp Ser Thr Val Ser Thr Gln Val Met Ala Val Tyr Glu Thr
 340 345 350
 Ile Ala Ile Asp Lys Val Arg Leu Gly
 355 360

<210> 159

<211> 1320

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1297)

<223> RXN00792

<400> 159

cacctttggt gctgagccag gccacccagg cctttgaggt tggcgcagat gccttaaacg 60

gcggccacgt	ggctgcccaa	tacacgatcg	gacccctgtc	atg	agc	caa	gaa	att	115
				Met	Ser	Gln	Glu	Ile	
				1				5	

ttg	agc	cat	ttt	gca	ccc	gca	tta	gag	cgc	att	cga	agc	ggc	gcc	gtc	163
Leu	Ser	His	Phe	Ala	Pro	Ala	Leu	Glu	Arg	Ile	Arg	Ser	Gly	Ala	Val	
				10				15					20			

gag	cgc	gaa	cag	cag	cgc	gcc	ttg	cca	gtg	gaa	gag	att	aaa	gag	ctg	211
Glu	Arg	Glu	Gln	Gln	Arg	Ala	Leu	Pro	Val	Glu	Glu	Ile	Lys	Glu	Leu	
			25				30						35			

gta	gag	cta	ggt	ttt	act	ggg	ctt	cga	gtg	ccc	gaa	gaa	cta	ggc	ggt	259
Val	Glu	Leu	Gly	Phe	Thr	Gly	Leu	Arg	Val	Pro	Glu	Glu	Leu	Gly	Gly	
		40					45					50				

gcg	ggc	gct	tcc	ctg	gaa	agc	gta	ggt	gag	tta	ctg	atc	gag	atc	gcg	307
Ala	Gly	Ala	Ser	Leu	Glu	Ser	Val	Val	Glu	Leu	Leu	Ile	Glu	Ile	Ala	
	55					60					65					

ggc	gcc	gat	tcc	aat	atc	gcc	caa	gcc	ctg	cgc	gga	cat	ttt	gcc	ttc	355
Gly	Ala	Asp	Ser	Asn	Ile	Ala	Gln	Ala	Leu	Arg	Gly	His	Phe	Ala	Phe	
70					75				80					85		

gtg	gaa	cta	ctc	ctg	gaa	gcg	ccg	gag	agc	gaa	ttc	cgc	acc	cat	tgg	403
Val	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Glu	Ser	Glu	Phe	Arg	Thr	His	Trp	
			90					95					100			

ctg	cgc	gaa	gtc	gcc	acc	gga	aga	ctt	gtg	ggc	aac	gcc	gaa	agt	gag	451
Leu	Arg	Glu	Val	Ala	Thr	Gly	Arg	Leu	Val	Gly	Asn	Ala	Glu	Ser	Glu	
			105					110					115			

aaa	cgc	ggc	gtt	tac	ggc	gat	ccg	cag	acc	ttc	atc	gat	gag	gtg	gag	499
Lys	Arg	Gly	Val	Tyr	Gly	Asp	Pro	Gln	Thr	Phe	Ile	Asp	Glu	Val	Glu	
		120					125					130				

act	gaa	aac	gga	ccg	att	ttc	gtg	ctc	aac	ggc	act	aag	ttt	tat	acc	547
Thr	Glu	Asn	Gly	Pro	Ile	Phe	Val	Leu	Asn	Gly	Thr	Lys	Phe	Tyr	Thr	
	135					140					145					

acc	ggc	acc	tat	ttt	gcg	gac	tac	acc	tgg	acc	acc	gcg	ctg	ctg	cgc	595
Thr	Gly	Thr	Tyr	Phe	Ala	Asp	Tyr	Thr	Trp	Thr	Thr	Ala	Leu	Leu	Arg	
150					155				160					165		

aac	ctt	aac	ggc	caa	gaa	act	ttg	gtc	agt	ttg	ccg	gtc	gat	ctg	cac	643
Asn	Leu	Asn	Gly	Gln	Glu	Thr	Leu	Val	Ser	Leu	Pro	Val	Asp	Leu	His	
			170					175						180		

gcg	ccg	ggc	gtg	gat	gtt	gct	gat	gat	tgg	agc	ggg	ttt	ggg	caa	aag	691
Ala	Pro	Gly	Val	Asp	Val	Ala	Asp	Asp	Trp	Ser	Gly	Phe	Gly	Gln	Lys	

185	190	195	
ctc acc gcc tct gga acg acc acg ttt aaa gac ctg gag gtg gat ccg Leu Thr Ala Ser Gly Thr Thr Thr Phe Lys Asp Leu Glu Val Asp Pro 200 205 210			739
cgg tgg atc att cca cgc act gat gcg ccc acg ctg gtg tgg acg tat Arg Trp Ile Ile Pro Arg Thr Asp Ala Pro Thr Leu Val Trp Thr Tyr 215 220 225			787
ctg cag ctg agc ctg ctg acc gtg ctg gtt ggc agt gcc gca gca gct Leu Gln Leu Ser Leu Leu Thr Val Leu Val Gly Ser Ala Ala Ala Ala 230 235 240 245			835
gtc gat gag gtg gtt gcc cgc gcc caa tcc tcc acc aga aat gcg tgg Val Asp Glu Val Val Ala Arg Ala Gln Ser Ser Thr Arg Asn Ala Trp 250 255 260			883
aac cct ggc gtc gag cgc cgc agc gat ccg gcc gca acc ata gcg atc Asn Pro Gly Val Glu Arg Arg Ser Asp Pro Ala Ala Thr Ile Ala Ile 265 270 275			931
ggc gac gca cgc agc cga gtc acc gtt att cgt gga gcg ctt ctc gac Gly Asp Ala Arg Ser Arg Val Thr Val Ile Arg Gly Ala Leu Leu Asp 280 285 290			979
gcc acc cgc cac gtt tcc aac gcc gcc acg atc gta acc ccc gaa gcc Ala Thr Arg His Val Ser Asn Ala Ala Thr Ile Val Thr Pro Glu Ala 295 300 305			1027
ttc aac gag gcg gac gct att gtt gca gcg ctc tgg ccc atc gtc tcc Phe Asn Glu Ala Asp Ala Ile Val Ala Ala Leu Trp Pro Ile Val Ser 310 315 320 325			1075
gga caa gct ttg gtg gtg aca tcc aac gtt ttc gat gcg gtg ggt gca Gly Gln Ala Leu Val Val Thr Ser Asn Val Phe Asp Ala Val Gly Ala 330 335 340			1123
tct gca gtg ctt ggt gag cat tcc att gat cgc cac tgg cgc aat gtg Ser Ala Val Leu Gly Glu His Ser Ile Asp Arg His Trp Arg Asn Val 345 350 355			1171
cgt acc gtg tcc tca aac aac ccg gtg ttc ctg gcc aag aat gca gtg Arg Thr Val Ser Ser Asn Asn Pro Val Phe Leu Ala Lys Asn Ala Val 360 365 370			1219
ggg gag tat gcc ctc aac ggc act cct gtg ggt acc aac att ggt aaa Gly Glu Tyr Ala Leu Asn Gly Thr Pro Val Gly Thr Asn Ile Gly Lys 375 380 385			1267
gca ctg agc cgt ccg gtg agc cta agc agc tagacgtgtg atttcgctgg Ala Leu Ser Arg Pro Val Ser Leu Ser Ser 390 395			1317
ttt			1320

<210> 160

<211> 399

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Ser Gln Glu Ile Leu Ser His Phe Ala Pro Ala Leu Glu Arg Ile
 1 5 10 15
 Arg Ser Gly Ala Val Glu Arg Glu Gln Gln Arg Ala Leu Pro Val Glu
 20 25 30
 Glu Ile Lys Glu Leu Val Glu Leu Gly Phe Thr Gly Leu Arg Val Pro
 35 40 45
 Glu Glu Leu Gly Gly Ala Gly Ala Ser Leu Glu Ser Val Val Glu Leu
 50 55 60
 Leu Ile Glu Ile Ala Gly Ala Asp Ser Asn Ile Ala Gln Ala Leu Arg
 65 70 75 80
 Gly His Phe Ala Phe Val Glu Leu Leu Leu Glu Ala Pro Glu Ser Glu
 85 90 95
 Phe Arg Thr His Trp Leu Arg Glu Val Ala Thr Gly Arg Leu Val Gly
 100 105 110
 Asn Ala Glu Ser Glu Lys Arg Gly Val Tyr Gly Asp Pro Gln Thr Phe
 115 120 125
 Ile Asp Glu Val Glu Thr Glu Asn Gly Pro Ile Phe Val Leu Asn Gly
 130 135 140
 Thr Lys Phe Tyr Thr Thr Gly Thr Tyr Phe Ala Asp Tyr Thr Trp Thr
 145 150 155 160
 Thr Ala Leu Leu Arg Asn Leu Asn Gly Gln Glu Thr Leu Val Ser Leu
 165 170 175
 Pro Val Asp Leu His Ala Pro Gly Val Asp Val Ala Asp Asp Trp Ser
 180 185 190
 Gly Phe Gly Gln Lys Leu Thr Ala Ser Gly Thr Thr Thr Phe Lys Asp
 195 200 205
 Leu Glu Val Asp Pro Arg Trp Ile Ile Pro Arg Thr Asp Ala Pro Thr
 210 215 220
 Leu Val Trp Thr Tyr Leu Gln Leu Ser Leu Leu Thr Val Leu Val Gly
 225 230 235 240
 Ser Ala Ala Ala Ala Val Asp Glu Val Val Ala Arg Ala Gln Ser Ser
 245 250 255
 Thr Arg Asn Ala Trp Asn Pro Gly Val Glu Arg Arg Ser Asp Pro Ala
 260 265 270
 Ala Thr Ile Ala Ile Gly Asp Ala Arg Ser Arg Val Thr Val Ile Arg
 275 280 285
 Gly Ala Leu Leu Asp Ala Thr Arg His Val Ser Asn Ala Ala Thr Ile
 290 295 300
 Val Thr Pro Glu Ala Phe Asn Glu Ala Asp Ala Ile Val Ala Ala Leu
 305 310 315 320

Trp Pro Ile Val Ser Gly Gln Ala Leu Val Val Thr Ser Asn Val Phe
 325 330 335

Asp Ala Val Gly Ala Ser Ala Val Leu Gly Glu His Ser Ile Asp Arg
 340 345 350

His Trp Arg Asn Val Arg Thr Val Ser Ser Asn Asn Pro Val Phe Leu
 355 360 365

Ala Lys Asn Ala Val Gly Glu Tyr Ala Leu Asn Gly Thr Pro Val Gly
 370 375 380

Thr Asn Ile Gly Lys Ala Leu Ser Arg Pro Val Ser Leu Ser Ser
 385 390 395

<210> 161

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> RXN00931

<400> 161

ccgtaacctta atcggtgaaa catcacctta ttgctgggct ttgcacgcta ctctttgtga 60

gtaacctcac cgaagtgcac aaattaattg ggagtgcata gtg aaa act att gaa 115
 Val Lys Thr Ile Glu
 1 5

gat att ttg acc ttg gaa gaa atc gac cgc gat att tac cgt ggt ccc 163
 Asp Ile Leu Thr Leu Glu Glu Ile Asp Arg Asp Ile Tyr Arg Gly Pro
 10 15 20

gtt atc gaa tct tat tta gcc agg act ttc ggt ggc cag gtc gct gcc 211
 Val Ile Glu Ser Tyr Leu Ala Arg Thr Phe Gly Gly Gln Val Ala Ala
 25 30 35

caa gct tta gta gca gca acg cat act gtt gat aaa gcc ttt act gtg 259
 Gln Ala Leu Val Ala Ala Thr His Thr Val Asp Lys Ala Phe Thr Val
 40 45 50

cat tct ttg cat ggc tac ttt ata gct cct ggt gat cca aca gca ccc 307
 His Ser Leu His Gly Tyr Phe Ile Ala Pro Gly Asp Pro Thr Ala Pro
 55 60 65

gca att tat tta gtg gat cga gtt cgc gac gga aaa agc tac gtc acc 355
 Ala Ile Tyr Leu Val Asp Arg Val Arg Asp Gly Lys Ser Tyr Val Thr
 70 75 80 85

cgc tcg gtg cgt ggc atc caa gac ggc gaa gta atc ttc agc atg cag 403
 Arg Ser Val Arg Gly Ile Gln Asp Gly Glu Val Ile Phe Ser Met Gln
 90 95 100

gcc agc ttt cat cgt ggg gat gaa ggc att gag cac atg gac aag atg 451
 Ala Ser Phe His Arg Gly Asp Glu Gly Ile Glu His Met Asp Lys Met
 105 110 115

cgt aaa gtt cca gct cct gat gag atc aag gga aca gta gaa cgt atg 499
 Arg Lys Val Pro Ala Pro Asp Glu Ile Lys Gly Thr Val Glu Arg Met
 120 125 130

ccg atc tca agt agg cga gtg ctt gat gaa tgg gcg gaa tgg gat atc 547
 Pro Ile Ser Ser Arg Arg Val Leu Asp Glu Trp Ala Glu Trp Asp Ile
 135 140 145

cgc gtt att ccg cag gat caa tta gaa ctc agc gat ttc acc gct act 595
 Arg Val Ile Pro Gln Asp Gln Leu Glu Leu Ser Asp Phe Thr Ala Thr
 150 155 160 165

gag caa gct gtg tgg att cgg tgc acc gct gat ctt ccg gat aat ccc 643
 Glu Gln Ala Val Trp Ile Arg Cys Thr Ala Asp Leu Pro Asp Asn Pro
 170 175 180

acc ttc cac cag tgc tca ctg act tat ctg tcc gat atg act ttg ctg 691
 Thr Phe His Gln Cys Ser Leu Thr Tyr Leu Ser Asp Met Thr Leu Leu
 185 190 195

cat agt gcc ctg gtg cca cac cca ggt gag aaa atg cag atg gcc tca 739
 His Ser Ala Leu Val Pro His Pro Gly Glu Lys Met Gln Met Ala Ser
 200 205 210

ctt gat cac gct gtg tgg ttc ctg cgt ccc ttc cgc gtc gat gaa tgg 787
 Leu Asp His Ala Val Trp Phe Leu Arg Pro Phe Arg Val Asp Glu Trp
 215 220 225

ttg ctt tat gat cag cgc tct cca tcg gcc tca agt ggg cga gcc ttg 835
 Leu Leu Tyr Asp Gln Arg Ser Pro Ser Ala Ser Ser Gly Arg Ala Leu
 230 235 240 245

act cac ggg cgg ctt ttc aac cag cag gga gat ttg gtc gct att gtc 883
 Thr His Gly Arg Leu Phe Asn Gln Gln Gly Asp Leu Val Ala Ile Val
 250 255 260

aat caa gag gga atg acc cgc aca ctc cac gag ggt gcg caa tca att 931
 Asn Gln Glu Gly Met Thr Arg Thr Leu His Glu Gly Ala Gln Ser Ile
 265 270 275

ccg atg cgc aaa gac taaaatgcag cgaacttgaa gat 969
 Pro Met Arg Lys Asp
 280

<210> 162

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Val Lys Thr Ile Glu Asp Ile Leu Thr Leu Glu Glu Ile Asp Arg Asp
 1 5 10 15

Ile Tyr Arg Gly Pro Val Ile Glu Ser Tyr Leu Ala Arg Thr Phe Gly
 20 25 30

Gly Gln Val Ala Ala Gln Ala Leu Val Ala Ala Thr His Thr Val Asp
 35 40 45

Lys Ala Phe Thr Val His Ser Leu His Gly Tyr Phe Ile Ala Pro Gly
 50 55 60
 Asp Pro Thr Ala Pro Ala Ile Tyr Leu Val Asp Arg Val Arg Asp Gly
 65 70 75 80
 Lys Ser Tyr Val Thr Arg Ser Val Arg Gly Ile Gln Asp Gly Glu Val
 85 90 95
 Ile Phe Ser Met Gln Ala Ser Phe His Arg Gly Asp Glu Gly Ile Glu
 100 105 110
 His Met Asp Lys Met Arg Lys Val Pro Ala Pro Asp Glu Ile Lys Gly
 115 120 125
 Thr Val Glu Arg Met Pro Ile Ser Ser Arg Arg Val Leu Asp Glu Trp
 130 135 140
 Ala Glu Trp Asp Ile Arg Val Ile Pro Gln Asp Gln Leu Glu Leu Ser
 145 150 155 160
 Asp Phe Thr Ala Thr Glu Gln Ala Val Trp Ile Arg Cys Thr Ala Asp
 165 170 175
 Leu Pro Asp Asn Pro Thr Phe His Gln Cys Ser Leu Thr Tyr Leu Ser
 180 185 190
 Asp Met Thr Leu Leu His Ser Ala Leu Val Pro His Pro Gly Glu Lys
 195 200 205
 Met Gln Met Ala Ser Leu Asp His Ala Val Trp Phe Leu Arg Pro Phe
 210 215 220
 Arg Val Asp Glu Trp Leu Leu Tyr Asp Gln Arg Ser Pro Ser Ala Ser
 225 230 235 240
 Ser Gly Arg Ala Leu Thr His Gly Arg Leu Phe Asn Gln Gln Gly Asp
 245 250 255
 Leu Val Ala Ile Val Asn Gln Glu Gly Met Thr Arg Thr Leu His Glu
 260 265 270
 Gly Ala Gln Ser Ile Pro Met Arg Lys Asp
 275 280

<210> 163

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> FRXA00931

<400> 163

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 gtaacctcac cgaagtgcata aaattaattg ggagtgatca gtg aaa act att gaa 115
 Val Lys Thr Ile Glu

	1	5	
gat att ttg acc ttg gaa gaa atc gac cgc gat att tac cgt ggt ccc			163
Asp Ile Leu Thr Leu Glu Glu Ile Asp Arg Asp Ile Tyr Arg Gly Pro	10	20	
ggt atc gaa tct tat tta gcc agg act ttc ggt ggc cag gtc gct gcc			211
Val Ile Glu Ser Tyr Leu Ala Arg Thr Phe Gly Gly Gln Val Ala Ala	25	35	
caa gct tta gta gca gca acg cat act gtt gat aaa gcc ttt act gtg			259
Gln Ala Leu Val Ala Ala Thr His Thr Val Asp Lys Ala Phe Thr Val	40	50	
cat tct ttg cat ggc tac ttt ata gct cct ggt gat cca aca gca ccc			307
His Ser Leu His Gly Tyr Phe Ile Ala Pro Gly Asp Pro Thr Ala Pro	55	65	
gca att tat tta gtg gat cga gtt cgc gac gga aaa agc tac gtc acc			355
Ala Ile Tyr Leu Val Asp Arg Val Arg Asp Gly Lys Ser Tyr Val Thr	70	85	
cgc tcg gtg cgt ggc atc caa gac ggc gaa gta atc ttc agc atg cag			403
Arg Ser Val Arg Gly Ile Gln Asp Gly Glu Val Ile Phe Ser Met Gln	90	100	
gcc agc ttt cat cgt ggg gat gaa ggc att gag cac atg gac aag atg			451
Ala Ser Phe His Arg Gly Asp Glu Gly Ile Glu His Met Asp Lys Met	105	115	
cgt aaa gtt cca gct cct gat gag atc aag gga aca gta gaa cgt atg			499
Arg Lys Val Pro Ala Pro Asp Glu Ile Lys Gly Thr Val Glu Arg Met	120	130	
ccg atc tca agt agg cga gtg ctt gat gaa tgg gcg gaa tgg gat atc			547
Pro Ile Ser Ser Arg Arg Val Leu Asp Glu Trp Ala Glu Trp Asp Ile	135	145	
cgc gtt att ccg cag gat caa tta gaa ctc agc gat ttc acc gct act			595
Arg Val Ile Pro Gln Asp Gln Leu Glu Leu Ser Asp Phe Thr Ala Thr	150	165	
gag caa gct gtg tgg att cgg tgc acc gct gat ctt ccg gat aat ccc			643
Glu Gln Ala Val Trp Ile Arg Cys Thr Ala Asp Leu Pro Asp Asn Pro	170	180	
acc ttc cac cag tgc tca ctg act tat ctg tcc gat atg act ttg ctg			691
Thr Phe His Gln Cys Ser Leu Thr Tyr Leu Ser Asp Met Thr Leu Leu	185	195	
cat agt gcc ctg gtg cca cac cca ggt gag aaa atg cag atg gcc tca			739
His Ser Ala Leu Val Pro His Pro Gly Glu Lys Met Gln Met Ala Ser	200	210	
ctt gat cac gct gtg tgg ttc ctg cgt ccc ttc cgc gtc gat gaa tgg			787
Leu Asp His Ala Val Trp Phe Leu Arg Pro Phe Arg Val Asp Glu Trp	215	225	
ttg ctt tat gat cag cgc tct cca tcg gcc tca agt ggg cga gcc ttg			835
Leu Leu Tyr Asp Gln Arg Ser Pro Ser Ala Ser Ser Gly Arg Ala Leu	230	245	

act cac ggg cgg ctt ttc aac cag cag gga gat ttg gtc gct att gtc 883
 Thr His Gly Arg Leu Phe Asn Gln Gln Gly Asp Leu Val Ala Ile Val
 250 255 260

aat caa gag gga atg acc cgc aca ctc cac gag ggt gcg caa tca att 931
 Asn Gln Glu Gly Met Thr Arg Thr Leu His Glu Gly Ala Gln Ser Ile
 265 270 275

ccg atg cgc aaa gac taaaatgcag cgaacttgaa gat 969
 Pro Met Arg Lys Asp
 280

<210> 164

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Val Lys Thr Ile Glu Asp Ile Leu Thr Leu Glu Glu Ile Asp Arg Asp
 1 5 10 15

Ile Tyr Arg Gly Pro Val Ile Glu Ser Tyr Leu Ala Arg Thr Phe Gly
 20 25 30

Gly Gln Val Ala Ala Gln Ala Leu Val Ala Ala Thr His Thr Val Asp
 35 40 45

Lys Ala Phe Thr Val His Ser Leu His Gly Tyr Phe Ile Ala Pro Gly
 50 55 60

Asp Pro Thr Ala Pro Ala Ile Tyr Leu Val Asp Arg Val Arg Asp Gly
 65 70 75 80

Lys Ser Tyr Val Thr Arg Ser Val Arg Gly Ile Gln Asp Gly Glu Val
 85 90 95

Ile Phe Ser Met Gln Ala Ser Phe His Arg Gly Asp Glu Gly Ile Glu
 100 105 110

His Met Asp Lys Met Arg Lys Val Pro Ala Pro Asp Glu Ile Lys Gly
 115 120 125

Thr Val Glu Arg Met Pro Ile Ser Ser Arg Arg Val Leu Asp Glu Trp
 130 135 140

Ala Glu Trp Asp Ile Arg Val Ile Pro Gln Asp Gln Leu Glu Leu Ser
 145 150 155 160

Asp Phe Thr Ala Thr Glu Gln Ala Val Trp Ile Arg Cys Thr Ala Asp
 165 170 175

Leu Pro Asp Asn Pro Thr Phe His Gln Cys Ser Leu Thr Tyr Leu Ser
 180 185 190

Asp Met Thr Leu Leu His Ser Ala Leu Val Pro His Pro Gly Glu Lys
 195 200 205

Met Gln Met Ala Ser Leu Asp His Ala Val Trp Phe Leu Arg Pro Phe
 210 215 220

Arg Val Asp Glu Trp Leu Leu Tyr Asp Gln Arg Ser Pro Ser Ala Ser
 225 230 235 240

Ser Gly Arg Ala Leu Thr His Gly Arg Leu Phe Asn Gln Gln Gly Asp
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Leu Val Ala Ile Val Asn Gln Glu Gly Met Thr Arg Thr Leu His Glu
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Gly Ala Gln Ser Ile Pro Met Arg Lys Asp
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 Met Thr Ser Lys Ser
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att agc ggc aag cgc ccg aat ctg ccg tcg ctc act gga gcg cgg tgg 163
 Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu Thr Gly Ala Arg Trp
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ctc gcg gcg ctc gct gtt tat ttt ttg cat gcg ttg gtg ttt ttg tcg 211
 Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala Leu Val Phe Leu Ser
 25 30 35

gtg tat ccg ttc cag cag tcg gaa ctg ttt gcc aca atc cat aaa ttt 259
 Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala Thr Ile His Lys Phe
 40 45 50

gtc ccc atg cag ctg ggt tca gct ggt gta acc ttc ttc ttt atc ttg 307
 Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr Phe Phe Phe Ile Leu
 55 60 65

tcc gga ttt ttg atc tat tgg tca aat agc cag ctc aag ggc atg aag 355
 Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln Leu Lys Gly Met Lys
 70 75 80 85

aat gtg ctg tat tac tgc aag cgc cgc atc acc aag att tat ccc atg 403
 Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr Lys Ile Tyr Pro Met
 90 95 100

cac ttg att gcg ttg ccg atg ttt att gag gcg tcg gcg aag ttc acg 451
 His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala Ser Ala Lys Phe Thr
 105 110 115

act aca ggc att acc tgg gtg ctg att ttg cgc gag taaagctgtg 497
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120

125

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510

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<213> Corynebacterium glutamicum

<400> 166

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Thr Gly Ala Arg Trp Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala
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Leu Val Phe Leu Ser Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala
 35 40 45

Thr Ile His Lys Phe Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr
 50 55 60

Phe Phe Phe Ile Leu Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln
 65 70 75 80

Leu Lys Gly Met Lys Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr
 85 90 95

Lys Ile Tyr Pro Met His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala
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Ser Ala Lys Phe Thr Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg
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Glu

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 Met Asn Val Asp Ile
 1 5

tca cga tcc aga gag ccg cta aac gtt gag ctc ctg aag gaa aaa ttg 163
 Ser Arg Ser Arg Glu Pro Leu Asn Val Glu Leu Leu Lys Glu Lys Leu
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ctc caa aac ggt gac ttt ggc cag gtc att tac gaa aaa gtg aca ggc 211

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Ser	Thr	Asn	Ala	Asp	Leu	Leu	Ala	Leu	Ala	Gly	Ser	Gly	Ala	Pro	Asn		
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Trp	Thr	Val	Lys	Thr	Val	Glu	Phe	Gln	Asp	His	Ala	Arg	Gly	Arg	Leu		
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ggc	cgc	ccg	tgg	tct	gcc	cct	gag	ggt	tcc	caa	aca	atc	gtg	tct	gtg	355	
Gly	Arg	Pro	Trp	Ser	Ala	Pro	Glu	Gly	Ser	Gln	Thr	Ile	Val	Ser	Val		
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Leu	Val	Gln	Leu	Ser	Ile	Asp	Gln	Val	Asp	Arg	Ile	Gly	Thr	Ile	Pro		
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gaa	ggt	gcc	gga	ctg	aaa	tgg	ccc	aac	gat	ggt	caa	atc	cac	ggc	aag	499	
Glu	Gly	Ala	Gly	Leu	Lys	Trp	Pro	Asn	Asp	Val	Gln	Ile	His	Gly	Lys		
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Lys	Leu	Cys	Gly	Ile	Leu	Val	Glu	Ala	Thr	Gly	Phe	Asp	Ser	Thr	Pro		
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Thr	Val	Val	Ile	Gly	Trp	Gly	Thr	Asn	Ile	Ser	Leu	Thr	Lys	Glu	Glu		
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ctt	cct	ggt	cct	cat	gca	act	tcc	ctc	gca	ttg	gaa	ggt	ggt	gaa	gtc	643	
Leu	Pro	Val	Pro	His	Ala	Thr	Ser	Leu	Ala	Leu	Glu	Gly	Val	Glu	Val		
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gac	aga	acc	aca	ttc	ctt	att	aat	atg	ctc	aca	cat	ctg	cat	act	cga	691	
Asp	Arg	Thr	Thr	Phe	Leu	Ile	Asn	Met	Leu	Thr	His	Leu	His	Thr	Arg		
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Leu	Asp	Gln	Trp	Gln	Gly	Pro	Ser	Val	Asp	Trp	Leu	Asp	Asp	Tyr	Arg		
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gcg	gta	tgt	tcc	agt	att	ggc	caa	gat	ggt	cga	gtg	ctt	cta	cct	ggg	787	
Ala	Val	Cys	Ser	Ser	Ile	Gly	Gln	Asp	Val	Arg	Val	Leu	Leu	Pro	Gly		
		215				220					225						
gat	aaa	gaa	ctc	tta	ggt	gaa	gcg	atc	ggt	gtc	gcg	act	ggc	gga	gaa	835	
Asp	Lys	Glu	Leu	Leu	Gly	Glu	Ala	Ile	Gly	Val	Ala	Thr	Gly	Gly	Glu		
		230			235					240					245		
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Ile	Arg	Val	Arg	Asp	Ala	Ser	Gly	Thr	Val	His	Thr	Leu	Asn	Ala	Gly		
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gaa	att	acg	cac	ctt	cgc	ctg	cag	taaggtgacg	gtatgggggaa	ttc						930	
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265

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<400> 168

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Glu Lys Val Thr Gly Ser Thr Asn Ala Asp Leu Leu Ala Leu Ala Gly
 35 40 45

Ser Gly Ala Pro Asn Trp Thr Val Lys Thr Val Glu Phe Gln Asp His
 50 55 60

Ala Arg Gly Arg Leu Gly Arg Pro Trp Ser Ala Pro Glu Gly Ser Gln
 65 70 75 80

Thr Ile Val Ser Val Leu Val Gln Leu Ser Ile Asp Gln Val Asp Arg
 85 90 95

Ile Gly Thr Ile Pro Leu Ala Ala Gly Leu Ala Val Met Asp Ala Leu
 100 105 110

Asn Asp Leu Gly Val Glu Gly Ala Gly Leu Lys Trp Pro Asn Asp Val
 115 120 125

Gln Ile His Gly Lys Lys Leu Cys Gly Ile Leu Val Glu Ala Thr Gly
 130 135 140

Phe Asp Ser Thr Pro Thr Val Val Ile Gly Trp Gly Thr Asn Ile Ser
 145 150 155 160

Leu Thr Lys Glu Glu Leu Pro Val Pro His Ala Thr Ser Leu Ala Leu
 165 170 175

Glu Gly Val Glu Val Asp Arg Thr Thr Phe Leu Ile Asn Met Leu Thr
 180 185 190

His Leu His Thr Arg Leu Asp Gln Trp Gln Gly Pro Ser Val Asp Trp
 195 200 205

Leu Asp Asp Tyr Arg Ala Val Cys Ser Ser Ile Gly Gln Asp Val Arg
 210 215 220

Val Leu Leu Pro Gly Asp Lys Glu Leu Leu Gly Glu Ala Ile Gly Val
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Ala Thr Gly Gly Glu Ile Arg Val Arg Asp Ala Ser Gly Thr Val His
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Thr Leu Asn Ala Gly Glu Ile Thr His Leu Arg Leu Gln
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 <223> RXN00563

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 Trp Ile Val Ala Ala Asn Leu Ser Ser Tyr Ser Asp Ile Asp Ala Ile
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 atc aac tgg gtc gga tcc gag cag acc acc acc gtc aac ggc gca tcc 144
 Ile Asn Trp Val Gly Ser Glu Gln Thr Thr Thr Val Asn Gly Ala Ser
 35 40 45
 aag ctg gtc aag cca gct ttg gtc cct acc ttg ctg ttc cca ttc gcg 192
 Lys Leu Val Lys Pro Ala Leu Val Pro Thr Leu Leu Phe Pro Phe Ala
 50 55 60
 gca cct cgc gtg tcc gga tcc atg gca gat gca ggc cca cag gca gaa 240
 Ala Pro Arg Val Ser Gly Ser Met Ala Asp Ala Gly Pro Gln Ala Glu
 65 70 75 80
 tcc cag atg cga ctt ctg ctc tgg tct gtt gag cgc ctc atc gca ggt 288
 Ser Gln Met Arg Leu Leu Leu Trp Ser Val Glu Arg Leu Ile Ala Gly
 85 90 95
 ctt gcg cca ttg ggc tcc tcc atc aac gtg ggt cac cgc ctg cac gtg 336
 Leu Ala Pro Leu Gly Ser Ser Ile Asn Val Gly His Arg Leu His Val
 100 105 110
 gtc atc cca ggt tca cca aac cgt gga cgc ttc ggt ggc gat ggt gca 384
 Val Ile Pro Gly Ser Pro Asn Arg Gly Arg Phe Gly Gly Asp Gly Ala
 115 120 125
 tac ggt gaa tcc aag gca gct ctc gac gcc gtg gtt acc cgt tgg aac 432
 Tyr Gly Glu Ser Lys Ala Ala Leu Asp Ala Val Val Thr Arg Trp Asn
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 gca gag caa gct gca tgg gga gca cac acc tcc ctc gtg cac gct cac 480
 Ala Glu Gln Ala Ala Trp Gly Ala His Thr Ser Leu Val His Ala His
 145 150 155 160
 atc ggt tgg gtt cgc ggc acc ggc ctc atg ggc ggc aac gat cct ttg 528
 Ile Gly Trp Val Arg Gly Thr Gly Leu Met Gly Gly Asn Asp Pro Leu
 165 170 175
 gtc aag gca gct gaa gaa gca ggc gtg gaa acc tac tcc acc caa gaa 576
 Val Lys Ala Ala Glu Glu Ala Gly Val Glu Thr Tyr Ser Thr Gln Glu
 180 185 190
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 Ile Ala Glu Lys Leu Leu Ser Gln Ala Thr Ser Thr Val Arg Glu Gln

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Ser	Asp	Leu	Asn	Leu	Ala	Glu	Met	Ala	Arg	Ala	Glu	Ala	Ala	Lys	Ala	
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Ala	Asn	Ala	Pro	Val	Val	Glu	Ala	Pro	Arg	Thr	Val	Ala	Ala	Leu	Pro	
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Thr	Pro	Tyr	Arg	Pro	Val	Val	Gln	Thr	Thr	Pro	Asp	Phe	Ala	Gly	Gln	
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Val	Thr	Gln	Asn	Leu	Asp	Glu	Met	Val	Val	Ile	Val	Gly	Ala	Gly	Glu	
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Leu	Gly	Pro	Leu	Gly	Ser	Ala	Arg	Thr	Arg	Phe	Asp	Ala	Glu	Leu	Asn	
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Gly	Ser	Leu	Ser	Ala	Ala	Gly	Val	Ile	Glu	Leu	Ala	Trp	Thr	Met	Gly	
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ctt	atc	cac	tgg	gat	gaa	gat	cca	aag	cca	ggc	tgg	tac	gac	gac	tcc	1008
Leu	Ile	His	Trp	Asp	Glu	Asp	Pro	Lys	Pro	Gly	Trp	Tyr	Asp	Asp	Ser	
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gac	gac	gca	gtg	gcc	gaa	gaa	gac	atc	ttc	gac	cgc	tac	cac	gac	gaa	1056
Asp	Asp	Ala	Val	Ala	Glu	Glu	Asp	Ile	Phe	Asp	Arg	Tyr	His	Asp	Glu	
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gtc	atg	gca	cgc	gtt	ggt	gtc	cgc	aag	tac	aat	gac	atg	cct	gag	tac	1104
Val	Met	Ala	Arg	Val	Gly	Val	Arg	Lys	Tyr	Asn	Asp	Met	Pro	Glu	Tyr	
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ggc	atg	atc	gac	aac	ttt	gca	cca	gag	ctg	acc	acc	gtc	tac	ctc	gac	1152
Gly	Met	Ile	Asp	Asn	Phe	Ala	Pro	Glu	Leu	Thr	Thr	Val	Tyr	Leu	Asp	
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cag	gac	ctc	acc	ttc	aac	gtg	gga	tcc	cgc	gaa	gag	gca	ctg	acc	tac	1200
Gln	Asp	Leu	Thr	Phe	Asn	Val	Gly	Ser	Arg	Glu	Glu	Ala	Leu	Thr	Tyr	
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gtc	gac	tcc	gag	cca	gaa	ctc	acc	ttt	gct	tct	ttc	gac	gaa	gca	gca	1248
Val	Asp	Ser	Glu	Pro	Glu	Leu	Thr	Phe	Ala	Ser	Phe	Asp	Glu	Ala	Ala	
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ggg	gag	tgg	aag	gtc	act	cgc	aag	gca	ggc	tcc	gca	atc	cgc	gta	cct	1296
Gly	Glu	Trp	Lys	Val	Thr	Arg	Lys	Ala	Gly	Ser	Ala	Ile	Arg	Val	Pro	
			420					425					430			
cgc	cgc	atg	gcg	atg	acc	cgc	ttc	gtt	ggt	gga	cag	gtt	cct	aag	gac	1344
Arg	Arg	Met	Ala	Met	Thr	Arg	Phe	Val	Gly	Gly	Gln	Val	Pro	Lys	Asp	
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Phe Asp Pro Ala Val Trp Gly Ile Pro Ala Asp Met Val Asp Asn Leu	
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Asp Thr Val Ala Leu Trp Asn Ile Val Cys Thr Val Asp Ala Phe Leu	
465 470 475 480	
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Ser Ala Gly Phe Thr Pro Ala Glu Leu Leu Ala Ser Val His Pro Ala	
485 490 495	
cgc gtg tcc tct acc caa ggc acc ggc atg ggc ggc atg gaa tcc ctc	1536
Arg Val Ser Ser Thr Gln Gly Thr Gly Met Gly Gly Met Glu Ser Leu	
500 505 510	
cgt ggc atc tac gtc gac cgc att ctg gca gag cca cgc gcc aac gac	1584
Arg Gly Ile Tyr Val Asp Arg Ile Leu Ala Glu Pro Arg Ala Asn Asp	
515 520 525	
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Val Leu Gln Glu Ala Leu Pro Asn Val Val Ala Ala His Val Met Gln	
530 535 540	
tcc tac gtc ggt ggc tac gga cag atg atc cac cca gtc gca gct tgt	1680
Ser Tyr Val Gly Gly Tyr Gly Gln Met Ile His Pro Val Ala Ala Cys	
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Ala Thr Ala Ala Val Ser Val Glu Glu Ala Leu Asp Lys Ile Arg Ile	
565 570 575	
ggc aag tcc gac ttc gtt gtc gca ggt ggc ttc gat gcc ctg tcc gtt	1776
Gly Lys Ser Asp Phe Val Val Ala Gly Gly Phe Asp Ala Leu Ser Val	
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Glu Gly Ile Thr Gly Phe Gly Asp Met Ala Ala Thr Ala Asp Ser Ala	
595 600 605	
gag atg gaa ggc aag gga att gag cac cgc ttc ttc tcc cgc gcc aac	1872
Glu Met Glu Gly Lys Gly Ile Glu His Arg Phe Phe Ser Arg Ala Asn	
610 615 620	
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Asp Arg Arg Arg Gly Gly Phe Ile Glu Ser Glu Gly Gly Gly Thr Val	
625 630 635 640	
ctt ctg gca cgc gga tca ctc gca gct gac ctg ggc ctt cca gta ctc	1968
Leu Leu Ala Arg Gly Ser Leu Ala Ala Asp Leu Gly Leu Pro Val Leu	
645 650 655	
ggt gtc atc gga ttc gca gag tcc ttt gca gat ggt gcc cac acc tcc	2016
Gly Val Ile Gly Phe Ala Glu Ser Phe Ala Asp Gly Ala His Thr Ser	
660 665 670	
atc cca gcc cca ggc ctc ggt gcc ctt ggt gct gct cgc gat ggt gtg	2064
Ile Pro Ala Pro Gly Leu Gly Ala Leu Gly Ala Ala Arg Asp Gly Val	
675 680 685	

gaa tct cgc ctt gca gta gca ctg cgt tcc gtc ggt gtc tct gct gat	2112
Glu Ser Arg Leu Ala Val Ala Leu Arg Ser Val Gly Val Ser Ala Asp	
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Glu Ile Ser Ile Ile Ser Lys His Asp Thr Ser Thr Asn Ala Asn Asp	
705 710 715 720	
cca aac gag tcc gac ctg cac gag cgc atc gca tcc gct atc ggt cgt	2208
Pro Asn Glu Ser Asp Leu His Glu Arg Ile Ala Ser Ala Ile Gly Arg	
725 730 735	
gca gac ggc aac ccg atg tac gtg att tcc cag aag tca ctc acc gga	2256
Ala Asp Gly Asn Pro Met Tyr Val Ile Ser Gln Lys Ser Leu Thr Gly	
740 745 750	
cac gcc aag ggt ggt gca gca gca ttc cag atg atc ggt ctc acc cag	2304
His Ala Lys Gly Gly Ala Ala Ala Phe Gln Met Ile Gly Leu Thr Gln	
755 760 765	
gtc ctc cga tcc gga ctg gtg cca gcc aac cgc gca ctc gac tgc gtt	2352
Val Leu Arg Ser Gly Leu Val Pro Ala Asn Arg Ala Leu Asp Cys Val	
770 775 780	
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Asp Pro Val Leu Ser Lys His Ser His Leu Val Trp Leu Arg Lys Pro	
785 790 795 800	
cta gac ctt cgt gcg aag gca cca aag gca ggt ctt gtt acc tcc ctt	2448
Leu Asp Leu Arg Ala Lys Ala Pro Lys Ala Gly Leu Val Thr Ser Leu	
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ggc ttc gga cac gtc tcc gct ctg gtt gcg att gtt cac cca gac gcc	2496
Gly Phe Gly His Val Ser Ala Leu Val Ala Ile Val His Pro Asp Ala	
820 825 830	
ttc tat gag gca gtt cgt gtg gca cgt ggt gct gag gca gct gac gta	2544
Phe Tyr Glu Ala Val Arg Val Ala Arg Gly Ala Glu Ala Ala Asp Val	
835 840 845	
tgg cgc gca tcc gcg atc gct cgc gaa gaa gca ggc ctt cgt acc atc	2592
Trp Arg Ala Ser Ala Ile Ala Arg Glu Glu Ala Gly Leu Arg Thr Ile	
850 855 860	
gtc gcc ggt atg cac ggt ggc gta ctg tac gaa cgc cca gtc gag cgc	2640
Val Ala Gly Met His Gly Gly Val Leu Tyr Glu Arg Pro Val Glu Arg	
865 870 875 880	
aac ctc ggt gtc cac gga gac gca gct aag gaa gtt gaa gct gca gtc	2688
Asn Leu Gly Val His Gly Asp Ala Ala Lys Glu Val Glu Ala Ala Val	
885 890 895	
ctc ctg gat tcc cgc gcc cgc cta gtt gac ggt gtc ctc cgc gcc gaa	2736
Leu Leu Asp Ser Arg Ala Arg Leu Val Asp Gly Val Leu Arg Ala Glu	
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ggc tagttggtta ttgcgttgag ccc	2762
Gly	

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 <213> Corynebacterium glutamicum

<400> 170

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Ile	Asn	Trp	Val	Gly	Ser	Glu	Gln	Thr	Thr	Thr	Val	Asn	Gly	Ala	Ser
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Ala	Pro	Arg	Val	Ser	Gly	Ser	Met	Ala	Asp	Ala	Gly	Pro	Gln	Ala	Glu
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Ser	Gln	Met	Arg	Leu	Leu	Leu	Trp	Ser	Val	Glu	Arg	Leu	Ile	Ala	Gly
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Gln Ala Ser Ala Trp Gln Gln Val Ile Ala Asp Ser Ser Glu Asp His
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 Asp Glu Pro Ala Arg Lys Val Leu Ile Asp Glu Ile Lys Thr Arg Glu
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 atc aac atc atc att aac tct gct ggc atc gca agc ttt ggg ccg ttc 403
 Ile Asn Ile Ile Ile Asn Ser Ala Gly Ile Ala Ser Phe Gly Pro Phe
 90 95 100
 aag gac cag gat tgg tct tat gag act gcc cag ttc tca ctt aat gcc 451
 Lys Asp Gln Asp Trp Ser Tyr Glu Thr Ala Gln Phe Ser Leu Asn Ala
 105 110 115
 aca gcc gtt ttt gag ctc acc cac gcg gtg ttg ggt ggc atg att gac 499
 Thr Ala Val Phe Glu Leu Thr His Ala Val Leu Gly Gly Met Ile Asp
 120 125 130
 cgt ggc acg ggc gct att tgc aat gtg gga tct gcg gct ggc aat gtg 547
 Arg Gly Thr Gly Ala Ile Cys Asn Val Gly Ser Ala Ala Gly Asn Val
 135 140 145

cca atc ccc aac aac gcc acg tat gtg ctc acc aag gct ggc gtg aac 595
 Pro Ile Pro Asn Asn Ala Thr Tyr Val Leu Thr Lys Ala Gly Val Asn
 150 155 160 165
 gcg ttc acc gag gca atg cat tat gag ctg cgc gga act ggt gtg gcg 643
 Ala Phe Thr Glu Ala Met His Tyr Glu Leu Arg Gly Thr Gly Val Ala
 170 175 180
 tgt act ttg ctc gca ccg gga cct gtc cgt gag gcg gag atc cct gag 691
 Cys Thr Leu Leu Ala Pro Gly Pro Val Arg Glu Ala Glu Ile Pro Glu
 185 190 195
 tct gag aag tcg atc gtg gac aag gtt gtc cct gat ttc ttg tgg acc 739
 Ser Glu Lys Ser Ile Val Asp Lys Val Val Pro Asp Phe Leu Trp Thr
 200 205 210
 acc tat gag tcc tgc tcc gca gag acc ttg cgt gcg ctg tct aag aat 787
 Thr Tyr Glu Ser Cys Ser Ala Glu Thr Leu Arg Ala Leu Ser Lys Asn
 215 220 225
 cag cgt cgc gtt gtt cca ggt ccg ctg tcc aag gcc atg aat ttt gtg 835
 Gln Arg Arg Val Val Pro Gly Pro Leu Ser Lys Ala Met Asn Phe Val
 230 235 240 245
 tcc tct gtt gct cca acc gct gtg ctc tcc cct gtt atg ggc tgg gtt 883
 Ser Ser Val Ala Pro Thr Ala Val Leu Ser Pro Val Met Gly Trp Val
 250 255 260
 tat aag aag atg ggt tagtttttaa aagtgtctga atc 921
 Tyr Lys Lys Met Gly
 265

<210> 174

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Met Ala Leu Pro Leu Pro Ser Lys Ser Ala Arg Ala Leu Val Thr Gly
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 Ala Ser Gln Gly Ile Gly Leu Ala Ile Ala Lys Asp Leu Ala Arg Tyr
 20 25 30
 Gly His Asn Leu Ile Leu Val Ala Arg Arg Glu Asp Val Leu Lys Glu
 35 40 45
 Ile Ala Ala Asp Leu Glu Lys Lys His Gly Val Ile Val Glu Val Arg
 50 55 60
 Pro Val Asp Leu Ser Asp Glu Pro Ala Arg Lys Val Leu Ile Asp Glu
 65 70 75 80
 Ile Lys Thr Arg Glu Ile Asn Ile Ile Ile Asn Ser Ala Gly Ile Ala
 85 90 95
 Ser Phe Gly Pro Phe Lys Asp Gln Asp Trp Ser Tyr Glu Thr Ala Gln
 100 105 110

Phe Ser Leu Asn Ala Thr Ala Val Phe Glu Leu Thr His Ala Val Leu
 115 120 125
 Gly Gly Met Ile Asp Arg Gly Thr Gly Ala Ile Cys Asn Val Gly Ser
 130 135 140
 Ala Ala Gly Asn Val Pro Ile Pro Asn Asn Ala Thr Tyr Val Leu Thr
 145 150 155 160
 Lys Ala Gly Val Asn Ala Phe Thr Glu Ala Met His Tyr Glu Leu Arg
 165 170 175
 Gly Thr Gly Val Ala Cys Thr Leu Leu Ala Pro Gly Pro Val Arg Glu
 180 185 190
 Ala Glu Ile Pro Glu Ser Glu Lys Ser Ile Val Asp Lys Val Val Pro
 195 200 205
 Asp Phe Leu Trp Thr Thr Tyr Glu Ser Cys Ser Ala Glu Thr Leu Arg
 210 215 220
 Ala Leu Ser Lys Asn Gln Arg Arg Val Val Pro Gly Pro Leu Ser Lys
 225 230 235 240
 Ala Met Asn Phe Val Ser Ser Val Ala Pro Thr Ala Val Leu Ser Pro
 245 250 255
 Val Met Gly Trp Val Tyr Lys Lys Met Gly
 260 265

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 <211> 1293
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1270)
 <223> RXN02062

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 Met Arg Val Gly Met
 1 5
 atg aca aga gag tat cca cca gag gtt tac ggc ggc gct ggc gtg cac 163
 Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly Gly Ala Gly Val His
 10 15 20
 gtc acc gaa ttg acc cga ttc atg cgt gag atc gct gaa gtt gat gtt 211
 Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile Ala Glu Val Asp Val
 25 30 35
 cac tgc atg ggt gca cct cgc gat atg gag gga gtt ttc gtc cac ggc 259
 His Cys Met Gly Ala Pro Arg Asp Met Glu Gly Val Phe Val His Gly
 40 45 50
 gtc gat cct gcc ttg gaa agc gcg aac cct gcg att aag aca ctg tcc 307

Val	Asp	Pro	Ala	Leu	Glu	Ser	Ala	Asn	Pro	Ala	Ile	Lys	Thr	Leu	Ser		
55						60					65						
acc	ggt	tta	cgc	atg	gca	gaa	gct	gca	aac	aac	gtg	gat	gtc	gtg	cac	355	
Thr	Gly	Leu	Arg	Met	Ala	Glu	Ala	Ala	Asn	Asn	Val	Asp	Val	Val	His		
70					75				80						85		
tca	cac	act	tgg	tat	gca	ggt	ctt	ggc	ggc	cac	ctt	gca	gct	cgt	ctc	403	
Ser	His	Thr	Trp	Tyr	Ala	Gly	Leu	Gly	Gly	His	Leu	Ala	Ala	Arg	Leu		
				90				95						100			
cac	ggc	att	cct	cac	gtg	gct	acc	gcg	cac	tct	ttg	gag	cca	gat	cgc	451	
His	Gly	Ile	Pro	His	Val	Ala	Thr	Ala	His	Ser	Leu	Glu	Pro	Asp	Arg		
			105					110						115			
cca	tgg	aag	cgt	gag	cag	ctt	ggc	ggt	gga	tac	gac	gtg	tcc	tcc	tgg	499	
Pro	Trp	Lys	Arg	Glu	Gln	Leu	Gly	Gly	Gly	Tyr	Asp	Val	Ser	Ser	Trp		
			120				125						130				
tct	gaa	aaa	aat	gcc	atg	gaa	tac	gct	gac	gcg	gtc	atc	gct	gtg	tcg	547	
Ser	Glu	Lys	Asn	Ala	Met	Glu	Tyr	Ala	Asp	Ala	Val	Ile	Ala	Val	Ser		
	135					140					145						
gct	cgc	atg	aaa	gat	tcc	atc	ctc	gct	gcg	tac	cct	cgc	atc	gag	ccg	595	
Ala	Arg	Met	Lys	Asp	Ser	Ile	Leu	Ala	Ala	Tyr	Pro	Arg	Ile	Glu	Pro		
150					155					160					165		
gac	aac	gtg	cgt	ggt	gtc	ctc	aac	ggc	atc	gac	act	gag	ttg	tgg	cag	643	
Asp	Asn	Val	Arg	Val	Val	Leu	Asn	Gly	Ile	Asp	Thr	Glu	Leu	Trp	Gln		
				170				175						180			
cct	cgc	ccg	act	ttc	gat	gac	gcg	gaa	gat	tcc	gta	ctc	cgc	tcc	cta	691	
Pro	Arg	Pro	Thr	Phe	Asp	Asp	Ala	Glu	Asp	Ser	Val	Leu	Arg	Ser	Leu		
			185					190						195			
ggc	ggt	gac	cca	cag	cgg	ccc	atc	gtc	gca	ttt	gtc	ggc	cgc	atc	acc	739	
Gly	Val	Asp	Pro	Gln	Arg	Pro	Ile	Val	Ala	Phe	Val	Gly	Arg	Ile	Thr		
		200					205					210					
cgc	caa	aaa	ggc	gtc	gag	cac	ctc	atc	aag	gca	gca	gcg	ctt	ttc	gac	787	
Arg	Gln	Lys	Gly	Val	Glu	His	Leu	Ile	Lys	Ala	Ala	Ala	Leu	Phe	Asp		
		215				220					225						
gag	tcc	gtg	cag	ctt	gtg	ctc	tgt	gcc	ggc	gcg	cca	gac	acc	ccc	gaa	835	
Glu	Ser	Val	Gln	Leu	Val	Leu	Cys	Ala	Gly	Ala	Pro	Asp	Thr	Pro	Glu		
230					235					240					245		
atc	gca	gct	cgc	acc	acc	gcc	ctg	gtg	gaa	gaa	ctc	cag	gca	aag	cgc	883	
Ile	Ala	Ala	Arg	Thr	Thr	Ala	Leu	Val	Glu	Glu	Leu	Gln	Ala	Lys	Arg		
				250				255						260			
gaa	ggc	att	ttc	tgg	ggt	cag	gac	atg	ctg	ggc	aag	gac	aaa	atc	caa	931	
Glu	Gly	Ile	Phe	Trp	Val	Gln	Asp	Met	Leu	Gly	Lys	Asp	Lys	Ile	Gln		
			265					270					275				
gag	att	ctc	acc	gct	gct	gac	acc	ttc	gtg	tgc	cca	tcc	att	tac	gag	979	
Glu	Ile	Leu	Thr	Ala	Ala	Asp	Thr	Phe	Val	Cys	Pro	Ser	Ile	Tyr	Glu		
		280					285					290					
cca	ctg	ggc	atc	gtg	aac	ttg	gaa	gca	atg	gcc	tgc	aac	acc	gca	gtt	1027	
Pro	Leu	Gly	Ile	Val	Asn	Leu	Glu	Ala	Met	Ala	Cys	Asn	Thr	Ala	Val		

295 300 305

gtc gca tcc gac gtt gga ggc atc cct gag gtt gtt gtc gac ggc acc 1075
 Val Ala Ser Asp Val Gly Gly Ile Pro Glu Val Val Val Asp Gly Thr
 310 315 320 325

acc ggc gcc ctc gtt cac tac gac gaa aat gat gtc gaa acc ttc gag 1123
 Thr Gly Ala Leu Val His Tyr Asp Glu Asn Asp Val Glu Thr Phe Glu
 330 335 340

cgc gat atc gcc gaa gcg gtg aat aaa atg gtc gct gat cga gag acc 1171
 Arg Asp Ile Ala Glu Ala Val Asn Lys Met Val Ala Asp Arg Glu Thr
 345 350 355

gca gcc aaa ttt ggt ctc gca ggg cgc gaa cgt gct atc aat gat ttc 1219
 Ala Ala Lys Phe Gly Leu Ala Gly Arg Glu Arg Ala Ile Asn Asp Phe
 360 365 370

tcc tgg gca acg att gct cag cag acc att gat gtg tac aaa tcc ttg 1267
 Ser Trp Ala Thr Ile Ala Gln Gln Thr Ile Asp Val Tyr Lys Ser Leu
 375 380 385

atg taaaaccgaa agccgggggaa cct 1293
 Met
 390

<210> 176
 <211> 390
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 176
 Met Arg Val Gly Met Met Thr Arg Glu Tyr Pro Pro Glu Val Tyr Gly
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Gly Ala Gly Val His Val Thr Glu Leu Thr Arg Phe Met Arg Glu Ile
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Ala Glu Val Asp Val His Cys Met Gly Ala Pro Arg Asp Met Glu Gly
 35 40 45

Val Phe Val His Gly Val Asp Pro Ala Leu Glu Ser Ala Asn Pro Ala
 50 55 60

Ile Lys Thr Leu Ser Thr Gly Leu Arg Met Ala Glu Ala Ala Asn Asn
 65 70 75 80

Val Asp Val Val His Ser His Thr Trp Tyr Ala Gly Leu Gly Gly His
 85 90 95

Leu Ala Ala Arg Leu His Gly Ile Pro His Val Ala Thr Ala His Ser
 100 105 110

Leu Glu Pro Asp Arg Pro Trp Lys Arg Glu Gln Leu Gly Gly Gly Tyr
 115 120 125

Asp Val Ser Ser Trp Ser Glu Lys Asn Ala Met Glu Tyr Ala Asp Ala
 130 135 140

Val Ile Ala Val Ser Ala Arg Met Lys Asp Ser Ile Leu Ala Ala Tyr

145	150	155	160
Pro Arg Ile Glu	Pro Asp Asn Val Arg	Val Val Leu Asn Gly Ile Asp	
	165	170	175
Thr Glu Leu Trp	Gln Pro Arg Pro Thr Phe Asp Asp	Ala Glu Asp Ser	
	180	185	190
Val Leu Arg Ser	Leu Gly Val Asp Pro Gln Arg Pro	Ile Val Ala Phe	
	195	200	205
Val Gly Arg Ile	Thr Arg Gln Lys Gly Val Glu His	Leu Ile Lys Ala	
	210	215	220
Ala Ala Leu Phe	Asp Glu Ser Val Gln Leu Val Leu Cys	Ala Gly Ala	
	225	230	235
Pro Asp Thr Pro	Glu Ile Ala Ala Arg Thr Thr	Ala Leu Val Glu Glu	
	245	250	255
Leu Gln Ala Lys	Arg Glu Gly Ile Phe Trp Val Gln Asp	Met Leu Gly	
	260	265	270
Lys Asp Lys Ile	Gln Glu Ile Leu Thr Ala Ala Asp	Thr Phe Val Cys	
	275	280	285
Pro Ser Ile Tyr	Glu Pro Leu Gly Ile Val Asn	Leu Glu Ala Met Ala	
	290	295	300
Cys Asn Thr Ala	Val Val Ala Ser Asp Val Gly Gly	Ile Pro Glu Val	
	305	310	315
Val Val Asp Gly	Thr Thr Gly Ala Leu Val His Tyr Asp	Glu Asn Asp	
	325	330	335
Val Glu Thr Phe	Glu Arg Asp Ile Ala Glu Ala Val Asn	Lys Met Val	
	340	345	350
Ala Asp Arg Glu	Thr Ala Ala Lys Phe Gly Leu Ala Gly	Arg Glu Arg	
	355	360	365
Ala Ile Asn Asp	Phe Ser Trp Ala Thr Ile Ala Gln	Gln Thr Ile Asp	
	370	375	380
Val Tyr Lys Ser	Leu Met		
	385	390	

<210> 177

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1243)

<223> RXN02148

<400> 177

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				Val	Ser	Ala	Ser	Arg	
				1				5	
aaa act ctc gtt gtg acc aat gat ttt cct cca cgg atc ggc gga atc	163								
Lys Thr Leu Val Val Thr Asn Asp Phe Pro Pro Arg Ile Gly Gly Ile									
	10 15 20								
caa agc tat ttg agg gat ttc atc gct act caa gat cct gag tcg atc	211								
Gln Ser Tyr Leu Arg Asp Phe Ile Ala Thr Gln Asp Pro Glu Ser Ile									
	25 30 35								
gtg gtg ttt gcg tcg act caa aac gct gag gaa gcg cat gcc tac gac	259								
Val Val Phe Ala Ser Thr Gln Asn Ala Glu Glu Ala His Ala Tyr Asp									
	40 45 50								
aag act ttg gac tat gag gtc att agg tgg cct cgt tcg gtg atg ctg	307								
Lys Thr Leu Asp Tyr Glu Val Ile Arg Trp Pro Arg Ser Val Met Leu									
	55 60 65								
ccc acc cca aca acg gca cac gct atg gcg gag atc att cgt gag cga	355								
Pro Thr Pro Thr Thr Ala His Ala Met Ala Glu Ile Ile Arg Glu Arg									
	70 75 80 85								
gag atc gat aat gtg tgg ttc ggt gct gcg gct ccg ttg gcg ttg atg	403								
Glu Ile Asp Asn Val Trp Phe Gly Ala Ala Ala Pro Leu Ala Leu Met									
	90 95 100								
gca ggc aca gcg aag cag gca ggt gcg agc aag gtt att gcc tcc act	451								
Ala Gly Thr Ala Lys Gln Ala Gly Ala Ser Lys Val Ile Ala Ser Thr									
	105 110 115								
cat ggg cat gag gtg ggg tgg tca atg ctt cct gga tcg aga caa tcg	499								
His Gly His Glu Val Gly Trp Ser Met Leu Pro Gly Ser Arg Gln Ser									
	120 125 130								
ttg cgc aaa atc ggc act gag gtg gac gtg ctg act tat atc tcg cag	547								
Leu Arg Lys Ile Gly Thr Glu Val Asp Val Leu Thr Tyr Ile Ser Gln									
	135 140 145								
tac acg ctg cgc aga ttc aaa agt gct ttt gga tcg cac ccg act ttt	595								
Tyr Thr Leu Arg Arg Phe Lys Ser Ala Phe Gly Ser His Pro Thr Phe									
	150 155 160 165								
gaa cat ttg cct tcc ggc gtg gac gtt aag aga ttc act ccg gcc acg	643								
Glu His Leu Pro Ser Gly Val Asp Val Lys Arg Phe Thr Pro Ala Thr									
	170 175 180								
cca gag gac aaa agc gca aca agg aaa aag cta gga ttc acg gac acc	691								
Pro Glu Asp Lys Ser Ala Thr Arg Lys Lys Leu Gly Phe Thr Asp Thr									
	185 190 195								
acc ccg gtt att gcc tgt aac tcg cgt tta gtg ccg agg aaa ggc cag	739								
Thr Pro Val Ile Ala Cys Asn Ser Arg Leu Val Pro Arg Lys Gly Gln									
	200 205 210								
gac tcg ctg atc aag gcg atg cca cag gtg att gcg gcg cgc cca gat	787								
Asp Ser Leu Ile Lys Ala Met Pro Gln Val Ile Ala Ala Arg Pro Asp									
	215 220 225								
gcg cag ttg ctc att gtg ggc agt ggg cga tac gag tcg act ttg ccg	835								

Ala Gln Leu Leu Ile Val Gly Ser Gly Arg Tyr Glu Ser Thr Leu Arg
 230 235 240 245

cgc ctt gcc act gac gtg agc cag aac gtg aaa ttc ctt ggg cgc ctt 883
 Arg Leu Ala Thr Asp Val Ser Gln Asn Val Lys Phe Leu Gly Arg Leu
 250 255 260

gaa tat caa gat atg atc aac acg ctt gcc gcc gca gat att ttc gcg 931
 Glu Tyr Gln Asp Met Ile Asn Thr Leu Ala Ala Ala Asp Ile Phe Ala
 265 270 275

atg cca gcg cgc acc cgc ggt ggc gga ctt gat gtt gaa ggc ttg ggc 979
 Met Pro Ala Arg Thr Arg Gly Gly Gly Leu Asp Val Glu Gly Leu Gly
 280 285 290

att gtc tat ctc gag gca caa gcc tgc gga gtg ccg gtg ata gcc ggc 1027
 Ile Val Tyr Leu Glu Ala Gln Ala Cys Gly Val Pro Val Ile Ala Gly
 295 300 305

acc tct ggc ggc gcg cca gag acg gtg act ccg gca act ggc ctg gtt 1075
 Thr Ser Gly Gly Ala Pro Glu Thr Val Thr Pro Ala Thr Gly Leu Val
 310 315 320 325

gtg gag ggg tcg gac gtc gat aag ctg tct gag ctt tta att gag ctt 1123
 Val Glu Gly Ser Asp Val Asp Lys Leu Ser Glu Leu Leu Ile Glu Leu
 330 335 340

ctc gac gat ccg atc cgc cgc gcc gcg atg ggc gct gca ggt agg gcg 1171
 Leu Asp Asp Pro Ile Arg Arg Ala Ala Met Gly Ala Ala Gly Arg Ala
 345 350 355

cat gtg gag gcc gaa tgg tcg tgg gaa atc atg ggg gag cgg ttg acc 1219
 His Val Glu Ala Glu Trp Ser Trp Glu Ile Met Gly Glu Arg Leu Thr
 360 365 370

aat att ttg cag agt gaa cca cga tgatgggttg acagctgttg ata 1266
 Asn Ile Leu Gln Ser Glu Pro Arg
 375 380

<210> 178

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Val Ser Ala Ser Arg Lys Thr Leu Val Val Thr Asn Asp Phe Pro Pro
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 20 25 30

Asp Pro Glu Ser Ile Val Val Phe Ala Ser Thr Gln Asn Ala Glu Glu
 35 40 45

Ala His Ala Tyr Asp Lys Thr Leu Asp Tyr Glu Val Ile Arg Trp Pro
 50 55 60

Arg Ser Val Met Leu Pro Thr Pro Thr Thr Ala His Ala Met Ala Glu
 65 70 75 80

Ile Ile Arg Glu Arg Glu Ile Asp Asn Val Trp Phe Gly Ala Ala Ala
 85 90 95
 Pro Leu Ala Leu Met Ala Gly Thr Ala Lys Gln Ala Gly Ala Ser Lys
 100 105 110
 Val Ile Ala Ser Thr His Gly His Glu Val Gly Trp Ser Met Leu Pro
 115 120 125
 Gly Ser Arg Gln Ser Leu Arg Lys Ile Gly Thr Glu Val Asp Val Leu
 130 135 140
 Thr Tyr Ile Ser Gln Tyr Thr Leu Arg Arg Phe Lys Ser Ala Phe Gly
 145 150 155 160
 Ser His Pro Thr Phe Glu His Leu Pro Ser Gly Val Asp Val Lys Arg
 165 170 175
 Phe Thr Pro Ala Thr Pro Glu Asp Lys Ser Ala Thr Arg Lys Lys Leu
 180 185 190
 Gly Phe Thr Asp Thr Thr Pro Val Ile Ala Cys Asn Ser Arg Leu Val
 195 200 205
 Pro Arg Lys Gly Gln Asp Ser Leu Ile Lys Ala Met Pro Gln Val Ile
 210 215 220
 Ala Ala Arg Pro Asp Ala Gln Leu Leu Ile Val Gly Ser Gly Arg Tyr
 225 230 235 240
 Glu Ser Thr Leu Arg Arg Leu Ala Thr Asp Val Ser Gln Asn Val Lys
 245 250 255
 Phe Leu Gly Arg Leu Glu Tyr Gln Asp Met Ile Asn Thr Leu Ala Ala
 260 265 270
 Ala Asp Ile Phe Ala Met Pro Ala Arg Thr Arg Gly Gly Gly Leu Asp
 275 280 285
 Val Glu Gly Leu Gly Ile Val Tyr Leu Glu Ala Gln Ala Cys Gly Val
 290 295 300
 Pro Val Ile Ala Gly Thr Ser Gly Gly Ala Pro Glu Thr Val Thr Pro
 305 310 315 320
 Ala Thr Gly Leu Val Val Glu Gly Ser Asp Val Asp Lys Leu Ser Glu
 325 330 335
 Leu Leu Ile Glu Leu Leu Asp Asp Pro Ile Arg Arg Ala Ala Met Gly
 340 345 350
 Ala Ala Gly Arg Ala His Val Glu Ala Glu Trp Ser Trp Glu Ile Met
 355 360 365
 Gly Glu Arg Leu Thr Asn Ile Leu Gln Ser Glu Pro Arg
 370 375 380

<210> 179

<211> 1287

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1264)

<223> RXN02595

<400> 179

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                                   Val Ile Val Val Ala
                                   1           5

atg gct tcc att atg gct tgt tta aaa gca gct aga ctg aat aac cct 163
Met Ala Ser Ile Met Ala Cys Leu Lys Ala Ala Arg Leu Asn Asn Pro
              10              15              20

atg aag atc ctt ttg ttg tgc tgg cgt gat acc act cat cct caa ggt 211
Met Lys Ile Leu Leu Leu Cys Trp Arg Asp Thr Thr His Pro Gln Gly
              25              30              35

ggc gga agt gaa cgc tat ctg gag cgg gtg ggt gag ttt ttg gcg gat 259
Gly Gly Ser Glu Arg Tyr Leu Glu Arg Val Gly Glu Phe Leu Ala Asp
              40              45              50

cag ggc cat gag gtg gtg ttt cgt act gct ggg cac acg gat gcg cca 307
Gln Gly His Glu Val Val Phe Arg Thr Ala Gly His Thr Asp Ala Pro
              55              60              65

cgg cgt tct ttc cgc gat ggt gtg agg tat tcc agg agc ggt ggg aag 355
Arg Arg Ser Phe Arg Asp Gly Val Arg Tyr Ser Arg Ser Gly Gly Lys
              70              75              80              85

ttt agt gtg tat ccc aag gcg tgg gtg gcc atg atg ttg ggt cgt gtg 403
Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met Met Leu Gly Arg Val
              90              95              100

ggg att ggc acg ttt tcc aag gtt gat gtg gtg gtg gat acg cag aat 451
Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val Val Asp Thr Gln Asn
              105              110              115

ggc att ccg ttt ttt gga aag ttt ttc tcc ggt aag ccg act gtg ttg 499
Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly Lys Pro Thr Val Leu
              120              125              130

ctc acg cat cat tgc cat aag gag cag tgg ccg gtg gtg ggt cgg gtg 547
Leu Thr His His Cys His Lys Glu Gln Trp Pro Val Val Gly Arg Val
              135              140              145

ctg gcg aag gtt ggt tgg ctg att gag agc cag atc gcg ccg cgc gct 595
Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln Ile Ala Pro Arg Ala
              150              155              160              165

tac aaa act gcg ccg tat gtg act gtt tca gag ccg agc gct gag gag 643
Tyr Lys Thr Ala Pro Tyr Val Thr Val Ser Glu Pro Ser Ala Glu Glu
              170              175              180

ctc att gcg ttg ggt gtg gat cag cag cgg att cat atc gtg cgc aat 691
Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile His Ile Val Arg Asn
              185              190              195

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ggc gtg gat ccc gtg ccg ctg cac acg ccg aag ctg gat cgc gat ggc 739
 Gly Val Asp Pro Val Pro Leu His Thr Pro Lys Leu Asp Arg Asp Gly
 200 205 210

cag cat gcg gtg acg ttg tgc cgc ctg gtt ccg cac aag cag att gag 787
 Gln His Ala Val Thr Leu Ser Arg Leu Val Pro His Lys Gln Ile Glu
 215 220 225

cat gcg atg gat gtc gtc gcg gcg ctc gac ggc gtg gtg ctg gat gta 835
 His Ala Met Asp Val Val Ala Ala Leu Asp Gly Val Val Leu Asp Val
 230 235 240 245

gtc gaa agc ggt tgg tgg cag aag gaa ctg gtc gat tat gcc cgc acg 883
 Val Glu Ser Gly Trp Trp Gln Lys Glu Leu Val Asp Tyr Ala Arg Thr
 250 255 260

ctg ggt gtg agc gat cgc gtg gtt ttc cac ggc cag gtc gcc gag gat 931
 Leu Gly Val Ser Asp Arg Val Val Phe His Gly Gln Val Ala Glu Asp
 265 270 275

cac aag cac gcc ctg ttg gag cgc gcc acg att cat ctc atg cct tgc 979
 His Lys His Ala Leu Leu Glu Arg Ala Thr Ile His Leu Met Pro Ser
 280 285 290

cgc aag gaa ggc tgg ggc ctg gcg gtc acg gag gcg gcg cag cac ggc 1027
 Arg Lys Glu Gly Trp Gly Leu Ala Val Thr Glu Ala Ala Gln His Gly
 295 300 305

gtt ccg acg atc ggt tac cga agc tca ggc ggc ctg cgc gat tcc gtc 1075
 Val Pro Thr Ile Gly Tyr Arg Ser Ser Gly Gly Leu Arg Asp Ser Val
 310 315 320 325

gtc gac ggc gaa acc ggc ctg ctt gtc gac tcc aag gcc gag ctt att 1123
 Val Asp Gly Glu Thr Gly Leu Leu Val Asp Ser Lys Ala Glu Leu Ile
 330 335 340

tca gcc acc aaa acc ctg ctt atc gac gcc tcc ctc cgc tcc aag ctc 1171
 Ser Ala Thr Lys Thr Leu Leu Ile Asp Ala Ser Leu Arg Ser Lys Leu
 345 350 355

ggc gcc agc gcg aag cag cgc gcc gaa aac tac aag tgg gac acc gcg 1219
 Gly Ala Ser Ala Lys Gln Arg Ala Glu Asn Tyr Lys Trp Asp Thr Ala
 360 365 370

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 Arg Ser Gly Gly Lys Phe Ser Val Tyr Pro Lys Ala Trp Val Ala Met
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 Met Leu Gly Arg Val Gly Ile Gly Thr Phe Ser Lys Val Asp Val Val
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 Val Asp Thr Gln Asn Gly Ile Pro Phe Phe Gly Lys Phe Phe Ser Gly
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 Lys Pro Thr Val Leu Leu Thr His His Cys His Lys Glu Gln Trp Pro
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 Val Val Gly Arg Val Leu Ala Lys Val Gly Trp Leu Ile Glu Ser Gln
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 Pro Ser Ala Glu Glu Leu Ile Ala Leu Gly Val Asp Gln Gln Arg Ile
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 His Ile Val Arg Asn Gly Val Asp Pro Val Pro Leu His Thr Pro Lys
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 His Lys Gln Ile Glu His Ala Met Asp Val Val Ala Ala Leu Asp Gly
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 Asp Tyr Ala Arg Thr Leu Gly Val Ser Asp Arg Val Val Phe His Gly
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His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
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Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
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Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
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Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
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Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
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His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
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Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala	
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Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu	
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Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser	
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Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val	
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Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln	
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Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp	
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His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu Leu Ala Ala Leu Gly			
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Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala Ile Tyr Pro Ser Gly			
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Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile Thr Arg Leu Ala Ala			
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Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp			
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gtg Val	gcg Ala	ttc Phe 265	cgt Arg	ttt Phe	gcg Ala	gtc Val	acc Thr	gat Asp 270	gag Glu	cag Gln	ttc Phe	gcg Ala 275	cag Gln	att Ile	tct Ser	931		
aag Lys	ctg Leu 280	cgt Arg	gtg Val	gct Ala	cga Arg	cgt Arg	ctg Leu 285	tgg Trp	gcc Ala	agg Arg	gtg Val	tgt Cys 290	gag Glu	gtg Val	ctt Leu	979		
ggg Gly 295	ttt Phe	cca Pro	gag Glu	ctg Leu	gcc Ala 300	gta Val	gca Ala	cca Pro	cag Gln	cat His	gcg Ala 305	gtg Val	act Thr	gca Ala	cga Arg	1027		
gcg Ala 310	atg Met	ttt Phe	agc Ser	cag Gln	cgt Arg 315	gat Asp	ccg Pro	tgg Trp	gtg Val	aat Asn 320	atg Met	ctg Leu	gcg Arg	agt Ser	act Thr 325	1075		
gtt Val	gca Ala	gct Ala	ttc Phe 330	gct Ala	gca Ala	ggc Gly	gtc Val	ggg Gly	gga Gly 335	gca Ala	acc Thr	gat Asp	gtg Val	gag Glu	gtt Val 340	1123		
cg Arg	ac Thr	tt Phe 345	ga Asp	ga Asp	gc Ala	at Ile	cc Pro	ga Asp 350	gga Gly	gtt Val	cct Pro	gga Gly 355	gtg Val	tcg Ser	agg Arg	1171		
aat Asn	ttc Phe 360	gct Ala	cac His	cg Arg	atc Ile	gcg Ala	cg Arg 365	aat Asn	act Thr	aat Asn	ttg Leu 370	ttg Leu	ttg Leu	cta Leu	gaa Glu	1219		
gag Glu 375	tca Ser	cat His	ctt Leu	ggg Gly	cac His	gtg Val 380	gtt Val	gat Asp	cct Pro	gct Ala	ggg Gly 385	gga Gly	tca Ser	tat Tyr	ttc Phe	1267		
gtg Val 390	gag Glu	agc Ser	ttc Phe	acc Thr	gat Asp 395	gat Asp	cta Leu	gcg Ala	gag Glu	aag Lys 400	gcg Ala	tgg Trp	gct Ala	gtg Val	ttc Phe 405	1315		
agt Ser	ggc Gly	atc Ile	gaa Glu	gct Ala 410	gag Glu	ggc Gly	gga Gly	tac Tyr	agt Ser 415	gca Ala	gct Ala	tgt Cys	gca Ala	tcc Ser 420	ggc Gly	1363		
acg Thr	gtg Val	act Thr	gcc Ala 425	atg Met	ctt Leu	gat Asp	cag Gln	acg Thr 430	tgg Trp	gag Glu	cag Gln	act Thr	cg Arg 435	gct Ala	gat Asp	1411		

gtg gcg tcg aga aag aag aag ctc act gga att aat gag ttc ccg aac 1459
 Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile Asn Glu Phe Pro Asn
 440 445 450

ttg gcg gag tct ccg ctg cca gct gat cgt cgg gta gaa cct gca ggt 1507
 Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg Val Glu Pro Ala Gly
 455 460 465

gtg cgt cga tgg gca gcg gat ttt gaa gcg ctg cgc aat cgt tcg gat 1555
 Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu Arg Asn Arg Ser Asp
 470 475 480 485

gct ttc ttg gaa aag aac ggc gcg agg cca cag atc acg atg att cct 1603
 Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln Ile Thr Met Ile Pro
 490 495 500

ctg gga ccg ttg tcc aag cac aat att cgc act ggt ttt act tcc aac 1651
 Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr Gly Phe Thr Ser Asn
 505 510 515

ctg ttg gct tcc ggt ggc att gaa gca atc aac ccg ggt caa ctt gtt 1699
 Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn Pro Gly Gln Leu Val
 520 525 530

ccc ggc act gac gct ttt gca gaa gct gca cag gcc gca ggc att gta 1747
 Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln Ala Ala Gly Ile Val
 535 540 545

gtg gtg tgt gga acg gac caa gag tat gcc gaa acg ggg gag gga gcc 1795
 Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu Thr Gly Glu Gly Ala
 550 555 560 565

gtc gaa aag ctc cgc gaa gcg ggc gtt gag cgc atc ctg ctt gct ggc 1843
 Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg Ile Leu Leu Ala Gly
 570 575 580

gcg ccg aag agc ttt gag ggc agc gcg cat gcg ccc gat ggt tat ttg 1891
 Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala Pro Asp Gly Tyr Leu
 585 590 595

aac atg aca att gat gcc gcg gcg acg ctg gct gac ctg cta gat gct 1939
 Asn Met Thr Ile Asp Ala Ala Thr Leu Ala Asp Leu Leu Asp Ala
 600 605 610

ttg gga gct taaatcatga cgtcgatccc taa 1971
 Leu Gly Ala
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<210> 184

<211> 616

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

Leu Thr Asp Leu Thr Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn
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Leu Glu Thr Trp Tyr Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln
 20 25 30

Lys Lys Asp Ile Gly Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile
 35 40 45
 Val Thr Thr Pro Asp Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala
 50 55 60
 Asp Glu Ser Gln Arg Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe
 65 70 75 80
 Thr Arg Gly Thr Thr Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr
 85 90 95
 Glu Thr Phe Gly His Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu
 100 105 110
 Asn Ala Leu Asn Ser Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu
 115 120 125
 Glu Phe Thr Ala Ala Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu
 130 135 140
 Asn Met Ala Pro Leu Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val
 145 150 155 160
 Ala Ala Ala Leu Tyr Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala
 165 170 175
 Ala Leu Thr Leu Gly Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser
 180 185 190
 His Ser Asp Thr Ile Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser
 195 200 205
 Lys Arg Ala Asn Val Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser
 210 215 220
 Asn Gln Gly Ala Ser Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala
 225 230 235 240
 Gly Val Asp Tyr Val Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu
 245 250 255
 Ala Ala Leu Lys Gln Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln
 260 265 270
 Phe Ala Gln Ile Ser Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg
 275 280 285
 Val Cys Glu Val Leu Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His
 290 295 300
 Ala Val Thr Ala Arg Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn
 305 310 315 320
 Met Leu Arg Ser Thr Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala
 325 330 335
 Thr Asp Val Glu Val Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val
 340 345 350

Pro Gly Val Ser Arg Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn
 355 360 365
 Leu Leu Leu Leu Glu Glu Ser His Leu Gly His Val Val Asp Pro Ala
 370 375 380
 Gly Gly Ser Tyr Phe Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys
 385 390 395 400
 Ala Trp Ala Val Phe Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala
 405 410 415
 Ala Cys Ala Ser Gly Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu
 420 425 430
 Gln Thr Arg Ala Asp Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile
 435 440 445
 Asn Glu Phe Pro Asn Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg
 450 455 460
 Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu
 465 470 475 480
 Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln
 485 490 495
 Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr
 500 505 510
 Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn
 515 520 525
 Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln
 530 535 540
 Ala Ala Gly Ile Val Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu
 545 550 555 560
 Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg
 565 570 575
 Ile Leu Leu Ala Gly Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala
 580 585 590
 Pro Asp Gly Tyr Leu Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala
 595 600 605
 Asp Leu Leu Asp Ala Leu Gly Ala
 610 615

<210> 185

<211> 1179

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1156)

<223> RXS02106

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aagcaaaatc tctttagcaa attcggttac tgtggggcgc atg aat aac cat ttt 115
                                         Met Asn Asn His Phe
                                         1           5

gag ctc aaa gta cct ggt gga aag ctt gtc gtc gtt gat gtg acc acc 163
Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val Val Asp Val Thr Thr
          10          15          20

gat ctg gat tcc att gct gac gtg aag att tcc ggc gat ttc ttc ctc 211
Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser Gly Asp Phe Phe Leu
          25          30          35

gaa ccc gat gag gca ttc ttc gcc ctt ggc cgg gcg ctg cag ggg gcg 259
Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg Ala Leu Gln Gly Ala
          40          45          50

tcg gtg ggt gat aac act gat cgt ttg cag gca aag ttg gat gca gcg 307
Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala Lys Leu Asp Ala Ala
          55          60          65

ttg gcg gaa tat gat gac gtt gag cta cac ggc ttt agc act gcg gat 355
Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly Phe Ser Thr Ala Asp
          70          75          80          85

att gct tta gct gtg cgt cgg gca gtc acc ggc gcg caa gat ttc acc 403
Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly Ala Gln Asp Phe Thr
          90          95          100

gat tat gaa tgg gaa atc ctg cac cca ggg gtg ctt cct acc cca ctt 451
Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val Leu Pro Thr Pro Leu
          105          110          115

aac gtt gcg ttg gat gag ctc ctt ttg gac caa gtt gcc agt ggt cag 499
Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln Val Ala Ser Gly Gln
          120          125          130

cgt ggc ccg acg atg cgc att tgg gat tgg gat gat cgc gcc aca gtg 547
Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp Asp Arg Ala Thr Val
          135          140          145

atc ggt agt ttc cag tca tat gtc aat gaa atc aac caa gaa ggc gtt 595
Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile Asn Gln Glu Gly Val
          150          155          160          165

aat gaa cat ggt gtg acc gtg gta cga cgc atg tct ggt gcc ggt gca 643
Asn Glu His Gly Val Thr Val Val Arg Arg Met Ser Gly Gly Gly Ala
          170          175          180

atg ttt atg gag ggc ggc aac tgc atc acc tat tcc ctg tat gca ccg 691
Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr Ser Leu Tyr Ala Pro
          185          190          195

gaa tct ctc gtt gct ggt ttg agc tat gag cag tcc tat gaa tat ttg 739
Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln Ser Tyr Glu Tyr Leu
          200          205          210

gat cgt tgg gtg att gct gcg ctg aag aca cac gat gtt gac gct tgg 787

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Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His Asp Val Asp Ala Trp
 215                               220                               225

tac gtg cct atc aat gac atc acc tcc acc ggc gga aaa atc ggt ggc 835
Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly Gly Lys Ile Gly Gly
230                               235                               240                               245

gct gca cag aaa cgt cgc agt ggc gca gtc ctc cac cac gtg acc atg 883
Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu His His Val Thr Met
                               250                               255                               260

tcc tat gac atc gat gcg gac atg atg acc cag gtg ttg cgc att gga 931
Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln Val Leu Arg Ile Gly
                               265                               270                               275

aag gtg aag att tcc gac aag ggt ctt cgc agc gca aag aag cgc gtt 979
Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser Ala Lys Lys Arg Val
                               280                               285                               290

gat cct ctg cgc cgc caa aca ggt gca tca cgt gag caa atc atc gac 1027
Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg Glu Gln Ile Ile Asp
295                               300                               305

acc cta aag tcc aca ttc agt gct agg tac ggc gcg caa gaa gta gag 1075
Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly Ala Gln Glu Val Glu
310                               315                               320                               325

ctc agc gat gaa gat ttc gcg gca ggc cac gac cta gta aaa acc aaa 1123
Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp Leu Val Lys Thr Lys
                               330                               335                               340

tac gcc acc gag gag tgg act aag cga gtt caa tagttttctat ggatctgcac 1176
Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
                               345                               350

aag 1179

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<210> 186

<211> 352

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

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Met Asn Asn His Phe Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val
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Val Asp Val Thr Thr Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser
                               20                               25                               30

Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg
                               35                               40                               45

Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala
                               50                               55                               60

Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly
                               65                               70                               75                               80

Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly
                               85                               90                               95

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Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val
 100 105 110
 Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln
 115 120 125
 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp
 130 135 140
 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile
 145 150 155 160
 Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met
 165 170 175
 Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr
 180 185 190
 Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln
 195 200 205
 Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His
 210 215 220
 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly
 225 230 235 240
 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu
 245 250 255
 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln
 260 265 270
 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser
 275 280 285
 Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg
 290 295 300
 Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly
 305 310 315 320
 Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp
 325 330 335
 Leu Val Lys Thr Lys Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
 340 345 350

<210> 187
 <211> 876
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(853)

<223> RXS01746

<400> 187

aaaccgccac tccccctttca ctgggggagtg gcggttttgt cgtttcatgc atgcagtggtg 60

tgacttatca	accttgtag	ggctaggggtg	gatatctatc	atg	act	gca	cca	aga	115
				Met	Thr	Ala	Pro	Arg	
				1				5	

gat	cct	ttt	ttc	ccc	gca	gat	ctt	tct	atc	cgc	gcg	tct	gca	gag	ccc	163
Asp	Pro	Phe	Phe	Pro	Ala	Asp	Leu	Ser	Ile	Arg	Ala	Ser	Ala	Glu	Pro	
				10					15					20		

att	gaa	att	cag	cgg	ttg	ggt	ttg	atc	gat	tat	caa	gag	gcc	tgg	gat	211
Ile	Glu	Ile	Gln	Arg	Leu	Gly	Leu	Ile	Asp	Tyr	Gln	Glu	Ala	Trp	Asp	
			25					30					35			

tat	caa	gca	gag	ctt	gct	acc	cgt	agg	gct	aat	gat	gaa	atc	cct	gat	259
Tyr	Gln	Ala	Glu	Leu	Ala	Thr	Arg	Arg	Ala	Asn	Asp	Glu	Ile	Pro	Asp	
		40					45					50				

cag	ctg	ctt	att	ttg	gag	cac	ccg	tcg	gtg	tat	acc	gca	ggt	aag	cgc	307
Gln	Leu	Leu	Ile	Leu	Glu	His	Pro	Ser	Val	Tyr	Thr	Ala	Gly	Lys	Arg	
	55					60					65					

acc	cag	ccg	gaa	gat	ctt	ccc	acc	aac	gga	ctg	ccg	gtg	atc	aat	gct	355
Thr	Gln	Pro	Glu	Asp	Leu	Pro	Thr	Asn	Gly	Leu	Pro	Val	Ile	Asn	Ala	
70					75					80					85	

gat	cgt	ggt	ggt	cgc	atc	acg	tgg	cat	ggt	cct	ggc	caa	ttg	gtg	atc	403
Asp	Arg	Gly	Gly	Arg	Ile	Thr	Trp	His	Gly	Pro	Gly	Gln	Leu	Val	Ile	
				90					95					100		

tat	ccg	atc	atc	aaa	tta	gcc	gat	ccg	atc	gat	gtg	gtt	gat	tac	gta	451
Tyr	Pro	Ile	Ile	Lys	Leu	Ala	Asp	Pro	Ile	Asp	Val	Val	Asp	Tyr	Val	
				105				110					115			

aga	cgc	ctc	gag	gaa	gcg	ctc	atc	caa	gtt	gtc	ggc	gat	atg	ggt	gtt	499
Arg	Arg	Leu	Glu	Glu	Ala	Leu	Ile	Gln	Val	Val	Gly	Asp	Met	Gly	Val	
		120				125						130				

gcc	ggc	gct	ggg	cgc	att	gat	ggg	cgt	tcg	ggt	gtg	tgg	gtg	cca	gct	547
Ala	Gly	Ala	Gly	Arg	Ile	Asp	Gly	Arg	Ser	Gly	Val	Trp	Val	Pro	Ala	
135						140					145					

cat	gat	ggt	tgg	gtg	gac	agc	aag	gtt	gcg	gcc	atc	ggc	att	cga	ata	595
His	Asp	Gly	Trp	Val	Asp	Ser	Lys	Val	Ala	Ala	Ile	Gly	Ile	Arg	Ile	
150					155					160					165	

act	cgt	ggt	gtt	gca	atg	cac	ggt	gtg	gcc	atc	aac	tgc	aac	aac	acg	643
Thr	Arg	Gly	Val	Ala	Met	His	Gly	Val	Ala	Ile	Asn	Cys	Asn	Asn	Thr	
				170				175						180		

ttg	gat	ttc	tat	gag	cac	atc	att	ccg	tgt	ggc	att	gct	gat	gca	ggc	691
Leu	Asp	Phe	Tyr	Glu	His	Ile	Ile	Pro	Cys	Gly	Ile	Ala	Asp	Ala	Gly	
			185					190					195			

ttg	agc	aca	ctc	tcg	agg	gaa	ctg	aaa	agg	gac	gtt	tca	gtt	gag	gaa	739
Leu	Ser	Thr	Leu	Ser	Arg	Glu	Leu	Lys	Arg	Asp	Val	Ser	Val	Glu	Glu	
		200					205					210				

tta gtc gag cca tcg atc cgc gca ttg gat gat gct ttg gct ggt cgg 787
 Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp Ala Leu Ala Gly Arg
 215 220 225

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835
 Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys
 230 235 240 245

aat ctc cct aaa cgg ggg tagtacgagg aattttgtcg gtg 876
 Asn Leu Pro Lys Arg Gly
 250

<210> 188

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Thr Ala Pro Arg Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg
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Ala Ser Ala Glu Pro Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr
 20 25 30

Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn
 35 40 45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr
 50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu
 65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro
 85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp
 100 105 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val
 115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly
 130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala
 145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile
 165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly
 180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp
 195 200 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp
 210 215 220

Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala
 225 230 235 240

Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly
 245 250

<210> 189

<211> 1167

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1144)

<223> RXS01747

<400> 189

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ctaaaaatat cactaactcg aaagatgtaa ggttgcattt gtg act atc gca cct 115
 Val Thr Ile Ala Pro
 1 5

gaa gga cga cga ctg cta cgc gtc gaa gct cga aac tca gaa acc ccg 163
 Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg Asn Ser Glu Thr Pro
 10 15 20

att gag acg aag cct cga tgg att aga aac cag gtc aaa aac gga cct 211
 Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln Val Lys Asn Gly Pro
 25 30 35

gag tat cag gat atg aag gaa cgt gtc gct ggc gca tca cta cac act 259
 Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly Ala Ser Leu His Thr
 40 45 50

gtg tgt cag gag gct ggc tgt cct aat atc cat gag tgt tgg gaa tcc 307
 Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His Glu Cys Trp Glu Ser
 55 60 65

cgt gag gca acc ttc ctc att ggt ggc gcc aac tgc tct cgc cgc tgt 355
 Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Arg Cys
 70 75 80 85

gat ttc tgc atg atc aac tcg gct cgc cct gag cca ctc gac cgc ggt 403
 Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu Pro Leu Asp Arg Gly
 90 95 100

gag cca ctg cgt gtc gct gag tct gtt cgt gag atg cag ctg aat tac 451
 Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu Met Gln Leu Asn Tyr
 105 110 115

tcc acc atc acc ggt gtt acc cgt gat gat ctg gat gat gaa ggc gca 499
 Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu Asp Asp Glu Gly Ala
 120 125 130

tgg ctg tac tca gaa gtg gtt cgt aag atc cac gag ctg aac cca cac 547
 Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His Glu Leu Asn Pro His
 135 140 145

acc ggt gtg gaa aac ctg gtg cct gat ttc tcc ggc aag aag gat ctg 595

Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu	
150 155 160 165	
ctg cag gaa gtt ttt gaa tcc cgc cca gag gtt ttc gct cac aac gtg	643
Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val Phe Ala His Asn Val	
170 175 180	
gaa act gtg cca cgt att ttc aag cgc att cgc cca gca ttc cgc tac	691
Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr	
185 190 195	
gag cgt tca ctt gat gtg atc cgt cag gct cgc gat ttc ggt ctg gtg	739
Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val	
200 205 210	
acc aag tcc aac ctg att ttg ggc atg ggt gaa acc aag gaa gaa atc	787
Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu Thr Lys Glu Glu Ile	
215 220 225	
acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc	835
Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr	
230 235 240 245	
atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt	883
Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg	
250 255 260	
tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa	931
Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Ala Lys Glu	
265 270 275	
atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac	979
Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr	
280 285 290	
cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa	1027
Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu	
295 300 305	
atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc	1075
Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr	
310 315 320 325	
gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac	1123
Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp	
330 335 340	
acc cca gtg gtg tcc ttc aac taagcccgaa gttttttaac cgc	1167
Thr Pro Val Val Ser Phe Asn	
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<210> 190

<211> 348

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Val Thr Ile Ala Pro Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg
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Asn Ser Glu Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln
 20 25 30
 Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly
 35 40 45
 Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
 50 55 60
 Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
 65 70 75 80
 Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu
 85 90 95
 Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu
 100 105 110
 Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
 115 120 125
 Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His
 130 135 140
 Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
 145 150 155 160
 Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val
 165 170 175
 Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
 180 185 190
 Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg
 195 200 205
 Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
 210 215 220
 Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly
 225 230 235 240
 Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe
 245 250 255
 His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala
 260 265 270
 Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu
 275 280 285
 Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu
 290 295 300
 Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr
 305 310 315 320
 Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr
 325 330 335
 Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn

345

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<223> RXC01748
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316

Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val Pro Val Tyr Glu Ile
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 atc acg ggc aac ggc gaa ggc cag acc cct atc gcg aag ctg cag cgt 691
 Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile Ala Lys Leu Gln Arg
 185 190 195
 gaa ctg gtc aag ctg cct cgc aac tac aag aag aac gac gtc gct gcc 739
 Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys Asn Asp Val Ala Ala
 200 205 210
 ctg gcc gct cgc att gag gct atg gac aat gtc gga aac gct cct gcc 787
 Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val Gly Asn Ala Pro Gly
 215 220 225
 gga tct ttg cct aag ggt cca ttg cca aag ggc gca agc atg tcc ggt 835
 Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly Ala Ser Met Ser Gly
 230 235 240 245
 atg aac cgc cgc gct cgc cga cag gct gaa cgc aag ggc gag gct 880
 Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg Lys Gly Glu Ala
 250 255 260
 taaagccttt tcgctttcgc gtc 903

<210> 192
 <211> 260
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 192
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 20 25 30
 Gln Val Phe Asn Met Gln Arg Lys Gln Asp Lys Ala Leu Ile Pro Leu
 35 40 45
 Leu Leu Leu Ala Ile Leu Gly Ile Pro Leu Val Leu Phe Leu Ile Gly
 50 55 60
 Leu Ile Trp Gly Gly Gln Trp Trp Met Leu Pro Ile Gly Ile Ala Ala
 65 70 75 80
 Gly Val Val Ala Ala Met Phe Ile Phe Thr Arg Arg Val Glu Arg Asp
 85 90 95
 Val Tyr Lys Arg Ala Glu Gly Gln Gln Gly Ala Ala Gly Trp Ala Val
 100 105 110
 Glu Asn Leu Arg Ser Gly Val Gly Met Thr Trp Arg Thr Lys Thr Ala
 115 120 125
 Val Ala Val Thr Thr Gln Met Asp Ala Val His Arg Val Ile Gly Leu
 130 135 140
 Cys Gly Val Val Leu Val Gly Glu Gly Ser Pro His Arg Leu Lys Pro
 145 150 155 160

Met Leu Ala Gln Gln Lys Lys Arg Leu Asn Arg Val Ala Pro Gly Val
 165 170 175

Pro Val Tyr Glu Ile Ile Thr Gly Asn Gly Glu Gly Gln Thr Pro Ile
 180 185 190

Ala Lys Leu Gln Arg Glu Leu Val Lys Leu Pro Arg Asn Tyr Lys Lys
 195 200 205

Asn Asp Val Ala Ala Leu Ala Ala Arg Ile Glu Ala Met Asp Asn Val
 210 215 220

Gly Asn Ala Pro Gly Gly Ser Leu Pro Lys Gly Pro Leu Pro Lys Gly
 225 230 235 240

Ala Ser Met Ser Gly Met Asn Arg Arg Ala Arg Arg Gln Ala Glu Arg
 245 250 255

Lys Gly Glu Ala
 260

<210> 193
 <211> 936
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(913)
 <223> RXC00354

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 ttctcgatta tgtacctcat ttacgcgtaa agtttggggc atg gga aag tta ctt 115
 Met Gly Lys Leu Leu
 1 5

ttc gta gac atc ggt ggc aca ctg ctg gat tac tca aat gaa gtt ccg 163
 Phe Val Asp Ile Gly Gly Thr Leu Leu Asp Tyr Ser Asn Glu Val Pro
 10 15 20

cgt tcg gcc gtt gac gcg atc cgt aag gca cgc gcc aaa gga cac cgc 211
 Arg Ser Ala Val Asp Ala Ile Arg Lys Ala Arg Ala Lys Gly His Arg
 25 30 35

gtg tac ttg agc tct ggt cga agc agc gct gag gtg act tct cag ttg 259
 Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu Val Thr Ser Gln Leu
 40 45 50

tgg gat atc gga gtg gat ggc ctc att ggc gca aat ggt gga tat gtg 307
 Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala Asn Gly Gly Tyr Val
 55 60 65

gaa agc gca cag gag tct gtg ttc cac cgc cgt ttg tcg ggt gag gag 355
 Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg Leu Ser Gly Glu Glu
 70 75 80 85

acc cgc cac att gtg gag tgg ctc tac aac cgt ggt ttg gag ttt tat 403

Thr	Arg	His	Ile	Val	Glu	Trp	Leu	Tyr	Asn	Arg	Gly	Leu	Glu	Phe	Tyr		
				90					95					100			
ctc	gag	tcc	aac	aac	ggt	ttg	tat	gca	agc	cgt	ggt	ttc	cgt	gag	gct	451	
Leu	Glu	Ser	Asn	Asn	Gly	Leu	Tyr	Ala	Ser	Arg	Gly	Phe	Arg	Glu	Ala		
			105					110					115				
tct	aag	cca	gtg	ctg	tct	cgc	ctt	tcg	gag	aag	acc	gac	gtg	aca	gtc	499	
Ser	Lys	Pro	Val	Leu	Ser	Arg	Leu	Ser	Glu	Lys	Thr	Asp	Val	Thr	Val		
		120					125					130					
gat	agc	atg	tac	ccg	gat	atg	ttc	tgg	ggc	gcg	agc	ctt	gat	cgt	gac	547	
Asp	Ser	Met	Tyr	Pro	Asp	Met	Phe	Trp	Gly	Ala	Ser	Leu	Asp	Arg	Asp		
		135				140					145						
gat	gtg	aac	aag	atc	agt	tac	atc	ttc	aat	tct	cag	gaa	gat	ttg	gac	595	
Asp	Val	Asn	Lys	Ile	Ser	Tyr	Ile	Phe	Asn	Ser	Gln	Glu	Asp	Leu	Asp		
					155					160					165		
gca	gcg	cgt	gag	gcg	ttc	cct	aac	ctg	gag	cac	acc	acg	tgg	ggt	ggt	643	
Ala	Ala	Arg	Glu	Ala	Phe	Pro	Asn	Leu	Glu	His	Thr	Thr	Trp	Gly	Gly		
				170					175					180			
cag	acg	ggt	gcg	ttg	ttc	ggc	acg	atc	ggt	gtg	tct	gtc	aac	aag	aag	691	
Gln	Thr	Gly	Ala	Leu	Phe	Gly	Thr	Ile	Gly	Val	Ser	Val	Asn	Lys	Lys		
			185					190					195				
atc	ggc	gtg	gat	cgc	ctg	ctg	aag	tac	ctg	aac	gca	gat	cgc	gca	aac	739	
Ile	Gly	Val	Asp	Arg	Leu	Leu	Lys	Tyr	Leu	Asn	Ala	Asp	Arg	Ala	Asn		
		200					205					210					
acc	att	gcg	ttc	ggc	gac	agc	gat	gag	gat	ctc	tcc	cta	ttt	gag	gcg	787	
Thr	Ile	Ala	Phe	Gly	Asp	Ser	Asp	Glu	Asp	Leu	Ser	Leu	Phe	Glu	Ala		
		215				220					225						
agc	gct	tac	ggc	gtc	gcg	atg	ggc	gag	gcc	acc	gaa	tcg	ctc	aag	gct	835	
Ser	Ala	Tyr	Gly	Val	Ala	Met	Gly	Glu	Ala	Thr	Glu	Ser	Leu	Lys	Ala		
		230			235				240					245			
gct	gct	gac	ctg	gtc	acg	gat	gct	gtt	ggg	cag	gac	ggc	ttg	cgc	aat	883	
Ala	Ala	Asp	Leu	Val	Thr	Asp	Ala	Val	Gly	Gln	Asp	Gly	Leu	Arg	Asn		
				250					255					260			
gcg	ttt	tta	aag	ctt	gag	ctt	atc	gac	gcc	tgaccccatc	aaagaacttc					933	
Ala	Phe	Leu	Lys	Leu	Glu	Leu	Ile	Asp	Ala								
			265					270									
cca																936	

<210> 194

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

Met	Gly	Lys	Leu	Leu	Phe	Val	Asp	Ile	Gly	Gly	Thr	Leu	Leu	Asp	Tyr
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Ser	Asn	Glu	Val	Pro	Arg	Ser	Ala	Val	Asp	Ala	Ile	Arg	Lys	Ala	Arg
		20						25					30		

Ala Lys Gly His Arg Val Tyr Leu Ser Ser Gly Arg Ser Ser Ala Glu
 35 40 45

Val Thr Ser Gln Leu Trp Asp Ile Gly Val Asp Gly Leu Ile Gly Ala
 50 55 60

Asn Gly Gly Tyr Val Glu Ser Ala Gln Glu Ser Val Phe His Arg Arg
 65 70 75 80

Leu Ser Gly Glu Glu Thr Arg His Ile Val Glu Trp Leu Tyr Asn Arg
 85 90 95

Gly Leu Glu Phe Tyr Leu Glu Ser Asn Asn Gly Leu Tyr Ala Ser Arg
 100 105 110

Gly Phe Arg Glu Ala Ser Lys Pro Val Leu Ser Arg Leu Ser Glu Lys
 115 120 125

Thr Asp Val Thr Val Asp Ser Met Tyr Pro Asp Met Phe Trp Gly Ala
 130 135 140

Ser Leu Asp Arg Asp Asp Val Asn Lys Ile Ser Tyr Ile Phe Asn Ser
 145 150 155 160

Gln Glu Asp Leu Asp Ala Ala Arg Glu Ala Phe Pro Asn Leu Glu His
 165 170 175

Thr Thr Trp Gly Gly Gln Thr Gly Ala Leu Phe Gly Thr Ile Gly Val
 180 185 190

Ser Val Asn Lys Lys Ile Gly Val Asp Arg Leu Leu Lys Tyr Leu Asn
 195 200 205

Ala Asp Arg Ala Asn Thr Ile Ala Phe Gly Asp Ser Asp Glu Asp Leu
 210 215 220

Ser Leu Phe Glu Ala Ser Ala Tyr Gly Val Ala Met Gly Glu Ala Thr
 225 230 235 240

Glu Ser Leu Lys Ala Ala Ala Asp Leu Val Thr Asp Ala Val Gly Gln
 245 250 255

Asp Gly Leu Arg Asn Ala Phe Leu Lys Leu Glu Leu Ile Asp Ala
 260 265 270

<210> 195

<211> 1740

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1717)

<223> RXC01749

<400> 195

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taacgctgag gtcgtactta atccatgaga tcatgaatgg gtg agc ttc ctt gta 115

																Val Ser Phe Leu Val	
																1	5
gaa aat caa tta ctc gcg ttg gtt gtc atc atg acg gtc gga cta ttg	Glu Asn Gln Leu Leu Ala Leu Val Val Ile Met Thr Val Gly Leu Leu	10	15	20	163												
ctc ggc cgc atc aaa att ttc ggg ttc cgt ctc ggc gtc gcc gct gta	Leu Gly Arg Ile Lys Ile Phe Gly Phe Arg Leu Gly Val Ala Ala Val	25	30	35	211												
ctg ttt gta ggt cta gcg cta tcc acc att gag ccg gat att tcc gtc	Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu Pro Asp Ile Ser Val	40	45	50	259												
cca tcc ctc att tac gtg gtt gga ctg tcg ctt ttt gtc tac acg atc	Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu Phe Val Tyr Thr Ile	55	60	65	307												
ggc ctg gaa gcc ggc cct gga ttc ttc acc tcc atg aaa acc act ggt	Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser Met Lys Thr Thr Gly	70	75	80	355												
ctg cgc aac aac gca ctg acc ttg ggc gcc atc atc gcc acc acg gca	Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile Ile Ala Thr Thr Ala	90	95	100	403												
ctc gca tgg gca ctc atc aca gtt ttg aac atc gat gcc gcc tcc ggc	Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile Asp Ala Ala Ser Gly	105	110	115	451												
gcc ggc atg ctc acc ggc gcg ctc acc aac acc cca gcc atg gcc gca	Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr Pro Ala Met Ala Ala	120	125	130	499												
gtt gtt gac gca ctt cct tcg ctt atc gac gac acc ggc cag ctt cac	Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp Thr Gly Gln Leu His	135	140	145	547												
ctc atc gcc gag ctg ccc gtc gtc gca tat tcc ttg gca tac ccc ctc	Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser Leu Ala Tyr Pro Leu	150	155	160	595												
ggc gtg ctc atc gtt att ctc tcc atc gcc atc ttc agc tct gtg ttc	Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile Phe Ser Ser Val Phe	170	175	180	643												
aaa gtc gac cac aac aaa gaa gcc gaa gaa gcg ggc gtt gcg gtc cag	Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala Gly Val Ala Val Gln	185	190	195	691												
gaa ctc aaa ggc cgt cgc atc cgc gtc acc gtc gct gat ctt cca gcc	Glu Leu Lys Gly Arg Arg Ile Arg Val Thr Val Ala Asp Leu Pro Ala	200	205	210	739												
ctg gag aac atc cca gag ctg ctc aac ctc cac gtc att gtg tcc cga	Leu Glu Asn Ile Pro Glu Leu Leu Asn Leu His Val Ile Val Ser Arg	215	220	225	787												
gtg gaa cga gac ggt gag caa ttc atc ccg ctt tat ggc gaa cac gca	Val Glu Arg Asp Gly Glu Gln Phe Ile Pro Leu Tyr Gly Glu His Ala				835												

230	235	240	245	
cgc atc ggc gat gtc tta aca gtg gtg ggt gcc gat gaa gaa ctc aac	883			
Arg Ile Gly Asp Val Leu Thr Val Val Gly Ala Asp Glu Glu Leu Asn				
250	255	260		
cgc gcg gaa aaa gcc atc ggt gaa ctc att gac ggc gac ccc tac agc	931			
Arg Ala Glu Lys Ala Ile Gly Glu Leu Ile Asp Gly Asp Pro Tyr Ser				
265	270	275		
aat gtg gaa ctt gat tac cga cgc atc ttc gtc tca aac aca gca gtc	979			
Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val Ser Asn Thr Ala Val				
280	285	290		
gtg ggc act ccc cta tcc aag ctc cag cca ctg ttt aaa gac atg ctg	1027			
Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu Phe Lys Asp Met Leu				
295	300	305		
atc acc cgc atc agg cgc ggc gac aca gat ttg gtg gcc tcc tcc gac	1075			
Ile Thr Arg Ile Arg Gly Asp Thr Asp Leu Val Ala Ser Ser Asp				
310	315	320	325	
atg act ttg cag ctc ggt gac cgt gtc cgc gtt gtc gca cca gca gaa	1123			
Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val Val Ala Pro Ala Glu				
330	335	340		
aaa ctc cgc gaa gca acc caa ttg ctc ggc gat tcc tac aag aaa ctc	1171			
Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp Ser Tyr Lys Lys Leu				
345	350	355		
tcc gat ttc aac ctg ctc cca ctc gct gcc ggc ctc atg atc ggt gtg	1219			
Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly Leu Met Ile Gly Val				
360	365	370		
ctt gtc ggc atg gtg gag ttc cca cta cca ggt gga agc tcc ctg aaa	1267			
Leu Val Gly Met Val Glu Phe Pro Leu Pro Gly Gly Ser Ser Leu Lys				
375	380	385		
ctg ggt aac gca ggt gga ccg cta gtt gtt gcg ctg ctg ctc ggc atg	1315			
Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala Leu Leu Leu Gly Met				
390	395	400	405	
atc aat cgc aca ggc aag ttc gtc tgg caa atc ccc tac gga gca aac	1363			
Ile Asn Arg Thr Gly Lys Phe Val Trp Gln Ile Pro Tyr Gly Ala Asn				
410	415	420		
ctt gcc ctt cgc caa ctg ggc atc aca cta ttt ttg gct gcc atc ggt	1411			
Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe Leu Ala Ala Ile Gly				
425	430	435		
acc tca gcg ggc gca gga ttt cga tca gcg atc agc gac ccc caa tca	1459			
Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile Ser Asp Pro Gln Ser				
440	445	450		
ctc acc atc atc ggc ttc ggt gcg ctg ctc act ttg ttc atc tcc atc	1507			
Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr Leu Phe Ile Ser Ile				
455	460	465		
acg gtg ctg ttc gtt ggc cac aaa ctg atg aaa atc ccc ttc ggt gaa	1555			
Thr Val Leu Phe Val Gly His Lys Leu Met Lys Ile Pro Phe Gly Glu				
470	475	480	485	

acc gct ggc atc ctc gcc ggt acg caa acc cac cct gct gtg ctg agt 1603
 Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His Pro Ala Val Leu Ser
 490 495 500

tat gtg tca gat gcc tcc cgc aac gag ctc cct gcc atg ggt tat acc 1651
 Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro Ala Met Gly Tyr Thr
 505 510 515

tct gtg tat ccg ctg gcg atg atc gca aag atc ctg gcc gcc caa acg 1699
 Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile Leu Ala Ala Gln Thr
 520 525 530

ttg ttg ttc cta ctt atc tagcattgac cccttaagcg cag 1740
 Leu Leu Phe Leu Leu Ile
 535

<210> 196

<211> 539

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Val Ser Phe Leu Val Glu Asn Gln Leu Leu Ala Leu Val Val Ile Met
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Thr Val Gly Leu Leu Leu Gly Arg Ile Lys Ile Phe Gly Phe Arg Leu
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Gly Val Ala Ala Val Leu Phe Val Gly Leu Ala Leu Ser Thr Ile Glu
 35 40 45

Pro Asp Ile Ser Val Pro Ser Leu Ile Tyr Val Val Gly Leu Ser Leu
 50 55 60

Phe Val Tyr Thr Ile Gly Leu Glu Ala Gly Pro Gly Phe Phe Thr Ser
 65 70 75 80

Met Lys Thr Thr Gly Leu Arg Asn Asn Ala Leu Thr Leu Gly Ala Ile
 85 90 95

Ile Ala Thr Thr Ala Leu Ala Trp Ala Leu Ile Thr Val Leu Asn Ile
 100 105 110

Asp Ala Ala Ser Gly Ala Gly Met Leu Thr Gly Ala Leu Thr Asn Thr
 115 120 125

Pro Ala Met Ala Ala Val Val Asp Ala Leu Pro Ser Leu Ile Asp Asp
 130 135 140

Thr Gly Gln Leu His Leu Ile Ala Glu Leu Pro Val Val Ala Tyr Ser
 145 150 155 160

Leu Ala Tyr Pro Leu Gly Val Leu Ile Val Ile Leu Ser Ile Ala Ile
 165 170 175

Phe Ser Ser Val Phe Lys Val Asp His Asn Lys Glu Ala Glu Glu Ala
 180 185 190

Gly Val Ala Val Gln Glu Leu Lys Gly Arg Arg Ile Arg Val Thr Val

195	200	205
Ala Asp Leu Pro Ala Leu Glu Asn Ile Pro Glu Leu Leu Asn Leu His 210 215 220		
Val Ile Val Ser Arg Val Glu Arg Asp Gly Glu Gln Phe Ile Pro Leu 225 230 235 240		
Tyr Gly Glu His Ala Arg Ile Gly Asp Val Leu Thr Val Val Gly Ala 245 250 255		
Asp Glu Glu Leu Asn Arg Ala Glu Lys Ala Ile Gly Glu Leu Ile Asp 260 265 270		
Gly Asp Pro Tyr Ser Asn Val Glu Leu Asp Tyr Arg Arg Ile Phe Val 275 280 285		
Ser Asn Thr Ala Val Val Gly Thr Pro Leu Ser Lys Leu Gln Pro Leu 290 295 300		
Phe Lys Asp Met Leu Ile Thr Arg Ile Arg Arg Gly Asp Thr Asp Leu 305 310 315 320		
Val Ala Ser Ser Asp Met Thr Leu Gln Leu Gly Asp Arg Val Arg Val 325 330 335		
Val Ala Pro Ala Glu Lys Leu Arg Glu Ala Thr Gln Leu Leu Gly Asp 340 345 350		
Ser Tyr Lys Lys Leu Ser Asp Phe Asn Leu Leu Pro Leu Ala Ala Gly 355 360 365		
Leu Met Ile Gly Val Leu Val Gly Met Val Glu Phe Pro Leu Pro Gly 370 375 380		
Gly Ser Ser Leu Lys Leu Gly Asn Ala Gly Gly Pro Leu Val Val Ala 385 390 395 400		
Leu Leu Leu Gly Met Ile Asn Arg Thr Gly Lys Phe Val Trp Gln Ile 405 410 415		
Pro Tyr Gly Ala Asn Leu Ala Leu Arg Gln Leu Gly Ile Thr Leu Phe 420 425 430		
Leu Ala Ala Ile Gly Thr Ser Ala Gly Ala Gly Phe Arg Ser Ala Ile 435 440 445		
Ser Asp Pro Gln Ser Leu Thr Ile Ile Gly Phe Gly Ala Leu Leu Thr 450 455 460		
Leu Phe Ile Ser Ile Thr Val Leu Phe Val Gly His Lys Leu Met Lys 465 470 475 480		
Ile Pro Phe Gly Glu Thr Ala Gly Ile Leu Ala Gly Thr Gln Thr His 485 490 495		
Pro Ala Val Leu Ser Tyr Val Ser Asp Ala Ser Arg Asn Glu Leu Pro 500 505 510		
Ala Met Gly Tyr Thr Ser Val Tyr Pro Leu Ala Met Ile Ala Lys Ile 515 520 525		

Leu Ala Ala Gln Thr Leu Leu Phe Leu Leu Ile
530 535

<210> 197

<211> 1023

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1000)

<223> RXA02268

<400> 197

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ttgccgagcg caagccggcc tacggcgcta gtgtgagcac atg tcc cag gaa aat 115
Met Ser Gln Glu Asn
1 5

tct ggt ttg ttc aag cgc gcg att aca cgt ggg gtg gct aag gtg cgc 163
Ser Gly Leu Phe Lys Arg Ala Ile Thr Arg Gly Val Ala Lys Val Arg
10 15 20

cgg aat ccg cgc gag gat ttt gcg gag gaa ttc acc caa gaa ctc tac 211
Arg Asn Pro Arg Glu Asp Phe Ala Glu Glu Phe Thr Gln Glu Leu Tyr
25 30 35

gat cac gca aca aat atc acc ctg ccc ctg acg gcg cgg ctg aag ccg 259
Asp His Ala Thr Asn Ile Thr Leu Pro Leu Thr Ala Arg Leu Lys Pro
40 45 50

aat ggg ttt ttc cag gat gat tgg cgg gcg cga cca agt ggt gcg cga 307
Asn Gly Phe Phe Gln Asp Asp Trp Arg Ala Arg Pro Ser Gly Ala Arg
55 60 65

ccg tgg ccg atc gtg cta att cac gga tcc ggg gcc agc aag ggt tca 355
Pro Trp Pro Ile Val Leu Ile His Gly Ser Gly Ala Ser Lys Gly Ser
70 75 80 85

tgg gag gaa atg ggc gct gag ctg cgc agc aaa ggt tgg gcc gtg ttt 403
Trp Glu Glu Met Gly Ala Glu Leu Arg Ser Lys Gly Trp Ala Val Phe
90 95 100

gcc cct gac ttt gga acg cgt gcc acc gag cca att gcg gcg tcg gct 451
Ala Pro Asp Phe Gly Thr Arg Ala Thr Glu Pro Ile Ala Ala Ser Ala
105 110 115

gcc caa att ggt gcg tat att gat gcc gtt ttg ttg gtg acg ggc gct 499
Ala Gln Ile Gly Ala Tyr Ile Asp Ala Val Leu Leu Val Thr Gly Ala
120 125 130

gcg cag att gtg ctg gtt ggg cat tcg caa ggc ggt gtc gtg gcg cgg 547
Ala Gln Ile Val Leu Val Gly His Ser Gln Gly Gly Val Val Ala Arg
135 140 145

tat tgg atg cgc acc tac ggc gga tac atg aag gtc agg cac atg att 595
Tyr Trp Met Arg Thr Tyr Gly Gly Tyr Met Lys Val Arg His Met Ile
150 155 160 165

tcc atc tct acg cca aat cac gga acg ctc atg gga ggc att tta aac 643
 Ser Ile Ser Thr Pro Asn His Gly Thr Leu Met Gly Gly Ile Leu Asn
 170 175 180

ccg atg acg aag gtg aaa tcg gga gag gga acg atc gaa aag ctg atg 691
 Pro Met Thr Lys Val Lys Ser Gly Glu Gly Thr Ile Glu Lys Leu Met
 185 190 195

cac aga cta ttc ggg ccc act ggt ttt gaa cag ctg cgc gga cac gac 739
 His Arg Leu Phe Gly Pro Thr Gly Phe Glu Gln Leu Arg Gly His Asp
 200 205 210

atc atc gag ttt ttg gcc gac ggt ggg gac ctc gat cca ggc gtc acc 787
 Ile Ile Glu Phe Leu Ala Asp Gly Gly Asp Leu Asp Pro Gly Val Thr
 215 220 225

tac acc tgc att ggt acc cat ttt gat cct ttc atc caa cct ccg gag 835
 Tyr Thr Cys Ile Gly Thr His Phe Asp Pro Phe Ile Gln Pro Pro Glu
 230 235 240 245

gtg gcc ttt ttg gag gtc aac gag gac gat gat cca aat cga gtc cac 883
 Val Ala Phe Leu Glu Val Asn Glu Asp Asp Asp Pro Asn Arg Val His
 250 255 260

aat att tgg gtc gaa gat gaa cac ccg cgc gca atg att gcc cac aac 931
 Asn Ile Trp Val Glu Asp Glu His Pro Arg Ala Met Ile Ala His Asn
 265 270 275

gat atg gtg cgc gat ccc agg gtg atc gaa atc gta cgc gca gag ctc 979
 Asp Met Val Arg Asp Pro Arg Val Ile Glu Ile Val Arg Ala Glu Leu
 280 285 290

gac cgg gtg gca cgc ctc ggc taagttgggg acatggttga cgc 1023
 Asp Arg Val Ala Arg Leu Gly
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<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

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 20 25 30

Thr Gln Glu Leu Tyr Asp His Ala Thr Asn Ile Thr Leu Pro Leu Thr
 35 40 45

Ala Arg Leu Lys Pro Asn Gly Phe Phe Gln Asp Asp Trp Arg Ala Arg
 50 55 60

Pro Ser Gly Ala Arg Pro Trp Pro Ile Val Leu Ile His Gly Ser Gly
 65 70 75 80

Ala Ser Lys Gly Ser Trp Glu Glu Met Gly Ala Glu Leu Arg Ser Lys
 85 90 95

Gly Trp Ala Val Phe Ala Pro Asp Phe Gly Thr Arg Ala Thr Glu Pro
 100 105 110
 Ile Ala Ala Ser Ala Ala Gln Ile Gly Ala Tyr Ile Asp Ala Val Leu
 115 120 125
 Leu Val Thr Gly Ala Ala Gln Ile Val Leu Val Gly His Ser Gln Gly
 130 135 140
 Gly Val Val Ala Arg Tyr Trp Met Arg Thr Tyr Gly Gly Tyr Met Lys
 145 150 155 160
 Val Arg His Met Ile Ser Ile Ser Thr Pro Asn His Gly Thr Leu Met
 165 170 175
 Gly Gly Ile Leu Asn Pro Met Thr Lys Val Lys Ser Gly Glu Gly Thr
 180 185 190
 Ile Glu Lys Leu Met His Arg Leu Phe Gly Pro Thr Gly Phe Glu Gln
 195 200 205
 Leu Arg Gly His Asp Ile Ile Glu Phe Leu Ala Asp Gly Gly Asp Leu
 210 215 220
 Asp Pro Gly Val Thr Tyr Thr Cys Ile Gly Thr His Phe Asp Pro Phe
 225 230 235 240
 Ile Gln Pro Pro Glu Val Ala Phe Leu Glu Val Asn Glu Asp Asp Asp
 245 250 255
 Pro Asn Arg Val His Asn Ile Trp Val Glu Asp Glu His Pro Arg Ala
 260 265 270
 Met Ile Ala His Asn Asp Met Val Arg Asp Pro Arg Val Ile Glu Ile
 275 280 285
 Val Arg Ala Glu Leu Asp Arg Val Ala Arg Leu Gly
 290 295 300

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 <223> RXA02269

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 Met Val Asp Ala Leu
 1 5
 aat gat ctc cgc cga gaa ctc aca aac gcg tta agg tcc gtg tgg aaa 163
 Asn Asp Leu Arg Arg Glu Leu Thr Asn Ala Leu Arg Ser Val Trp Lys
 10 15 20

aac ctc ccc act gat aac gcc ccg cag gcc gat gcc ttg cca gac gat	211
Asn Leu Pro Thr Asp Asn Ala Pro Gln Ala Asp Ala Leu Pro Asp Asp	
25 30 35	
gta gtg gaa gag att gcg ata aat ttc tac cgt gat ccc aaa aac cgc	259
Val Val Glu Glu Ile Ala Ile Asn Phe Tyr Arg Asp Pro Lys Asn Arg	
40 45 50	
ggc aaa ctc aac gaa gac aaa aca gat tcc ttg ccg atg ctc gcg cgc	307
Gly Lys Leu Asn Glu Asp Lys Thr Asp Ser Leu Pro Met Leu Ala Arg	
55 60 65	
ata cgt tca cgt gga ctt ttt gaa gac gat tgg cgc gcc cgc ccc acc	355
Ile Arg Ser Arg Gly Leu Phe Glu Asp Asp Trp Arg Ala Arg Pro Thr	
70 75 80 85	
gaa gac cgc ccc tgg cca gtg gta tta gtc cac gga act gga tca aca	403
Glu Asp Arg Pro Trp Pro Val Val Leu Val His Gly Thr Gly Ser Thr	
90 95 100	
aaa ggt gat tgg caa gac ttg gga gcc gat cta cgc cgc gac ggc tgg	451
Lys Gly Asp Trp Gln Asp Leu Gly Ala Asp Leu Arg Arg Asp Gly Trp	
105 110 115	
gca gtg ttt gca ccc gaa ttt ggc caa cgc gcc acc ggt tca gtc gca	499
Ala Val Phe Ala Pro Glu Phe Gly Gln Arg Ala Thr Gly Ser Val Ala	
120 125 130	
gaa tca tcc gca caa att ggc gcc tat ata gat aca gta ttg ctt gct	547
Glu Ser Ser Ala Gln Ile Gly Ala Tyr Ile Asp Thr Val Leu Leu Ala	
135 140 145	
aca gga gcc tca aaa gtc att gtc gtt ggc cac tcc caa ggc ggc gtg	595
Thr Gly Ala Ser Lys Val Ile Val Val Gly His Ser Gln Gly Gly Val	
150 155 160 165	
ttg ctg aga tac tgg atg cgt gtt ttg ggt ggt gca tcc aaa gtc aaa	643
Leu Leu Arg Tyr Trp Met Arg Val Leu Gly Gly Ala Ser Lys Val Lys	
170 175 180	
cac atg gtc tcc ctc gct gtc ccc aat cac ggc acc acc atg ggc gga	691
His Met Val Ser Leu Ala Val Pro Asn His Gly Thr Thr Met Gly Gly	
185 190 195	
atc gtc agc ccg cta atc cgt aac aat cgt ggc gaa agt gtg gtt aat	739
Ile Val Ser Pro Leu Ile Arg Asn Asn Arg Gly Glu Ser Val Val Asn	
200 205 210	
tct gtc gtt caa tca tgg ttc ggc gaa gct gga ttt gaa atg atc cgc	787
Ser Val Val Gln Ser Trp Phe Gly Glu Ala Gly Phe Glu Met Ile Arg	
215 220 225	
gga cac gac acc atc aac gcc atc aat gaa ggc ggc gat ttg gat cca	835
Gly His Asp Thr Ile Asn Ala Ile Asn Glu Gly Gly Asp Leu Asp Pro	
230 235 240 245	
gac gtg aca tat ctg tgc atc gcc acc cac ttt gac acc gtg att cag	883
Asp Val Thr Tyr Leu Cys Ile Ala Thr His Phe Asp Thr Val Ile Gln	
250 255 260	

ccc cct gaa acc tgc ttc cta gag gcc cgg aac ccc gaa gaa ctc aag 931
 Pro Pro Glu Thr Cys Phe Leu Glu Ala Arg Asn Pro Glu Glu Leu Lys
 265 270 275
 cgg gtc caa aac atc tgg gtg gaa aac ctc gac ccc aat tca gtc gtg 979
 Arg Val Gln Asn Ile Trp Val Glu Asn Leu Asp Pro Asn Ser Val Val
 280 285 290
 ctc cac gaa gca atg cct tac gat ccc cgc gta cgc gca ctg gtc agg 1027
 Leu His Glu Ala Met Pro Tyr Asp Pro Arg Val Arg Ala Leu Val Arg
 295 300 305
 gcg gat ttg agc aaa ttg gtg gag att tcc gag act gcg gag aac 1072
 Ala Asp Leu Ser Lys Leu Val Glu Ile Ser Glu Thr Ala Glu Asn
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<210> 200

<211> 324

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

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 35 40 45
 Asp Pro Lys Asn Arg Gly Lys Leu Asn Glu Asp Lys Thr Asp Ser Leu
 50 55 60
 Pro Met Leu Ala Arg Ile Arg Ser Arg Gly Leu Phe Glu Asp Asp Trp
 65 70 75 80
 Arg Ala Arg Pro Thr Glu Asp Arg Pro Trp Pro Val Val Leu Val His
 85 90 95
 Gly Thr Gly Ser Thr Lys Gly Asp Trp Gln Asp Leu Gly Ala Asp Leu
 100 105 110
 Arg Arg Asp Gly Trp Ala Val Phe Ala Pro Glu Phe Gly Gln Arg Ala
 115 120 125
 Thr Gly Ser Val Ala Glu Ser Ser Ala Gln Ile Gly Ala Tyr Ile Asp
 130 135 140
 Thr Val Leu Leu Ala Thr Gly Ala Ser Lys Val Ile Val Val Gly His
 145 150 155 160
 Ser Gln Gly Gly Val Leu Leu Arg Tyr Trp Met Arg Val Leu Gly Gly
 165 170 175
 Ala Ser Lys Val Lys His Met Val Ser Leu Ala Val Pro Asn His Gly
 180 185 190

Thr Thr Met Gly Gly Ile Val Ser Pro Leu Ile Arg Asn Asn Arg Gly
 195 200 205
 Glu Ser Val Val Asn Ser Val Val Gln Ser Trp Phe Gly Glu Ala Gly
 210 215 220
 Phe Glu Met Ile Arg Gly His Asp Thr Ile Asn Ala Ile Asn Glu Gly
 225 230 235 240
 Gly Asp Leu Asp Pro Asp Val Thr Tyr Leu Cys Ile Ala Thr His Phe
 245 250 255
 Asp Thr Val Ile Gln Pro Pro Glu Thr Cys Phe Leu Glu Ala Arg Asn
 260 265 270
 Pro Glu Glu Leu Lys Arg Val Gln Asn Ile Trp Val Glu Asn Leu Asp
 275 280 285
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 Arg Ala Leu Val Arg Ala Asp Leu Ser Lys Leu Val Glu Ile Ser Glu
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1123)
 <223> RXA01614

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 Met Asn Gln Met Gln
 1 5
 cag tgg aaa cca gac ttc ctg gga gag ggc tac caa aac ctc acc atc 163
 Gln Trp Lys Pro Asp Phe Leu Gly Glu Gly Tyr Gln Asn Leu Thr Ile
 10 15 20
 gag ctc ggc gac gac ccg gat aat gaa aca gat gtt gtg aca acg gtt 211
 Glu Leu Gly Asp Asp Pro Asp Asn Glu Thr Asp Val Val Thr Thr Val
 25 30 35
 gtg cgc tac aac cca gac aat cac gcg gac gag tct ttt gct gcc cgc 259
 Val Arg Tyr Asn Pro Asp Asn His Ala Asp Glu Ser Phe Ala Ala Arg
 40 45 50
 cca gcg ttg ctg tgg gtt cac ggc atg acg gac tac ttc ttc cac act 307
 Pro Ala Leu Leu Trp Val His Gly Met Thr Asp Tyr Phe Phe His Thr
 55 60 65

gaa ttc gcg gag ttt ttc cac aat gcc ggt ttt gct gtg tac ggc att	355
Glu Phe Ala Glu Phe Phe His Asn Ala Gly Phe Ala Val Tyr Gly Ile	
70 75 80 85	
gat ctt aga aaa tgt gga cgc tcc tac cgt cca gga cag cag tgg cac	403
Asp Leu Arg Lys Cys Gly Arg Ser Tyr Arg Pro Gly Gln Gln Trp His	
90 95 100	
tac acc tct gat ctt gcc cat tac ttc cct gac tta aca gct gct gcc	451
Tyr Thr Ser Asp Leu Ala His Tyr Phe Pro Asp Leu Thr Ala Ala Ala	
105 110 115	
gag gtc atc tct tcc acc cac cct gag cta gtc ccc gtc gcc cat tcc	499
Glu Val Ile Ser Ser Thr His Pro Glu Leu Val Pro Val Ala His Ser	
120 125 130	
act ggt gga ctc atc gtt cct ctg tgg atg tcc cag atg cgc aca agc	547
Thr Gly Gly Leu Ile Val Pro Leu Trp Met Ser Gln Met Arg Thr Ser	
135 140 145	
aat cca gct gcc att gag aag att cca gcg ctg gtc ctc aac agt ccg	595
Asn Pro Ala Ala Ile Glu Lys Ile Pro Ala Leu Val Leu Asn Ser Pro	
150 155 160 165	
tgg ctg gac atg atg tat cca cca ctg ttc atc aag ctg atc acc cct	643
Trp Leu Asp Met Met Tyr Pro Pro Leu Phe Ile Lys Leu Ile Thr Pro	
170 175 180	
atg gtg agg gtg ttg ggc aaa cgc tcc ccc aca acc atc atc cca ggc	691
Met Val Arg Val Leu Gly Lys Arg Ser Pro Thr Thr Ile Ile Pro Gly	
185 190 195	
gga ggt ttg gga gca tac gga aaa tcg atc cat aag aac ttt tac ggc	739
Gly Gly Leu Gly Ala Tyr Gly Lys Ser Ile His Lys Asn Phe Tyr Gly	
200 205 210	
gaa tgg gac ttt gac acc acc atc aag cct gta gaa gga cat aaa aag	787
Glu Trp Asp Phe Asp Thr Thr Ile Lys Pro Val Glu Gly His Lys Lys	
215 220 225	
agc atc gga tgg ctt cgg gca gtc atg gct ggc caa gca gaa atc cat	835
Ser Ile Gly Trp Leu Arg Ala Val Met Ala Gly Gln Ala Glu Ile His	
230 235 240 245	
cac gac cac gtg aat gtc gga gtg gac gtg ctc acg ctg tgt tca aat	883
His Asp His Val Asn Val Gly Val Asp Val Leu Thr Leu Cys Ser Asn	
250 255 260	
aag tcc tgg ttg aag tct gaa tac aca gag gac acc aac act tca gac	931
Lys Ser Trp Leu Lys Ser Glu Tyr Thr Glu Asp Thr Asn Thr Ser Asp	
265 270 275	
gcg gtt ttg gat gtg aaa cac att caa aag tgg gct cct cat ttg agc	979
Ala Val Leu Asp Val Lys His Ile Gln Lys Trp Ala Pro His Leu Ser	
280 285 290	
tcg cca tcg tcc agg gtt gat gtt gag atc atc gac aac gct cgc cac	1027
Ser Pro Ser Ser Arg Val Asp Val Glu Ile Ile Asp Asn Ala Arg His	
295 300 305	
gat att ttc ctc tca agg aaa ccc gcc aga gat cac gcc tct gaa gta	1075

Asp Ile Phe Leu Ser Arg Lys Pro Ala Arg Asp His Ala Ser Glu Val
 310 315 320 325

ctc aac aac tgg ctg caa tcg aag ctt tcc agc ctc aaa cca tct caa 1123
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taacaccgcg aattatagac tga 1146

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<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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Gln Asn Leu Thr Ile Glu Leu Gly Asp Asp Pro Asp Asn Glu Thr Asp
 20 25 30

Val Val Thr Thr Val Val Arg Tyr Asn Pro Asp Asn His Ala Asp Glu
 35 40 45

Ser Phe Ala Ala Arg Pro Ala Leu Leu Trp Val His Gly Met Thr Asp
 50 55 60

Tyr Phe Phe His Thr Glu Phe Ala Glu Phe Phe His Asn Ala Gly Phe
 65 70 75 80

Ala Val Tyr Gly Ile Asp Leu Arg Lys Cys Gly Arg Ser Tyr Arg Pro
 85 90 95

Gly Gln Gln Trp His Tyr Thr Ser Asp Leu Ala His Tyr Phe Pro Asp
 100 105 110

Leu Thr Ala Ala Ala Glu Val Ile Ser Ser Thr His Pro Glu Leu Val
 115 120 125

Pro Val Ala His Ser Thr Gly Gly Leu Ile Val Pro Leu Trp Met Ser
 130 135 140

Gln Met Arg Thr Ser Asn Pro Ala Ala Ile Glu Lys Ile Pro Ala Leu
 145 150 155 160

Val Leu Asn Ser Pro Trp Leu Asp Met Met Tyr Pro Pro Leu Phe Ile
 165 170 175

Lys Leu Ile Thr Pro Met Val Arg Val Leu Gly Lys Arg Ser Pro Thr
 180 185 190

Thr Ile Ile Pro Gly Gly Gly Leu Gly Ala Tyr Gly Lys Ser Ile His
 195 200 205

Lys Asn Phe Tyr Gly Glu Trp Asp Phe Asp Thr Thr Ile Lys Pro Val
 210 215 220

Glu Gly His Lys Lys Ser Ile Gly Trp Leu Arg Ala Val Met Ala Gly
 225 230 235 240

Gln Ala Glu Ile His His Asp His Val Asn Val Gly Val Asp Val Leu
 245 250 255

Thr Leu Cys Ser Asn Lys Ser Trp Leu Lys Ser Glu Tyr Thr Glu Asp
 260 265 270

Thr Asn Thr Ser Asp Ala Val Leu Asp Val Lys His Ile Gln Lys Trp
 275 280 285

Ala Pro His Leu Ser Ser Pro Ser Ser Arg Val Asp Val Glu Ile Ile
 290 295 300

Asp Asn Ala Arg His Asp Ile Phe Leu Ser Arg Lys Pro Ala Arg Asp
 305 310 315 320

His Ala Ser Glu Val Leu Asn Asn Trp Leu Gln Ser Lys Leu Ser Ser
 325 330 335

Leu Lys Pro Ser Gln
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 <213> Corynebacterium glutamicum

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 <223> RXA01983

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 Met Glu Gly Tyr Gly
 1 5

cct acc cag atc gaa aag ctc tta cct gca tac aca cag gtc aac aca 163
 Pro Thr Gln Ile Glu Lys Leu Leu Pro Ala Tyr Thr Gln Val Asn Thr
 10 15 20

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 Ala Gly Asn Asn Pro Ala Thr Thr Pro Glu Gln Asp Leu Leu Gly Gly
 25 30 35

gct gca acc tcg ccg gaa aac tac gac cac cag ctg cag tac gca gtc 259
 Ala Ala Thr Ser Pro Glu Asn Tyr Asp His Gln Leu Gln Tyr Ala Val
 40 45 50

gac gcc agt ccg gtg cat cag aat gcg gca cag gca ccg ccc ttc ctg 307
 Asp Ala Ser Pro Val His Gln Asn Ala Ala Gln Ala Pro Pro Phe Leu
 55 60 65

atc atg cac ggc act ggt gac cgg atg gtc cct ccg gag caa tcg gct 355
 Ile Met His Gly Thr Gly Asp Arg Met Val Pro Pro Glu Gln Ser Ala
 70 75 80 85

gcg ctg cac acc cat ctt gtg cag gct ggt ccg cag tcc acc ctg gta 403
 Ala Leu His Thr His Leu Val Gln Ala Gly Arg Gln Ser Thr Leu Val

90	95	100	
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gag ctg ggg cca aac gtt cga cta gac aat ggt cgg ctc gag cgg gag Glu Leu Gly Pro Asn Val Arg Leu Asp Asn Gly Arg Leu Glu Arg Glu 120 125 130			499
cct cag aca aat ttc agc gcg cag cag agt ccg gga aac ccc ttt gaa Pro Gln Thr Asn Phe Ser Ala Gln Gln Ser Pro Gly Asn Pro Phe Glu 135 140 145			547
cta cag gga ctt gcc gcc gac cat gag atg atc aag cgc ttt ttc acc Leu Gln Gly Leu Ala Ala Asp His Glu Met Ile Lys Arg Phe Phe Thr 150 155 160 165			595
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<400> 204
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 35 40 45
 Leu Gln Tyr Ala Val Asp Ala Ser Pro Val His Gln Asn Ala Ala Gln
 50 55 60
 Ala Pro Pro Phe Leu Ile Met His Gly Thr Gly Asp Arg Met Val Pro
 65 70 75 80
 Pro Glu Gln Ser Ala Ala Leu His Thr His Leu Val Gln Ala Gly Arg
 85 90 95
 Gln Ser Thr Leu Val Leu Ile Glu Gly Phe Gly His Gly Phe Leu Asn
 100 105 110
 Pro Gly Glu Val Ala Glu Leu Gly Pro Asn Val Arg Leu Asp Asn Gly
 115 120 125
 Arg Leu Glu Arg Glu Pro Gln Thr Asn Phe Ser Ala Gln Gln Ser Pro
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 Gly Asn Pro Phe Glu Leu Gln Gly Leu Ala Ala Asp His Glu Met Ile
 145 150 155 160
 Lys Arg Phe Phe Thr Leu His Leu Arg
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<210> 205
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1414)
 <223> RXN02947

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acc aaa cct gac ctc acc acc acg gct gga aag ctg tcc gat ctt cgc 163
Thr Lys Pro Asp Leu Thr Thr Thr Ala Gly Lys Leu Ser Asp Leu Arg
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tcc cgt ctt gca gaa gct caa gct cca atg ggc gaa gca act gta gaa 211
Ser Arg Leu Ala Glu Ala Gln Ala Pro Met Gly Glu Ala Thr Val Glu
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aaa gtg cac gct gct ggc agg aag act gcc cgc gaa cgt atc gag tat 259
Lys Val His Ala Ala Gly Arg Lys Thr Ala Arg Glu Arg Ile Glu Tyr
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ttg ctc gat gag ggc tct ttc gta gag atc gat gct ctt gct cgt cac 307
Leu Leu Asp Glu Gly Ser Phe Val Glu Ile Asp Ala Leu Ala Arg His
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cgt tcc aag aac ttc ggc ctg gat gcc aag cgt cca gtt act gac ggt 355
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Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg Lys Val Cys Val Phe
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Ser Gln Asp Gly Ala Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly
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Glu Lys Ile Val Lys Val Met Asp Leu Ala Ile Lys Thr Gly Val Pro
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ttg atc gga atc aat gag ggt gct ggt gcg cgt atc cag gaa ggt gtt 547
Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg Ile Gln Glu Gly Val
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gtg tct ctg ggt ctg tac tca cag atc ttc tac cgc aac acc cag gcg 595
Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr Arg Asn Thr Gln Ala
                        150 155 160 165

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Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Ala Cys Ala Gly

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170										175										180									
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Arg	Ala	Glu	Thr	Pro	Arg	Gln	Glu	Ala	Asp	Ile	Met	Ile	Gly	Ser	Ile														
			265						270					275															
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Gln	Glu	Asn	Ile	Asn	Asp	Val	Asp	Leu	Glu	Leu	Asp	Thr	Ile	Ile	Pro														
		280						285					290																
gat	tcc	ccg	aac	cag	cct	tat	gac	atg	aag	gaa	gtt	att	tcc	cgc	atc					1027									
Asp	Ser	Pro	Asn	Gln	Pro	Tyr	Asp	Met	Lys	Glu	Val	Ile	Ser	Arg	Ile														
		295				300						305																	
gtc	gac	gac	gcc	gag	ttc	ttc	gag	atc	cag	gaa	gac	tac	gca	gag	aac					1075									
Val	Asp	Asp	Ala	Glu	Phe	Phe	Glu	Ile	Gln	Glu	Asp	Tyr	Ala	Glu	Asn														
		310				315				320				325															
atc	ctg	tgt	ggc	ttc	gct	cgc	gtt	gag	gtc	cgt	tct	gtt	ggc	atc	gtg					1123									
Ile	Leu	Cys	Gly	Phe	Ala	Arg	Val	Glu	Val	Arg	Ser	Val	Gly	Ile	Val														
			330						335					340															
gct	aac	cag	cca	acc	cag	ttc	gct	ggc	tgc	ttg	gat	att	aag	gca	tct					1171									
Ala	Asn	Gln	Pro	Thr	Gln	Phe	Ala	Gly	Cys	Leu	Asp	Ile	Lys	Ala	Ser														
			345						350					355															
gag	aag	gct	gcc	cgt	ttc	atc	cgc	acc	tgc	gat	gcc	ttc	aac	atc	cca					1219									
Glu	Lys	Ala	Ala	Arg	Phe	Ile	Arg	Thr	Cys	Asp	Ala	Phe	Asn	Ile	Pro														
		360						365					370																
atc	ctt	gag	ttc	gtg	gac	gtt	cca	ggc	ttc	ctg	cct	ggc	acc	aac	cag					1267									
Ile	Leu	Glu	Phe	Val	Asp	Val	Pro	Gly	Phe	Leu	Pro	Gly	Thr	Asn	Gln														
		375					380						385																
gaa	ttc	gac	ggc	atc	atc	cgc	cgc	ggc	gca	aag	ctg	ctt	tac	gct	tac					1315									
Glu	Phe	Asp	Gly	Ile	Ile	Arg	Arg	Gly	Ala	Lys	Leu	Leu	Tyr	Ala	Tyr														
		390					395			400				405															
gct	gaa	gca	acc	gtc	ggc	aag	atc	acc	gtc	atc	acc	cgc	aag	tcc	tac					1363									
Ala	Glu	Ala	Thr	Val	Gly	Lys	Ile	Thr	Val	Ile	Thr	Arg	Lys	Ser	Tyr														
			410							415				420															

ggc gga gcg tac tgc gtg atg ggt tcc aag gat atg ggc gct ggc ctg 1411
 Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp Met Gly Ala Gly Leu
 425 430 435

gta
 Val 1414

<210> 206

<211> 438

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

Met Thr Ala Ala Gln Thr Lys Pro Asp Leu Thr Thr Thr Ala Gly Lys
 1 5 10 15

Leu Ser Asp Leu Arg Ser Arg Leu Ala Glu Ala Gln Ala Pro Met Gly
 20 25 30

Glu Ala Thr Val Glu Lys Val His Ala Ala Gly Arg Lys Thr Ala Arg
 35 40 45

Glu Arg Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Ile Asp
 50 55 60

Ala Leu Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ala Lys Arg
 65 70 75 80

Pro Val Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg
 85 90 95

Lys Val Cys Val Phe Ser Gln Asp Gly Ala Val Phe Gly Gly Ala Leu
 100 105 110

Gly Glu Val Tyr Gly Glu Lys Ile Val Lys Val Met Asp Leu Ala Ile
 115 120 125

Lys Thr Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg
 130 135 140

Ile Gln Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr
 145 150 155 160

Arg Asn Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met
 165 170 175

Gly Ala Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe
 180 185 190

Ile Val Met Val Asp Gln Thr Ser Lys Met Phe Ile Thr Gly Pro Asp
 195 200 205

Val Ile Lys Thr Val Thr Gly Glu Asp Val Thr Gln Glu Glu Leu Gly
 210 215 220

Gly Ala His Thr His Met Ala Thr Ser Gly Thr Ser His Tyr Ser Ala
 225 230 235 240

Ser Asp Asp Ser Asp Ala Leu Asp Trp Val Arg Glu Leu Thr Ser Tyr
 245 250 255
 Leu Pro Ser Asn Asn Arg Ala Glu Thr Pro Arg Gln Glu Ala Asp Ile
 260 265 270
 Met Ile Gly Ser Ile Gln Glu Asn Ile Asn Asp Val Asp Leu Glu Leu
 275 280 285
 Asp Thr Ile Ile Pro Asp Ser Pro Asn Gln Pro Tyr Asp Met Lys Glu
 290 295 300
 Val Ile Ser Arg Ile Val Asp Asp Ala Glu Phe Phe Glu Ile Gln Glu
 305 310 315 320
 Asp Tyr Ala Glu Asn Ile Leu Cys Gly Phe Ala Arg Val Glu Val Arg
 325 330 335
 Ser Val Gly Ile Val Ala Asn Gln Pro Thr Gln Phe Ala Gly Cys Leu
 340 345 350
 Asp Ile Lys Ala Ser Glu Lys Ala Ala Arg Phe Ile Arg Thr Cys Asp
 355 360 365
 Ala Phe Asn Ile Pro Ile Leu Glu Phe Val Asp Val Pro Gly Phe Leu
 370 375 380
 Pro Gly Thr Asn Gln Glu Phe Asp Gly Ile Ile Arg Arg Gly Ala Lys
 385 390 395 400
 Leu Leu Tyr Ala Tyr Ala Glu Ala Thr Val Gly Lys Ile Thr Val Ile
 405 410 415
 Thr Arg Lys Ser Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Asp
 420 425 430
 Met Gly Ala Gly Leu Val
 435

<210> 207
 <211> 688
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(688)
 <223> FRXA02320

<400> 207
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 attattcact ctcacccttc aggatttaga ctaagaaacc atg act gca gca cag 115
 Met Thr Ala Ala Gln
 1 5
 acc aaa cct gac ctc acc acc acg gct gga aag ctg tcc gat ctt cgc 163
 Thr Lys Pro Asp Leu Thr Thr Thr Ala Gly Lys Leu Ser Asp Leu Arg
 10 15 20

tcc cgt ctt gca gaa gct caa gct cca atg ggc gaa gca act gta gaa 211
 Ser Arg Leu Ala Glu Ala Gln Ala Pro Met Gly Glu Ala Thr Val Glu
 25 30 35
 aaa gtg cac gct gct ggc agg aag act gcc cgc gaa cgt atc gag tat 259
 Lys Val His Ala Ala Gly Arg Lys Thr Ala Arg Glu Arg Ile Glu Tyr
 40 45 50
 ttg ctc gat gag ggc tct ttc gta gag atc gat gct ctt gct cgt cac 307
 Leu Leu Asp Glu Gly Ser Phe Val Glu Ile Asp Ala Leu Ala Arg His
 55 60 65
 cgt tcc aag aac ttc ggc ctg gat gcc aag cgt cca gtt act gac ggt 355
 Arg Ser Lys Asn Phe Gly Leu Asp Ala Lys Arg Pro Val Thr Asp Gly
 70 75 80 85
 gtt gtg act ggt tac ggc acc atc gat ggc cgt aag gtc tgt gtg ttc 403
 Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg Lys Val Cys Val Phe
 90 95 100
 tcc cag gac ggc gct gta ttc ggt ggc gct ttg ggt gaa gtt tat ggt 451
 Ser Gln Asp Gly Ala Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly
 105 110 115
 gaa aag atc gtt aag gtt atg gat ctt gcg atc aag acc ggt gtg cct 499
 Glu Lys Ile Val Lys Val Met Asp Leu Ala Ile Lys Thr Gly Val Pro
 120 125 130
 ttg atc gga atc aat gag ggt gct ggt gcg cgt atc cag gaa ggt gtt 547
 Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg Ile Gln Glu Gly Val
 135 140 145
 gtg tct ctg ggt ctg tac tca cag atc ttc tac cgc aac acc cag gcg 595
 Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr Arg Asn Thr Gln Ala
 150 155 160 165
 tct ggc gtt atc cca cag atc tct ttg atc atg ggt gcc tgc gct ggt 643
 Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Ala Cys Ala Gly
 170 175 180
 ggt cac gtg tac tcc cct gct ctg act gac ttc atc gtc atg gtg 688
 Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe Ile Val Met Val
 185 190 195

<210> 208

<211> 196

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 208

Met Thr Ala Ala Gln Thr Lys Pro Asp Leu Thr Thr Thr Ala Gly Lys
 1 5 10 15

Leu Ser Asp Leu Arg Ser Arg Leu Ala Glu Ala Gln Ala Pro Met Gly
 20 25 30

Glu Ala Thr Val Glu Lys Val His Ala Ala Gly Arg Lys Thr Ala Arg
 35 40 45

Glu Arg Ile Glu Tyr Leu Leu Asp Glu Gly Ser Phe Val Glu Ile Asp

50 55 60
 Ala Leu Ala Arg His Arg Ser Lys Asn Phe Gly Leu Asp Ala Lys Arg
 65 70 75 80
 Pro Val Thr Asp Gly Val Val Thr Gly Tyr Gly Thr Ile Asp Gly Arg
 85 90 95
 Lys Val Cys Val Phe Ser Gln Asp Gly Ala Val Phe Gly Gly Ala Leu
 100 105 110
 Gly Glu Val Tyr Gly Glu Lys Ile Val Lys Val Met Asp Leu Ala Ile
 115 120 125
 Lys Thr Gly Val Pro Leu Ile Gly Ile Asn Glu Gly Ala Gly Ala Arg
 130 135 140
 Ile Gln Glu Gly Val Val Ser Leu Gly Leu Tyr Ser Gln Ile Phe Tyr
 145 150 155 160
 Arg Asn Thr Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met
 165 170 175
 Gly Ala Cys Ala Gly Gly His Val Tyr Ser Pro Ala Leu Thr Asp Phe
 180 185 190
 Ile Val Met Val
 195

<210> 209

<211> 519

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(519)

<223> FRXA02851

<400> 209

cct cgc cag aag gcc gac atc atg atc ggt tcc atc cag gaa aac atc 48
 Pro Arg Gln Lys Ala Asp Ile Met Ile Gly Ser Ile Gln Glu Asn Ile
 1 5 10 15
 aac gat gtg gat ctg gaa ttg gac acc atc atc ccg gat tcc ccg aac 96
 Asn Asp Val Asp Leu Glu Leu Asp Thr Ile Ile Pro Asp Ser Pro Asn
 20 25 30
 cag cct tat gac atg aag gaa gtt att tcc cgc atc gtn gac gac gcc 144
 Gln Pro Tyr Asp Met Lys Glu Val Ile Ser Arg Ile Val Asp Asp Ala
 35 40 45
 gag ttc ttc gag atc cag gaa gac tac gca gag aac atc ctg tgt ggc 192
 Glu Phe Phe Glu Ile Gln Glu Asp Tyr Ala Glu Asn Ile Leu Cys Gly
 50 55 60
 ttc gct cgc gtt gag gnc cgt tnt gtt ggc atc gtg gct aac cag cca 240
 Phe Ala Arg Val Glu Xaa Arg Xaa Val Gly Ile Val Ala Asn Gln Pro
 65 70 75 80

acc cag ttc gct ggc tgn ttg gat att aag gca tct gag aag gct gcc 288
 Thr Gln Phe Ala Gly Xaa Leu Asp Ile Lys Ala Ser Glu Lys Ala Ala
 85 90 95

cgt ttc atc cgc acc tgc gat gcc ttc aac atc cca atc ctt gag ttc 336
 Arg Phe Ile Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Leu Glu Phe
 100 105 110

gtg gac gtt cca ggc ttc ctg cct ggc acc aac cag gaa ttc gac ggc 384
 Val Asp Val Pro Gly Phe Leu Pro Gly Thr Asn Gln Glu Phe Asp Gly
 115 120 125

atc atc cgc cgc ggc gca aag ctg ctt tac gct tac gct gaa gca acc 432
 Ile Ile Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Ala Glu Ala Thr
 130 135 140

gtc ggc aag atc acc gtc atc acc cgc aag tcc tac ggc gga gcg tac 480
 Val Gly Lys Ile Thr Val Ile Thr Arg Lys Ser Tyr Gly Gly Ala Tyr
 145 150 155 160

tgc gtg atg ggt tcc aag gat atg ggc gct ggc ctg gta 519
 Cys Val Met Gly Ser Lys Asp Met Gly Ala Gly Leu Val
 165 170

<210> 210

<211> 173

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

Pro Arg Gln Lys Ala Asp Ile Met Ile Gly Ser Ile Gln Glu Asn Ile
 1 5 10 15

Asn Asp Val Asp Leu Glu Leu Asp Thr Ile Ile Pro Asp Ser Pro Asn
 20 25 30

Gln Pro Tyr Asp Met Lys Glu Val Ile Ser Arg Ile Val Asp Asp Ala
 35 40 45

Glu Phe Phe Glu Ile Gln Glu Asp Tyr Ala Glu Asn Ile Leu Cys Gly
 50 55 60

Phe Ala Arg Val Glu Xaa Arg Xaa Val Gly Ile Val Ala Asn Gln Pro
 65 70 75 80

Thr Gln Phe Ala Gly Xaa Leu Asp Ile Lys Ala Ser Glu Lys Ala Ala
 85 90 95

Arg Phe Ile Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Leu Glu Phe
 100 105 110

Val Asp Val Pro Gly Phe Leu Pro Gly Thr Asn Gln Glu Phe Asp Gly
 115 120 125

Ile Ile Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Ala Glu Ala Thr
 130 135 140

Val Gly Lys Ile Thr Val Ile Thr Arg Lys Ser Tyr Gly Gly Ala Tyr
 145 150 155 160

Cys Val Met Gly Ser Lys Asp Met Gly Ala Gly Leu Val
 165 170

<210> 211
 <211> 1752
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1729)
 <223> RXN02321

<400> 211
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 ttgtggacgt tcccccgcc taccgctacg atttcaaac atg acc att tcc tca 115
 Met Thr Ile Ser Ser
 1 5
 cct ttg att gac gtc gcc aac ctt cca gac atc aac acc act gcc ggc 163
 Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly
 10 15 20
 aag atc gcc gac ctt aag gct cgc cgc ggc gaa gcc cat ttc ccc atg 211
 Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met
 25 30 35
 ggt gaa aag gca gta gag aag gtc cac gct gct gga cgc ctc act gcc 259
 Gly Glu Lys Ala Val Glu Lys Val His Ala Ala Gly Arg Leu Thr Ala
 40 45 50
 cgt gag cgc ttg gat tac tta ctc gat gag ggc tcc ttc atc gag acc 307
 Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr
 55 60 65
 gat cag ctg gct cgc cac cgc acc acc gct ttc tgc ctg ggc gct aag 355
 Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe Cys Leu Gly Ala Lys
 70 75 80 85
 cgt cct gca acc gac ggt atc gtg acc ggc tgg ggc acc att gat gga 403
 Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly
 90 95 100
 cgc gaa gtc tgc atc ttc tcg cag gac ggc acc gta ttc ggt ggc gcg 451
 Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr Val Phe Gly Gly Ala
 105 110 115
 ctt ggt gag gtg tac ggc gaa aag atg atc aag atc atg gag ctg gca 499
 Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys Ile Met Glu Leu Ala
 120 125 130
 atc gac acc ggc cgc cca ttg atc ggt ctt tac gaa ggc gct ggc gct 547
 Ile Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr Glu Gly Ala Gly Ala
 135 140 145
 cgt att cag gac ggc gct gtc tcc ctg gac ttc att tcc cag acc ttc 595
 Arg Ile Gln Asp Gly Ala Val Ser Leu Asp Phe Ile Ser Gln Thr Phe
 150 155 160 165

<p> cac caa aac att cag gct tct ggc gtt atc cca cag atc tcc gtc atc Tyr Gln Asn Ile Gln Ala Ser Gly Val Ile Pro Gln Ile Ser Val Ile 170 175 180 </p>	643
<p> atg ggc gca tgt gca ggt ggc aac gct tac ggc cca gct ctg acc gac Met Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly Pro Ala Leu Thr Asp 185 190 195 </p>	691
<p> ttc gtg gtc atg gtg gac aag acc tcc aag atg ttc gtt acc ggc cca Phe Val Val Met Val Asp Lys Thr Ser Lys Met Phe Val Thr Gly Pro 200 205 210 </p>	739
<p> gac gtg atc aag acc gtc acc ggc gag gaa atc acc cag gaa gag ctt Asp Val Ile Lys Thr Val Thr Gly Glu Glu Ile Thr Gln Glu Glu Leu 215 220 225 </p>	787
<p> ggc gga gca acc acc cac atg gtg acc gct ggt aac tcc cac tac acc Gly Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser His Tyr Thr 230 235 240 245 </p>	835
<p> gct gcg acc gat gag gaa gca ctg gat tgg gta cag gac ctg gtg tcc Ala Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp Leu Val Ser 250 255 260 </p>	883
<p> ttc ctc cca tcc aac aat cgc tcc tac gca ccg atg gaa gac ttc gac Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Met Glu Asp Phe Asp 265 270 275 </p>	931
<p> gag gaa gaa ggc ggc gtt gaa gaa aac atc acc gct gac gat ctg aag Glu Glu Glu Gly Gly Val Glu Glu Asn Ile Thr Ala Asp Asp Leu Lys 280 285 290 </p>	979
<p> ctc gac gag atc atc cca gat tcc gcg acc gtt cct tac gac gtc cgc Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr Asp Val Arg 295 300 305 </p>	1027
<p> gat gtc atc gaa tgc ctc acc gac gat ggc gaa tac ctg gaa atc cag Asp Val Ile Glu Cys Leu Thr Asp Asp Gly Glu Tyr Leu Glu Ile Gln 310 315 320 325 </p>	1075
<p> gca gac cgc gca gaa aac gtt gtt att gca ttc ggc cgc atc gaa ggc Ala Asp Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg Ile Glu Gly 330 335 340 </p>	1123
<p> cag tcc gtt ggc ttt gtt gcc aac cag cca acc cag ttc gct ggc tgc Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr Gln Phe Ala Gly Cys 345 350 355 </p>	1171
<p> ctg gac atc gac tcc tct gag aag gca gct cgc ttc gtc cgc acc tgc Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val Arg Thr Cys 360 365 370 </p>	1219
<p> gac gcg ttc aac atc cca atc gtc atg ctt gtc gac gtc ccc ggc ttc Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val Pro Gly Phe 375 380 385 </p>	1267
<p> ctc cca ggc gca ggc cag gag tac ggt ggc att ctg cgt cgt ggc gca Leu Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala 390 395 400 405 </p>	1315
<p> aag ctg ctc tac gca tac ggc gaa gca acc gtt cca aag atc acc gtc </p>	1363

Lys Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val Pro Lys Ile Thr Val
 410 415 420
 acc atg cgt aag gct tac ggc gga gcg tac tgc gtg atg ggt tcc aag 1411
 Thr Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys Val Met Gly Ser Lys
 425 430 435
 ggc ttg ggc tct gac atc aac ctt gca tgg cca acc gca cag atc gcc 1459
 Gly Leu Gly Ser Asp Ile Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala
 440 445 450
 gtc atg ggc gct gct ggc gca gtt gga ttc atc tac cgc aag gag ctc 1507
 Val Met Gly Ala Ala Gly Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu
 455 460 465
 atg gca gct gat gcc aag ggc ctc gat acc gta gct ctg gct aag tcc 1555
 Met Ala Ala Asp Ala Lys Gly Leu Asp Thr Val Ala Leu Ala Lys Ser
 470 475 480 485
 ttc gag cgc gag tat gaa gac cac atg ctc aac ccg tac cac gct gca 1603
 Phe Glu Arg Glu Tyr Glu Asp His Met Leu Asn Pro Tyr His Ala Ala
 490 495 500
 gaa cgt ggc ctg atc gac gcc gtg atc ctg cca agc gaa acc cgc gga 1651
 Glu Arg Gly Leu Ile Asp Ala Val Ile Leu Pro Ser Glu Thr Arg Gly
 505 510 515
 cag att tcc cgc aac ctt cgc ctg ctc aag cac aag aac gtc act cgc 1699
 Gln Ile Ser Arg Asn Leu Arg Leu Leu Lys His Lys Asn Val Thr Arg
 520 525 530
 cct gct cgc aag cac ggc aac atg cca ctg taaatcggcg aatccataaaa 1749
 Pro Ala Arg Lys His Gly Asn Met Pro Leu
 535 540
 ggt 1752

<210> 212

<211> 543

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 212

Met Thr Ile Ser Ser Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile
 1 5 10 15
 Asn Thr Thr Ala Gly Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu
 20 25 30
 Ala His Phe Pro Met Gly Glu Lys Ala Val Glu Lys Val His Ala Ala
 35 40 45
 Gly Arg Leu Thr Ala Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly
 50 55 60
 Ser Phe Ile Glu Thr Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe
 65 70 75 80
 Cys Leu Gly Ala Lys Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp
 85 90 95

Gly Thr Ile Asp Gly Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr
 100 105 110
 Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys
 115 120 125
 Ile Met Glu Leu Ala Ile Asp Thr Gly Arg Pro Leu Ile Gly Leu Tyr
 130 135 140
 Glu Gly Ala Gly Ala Arg Ile Gln Asp Gly Ala Val Ser Leu Asp Phe
 145 150 155 160
 Ile Ser Gln Thr Phe Tyr Gln Asn Ile Gln Ala Ser Gly Val Ile Pro
 165 170 175
 Gln Ile Ser Val Ile Met Gly Ala Cys Ala Gly Gly Asn Ala Tyr Gly
 180 185 190
 Pro Ala Leu Thr Asp Phe Val Val Met Val Asp Lys Thr Ser Lys Met
 195 200 205
 Phe Val Thr Gly Pro Asp Val Ile Lys Thr Val Thr Gly Glu Glu Ile
 210 215 220
 Thr Gln Glu Glu Leu Gly Gly Ala Thr Thr His Met Val Thr Ala Gly
 225 230 235 240
 Asn Ser His Tyr Thr Ala Ala Thr Asp Glu Glu Ala Leu Asp Trp Val
 245 250 255
 Gln Asp Leu Val Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro
 260 265 270
 Met Glu Asp Phe Asp Glu Glu Glu Gly Gly Val Glu Glu Asn Ile Thr
 275 280 285
 Ala Asp Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val
 290 295 300
 Pro Tyr Asp Val Arg Asp Val Ile Glu Cys Leu Thr Asp Asp Gly Glu
 305 310 315 320
 Tyr Leu Glu Ile Gln Ala Asp Arg Ala Glu Asn Val Val Ile Ala Phe
 325 330 335
 Gly Arg Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr
 340 345 350
 Gln Phe Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg
 355 360 365
 Phe Val Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val
 370 375 380
 Asp Val Pro Gly Phe Leu Pro Gly Ala Gly Gln Glu Tyr Gly Gly Ile
 385 390 395 400
 Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Tyr Gly Glu Ala Thr Val
 405 410 415

Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr Gly Gly Ala Tyr Cys
 420 425 430

Val Met Gly Ser Lys Gly Leu Gly Ser Asp Ile Asn Leu Ala Trp Pro
 435 440 445

Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly Ala Val Gly Phe Ile
 450 455 460

Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys Gly Leu Asp Thr Val
 465 470 475 480

Ala Leu Ala Lys Ser Phe Glu Arg Glu Tyr Glu Asp His Met Leu Asn
 485 490 495

Pro Tyr His Ala Ala Glu Arg Gly Leu Ile Asp Ala Val Ile Leu Pro
 500 505 510

Ser Glu Thr Arg Gly Gln Ile Ser Arg Asn Leu Arg Leu Leu Lys His
 515 520 525

Lys Asn Val Thr Arg Pro Ala Arg Lys His Gly Asn Met Pro Leu
 530 535 540

<210> 213

<211> 467

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(444)

<223> FRXA02321

<400> 213

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Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Ser	
1 5 10 15	
gnn gaa gca ccg gtt cca aag atc acc gtc acc atg cgt aag gct tac	96
Xaa Glu Ala Pro Val Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr	
20 25 30	
ggc gga gcg tac tgc gtg atg ggt tcc aag ggc ttg ggc tct gac atc	144
Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Gly Leu Gly Ser Asp Ile	
35 40 45	
aac ctt gca tgg cca acc gca cag atc gcc gtc atg ggc gct gct ggc	192
Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly	
50 55 60	
gca gtt gga ttc atc tac cgc aag gag ctc atg gca gct gat gcc aag	240
Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys	
65 70 75 80	
ggc ctc gat acc gta gct ctg gct aag tcc ttc gag cgc gag tat gaa	288
Gly Leu Asp Thr Val Ala Leu Ala Lys Ser Phe Glu Arg Glu Tyr Glu	
85 90 95	
gac cac atg ctc aac ccg tac cac gct gca gaa cgt ggc ctg atc gac	336

Asp His Met Leu Asn Pro Tyr His Ala Ala Glu Arg Gly Leu Ile Asp
 100 105 110

gcc gtg atc ctg cca agc gaa acc cgc gga cag att tcc cgc aac ctt 384
 Ala Val Ile Leu Pro Ser Glu Thr Arg Gly Gln Ile Ser Arg Asn Leu
 115 120 125

cgc ctg ctc aag cac aag aac gtc act cgc cct gct cgc aag cac ggc 432
 Arg Leu Leu Lys His Lys Asn Val Thr Arg Pro Ala Arg Lys His Gly
 130 135 140

aac atg cca ctg taaatcggcg aatccataaa ggt 467
 Asn Met Pro Leu
 145

<210> 214
 <211> 148
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 214
 Glu Tyr Gly Gly Ile Leu Arg Arg Gly Ala Lys Leu Leu Tyr Ala Ser
 1 5 10 15

Xaa Glu Ala Pro Val Pro Lys Ile Thr Val Thr Met Arg Lys Ala Tyr
 20 25 30

Gly Gly Ala Tyr Cys Val Met Gly Ser Lys Gly Leu Gly Ser Asp Ile
 35 40 45

Asn Leu Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly Ala Ala Gly
 50 55 60

Ala Val Gly Phe Ile Tyr Arg Lys Glu Leu Met Ala Ala Asp Ala Lys
 65 70 75 80

Gly Leu Asp Thr Val Ala Leu Ala Lys Ser Phe Glu Arg Glu Tyr Glu
 85 90 95

Asp His Met Leu Asn Pro Tyr His Ala Ala Glu Arg Gly Leu Ile Asp
 100 105 110

Ala Val Ile Leu Pro Ser Glu Thr Arg Gly Gln Ile Ser Arg Asn Leu
 115 120 125

Arg Leu Leu Lys His Lys Asn Val Thr Arg Pro Ala Arg Lys His Gly
 130 135 140

Asn Met Pro Leu
 145

<210> 215
 <211> 514
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(514)

<223> FRXA02343

<400> 215

tttaaaaaact acccgcacgc agcacgaacc tgttcagtga tgtaaatacac cgcggaaata 60

ttgtggacgt tcccccgcc taccgctacg atttcaaaac atg acc att tcc tca 115
 Met Thr Ile Ser Ser
 1 5

cct ttg att gac gtc gcc aac ctt cca gac atc aac acc act gcc ggc 163
 Pro Leu Ile Asp Val Ala Asn Leu Pro Asp Ile Asn Thr Thr Ala Gly
 10 15 20

aag atc gcc gac ctt aag gct cgc cgc ggc gaa gcc cat ttc ccc atg 211
 Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu Ala His Phe Pro Met
 25 30 35

ggt gaa aag gca gta gag aag gtc cac gct gct gga cgc ctc act gcc 259
 Gly Glu Lys Ala Val Glu Lys Val His Ala Ala Gly Arg Leu Thr Ala
 40 45 50

cgt gag cgc ttg gat tac tta ctc gat gag ggc tcc ttc atc gag acc 307
 Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly Ser Phe Ile Glu Thr
 55 60 65

gat cag ctg gct cgc cac cgc acc acc gct ttc tgc ctg ggc gct aag 355
 Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe Cys Leu Gly Ala Lys
 70 75 80 85

cgt cct gca acc gac ggc atc gtg acc ggc tgg ggc acc att gat gga 403
 Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp Gly Thr Ile Asp Gly
 90 95 100

cgc gaa gtc tgc atc ttc tcg cag gac ggc acc gta ttc ggt ggc gcg 451
 Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr Val Phe Gly Gly Ala
 105 110 115

ctt ggt gag gtg tac ggc gaa aag atg atc aag atc atg gag ctg gca 499
 Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys Ile Met Glu Leu Ala
 120 125 130

atc gac acc ggc cgc 514
 Ile Asp Thr Gly Arg
 135

<210> 216

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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Asn Thr Thr Ala Gly Lys Ile Ala Asp Leu Lys Ala Arg Arg Ala Glu
 20 25 30

Ala His Phe Pro Met Gly Glu Lys Ala Val Glu Lys Val His Ala Ala
 35 40 45

Gly Arg Leu Thr Ala Arg Glu Arg Leu Asp Tyr Leu Leu Asp Glu Gly
 50 55 60

Ser Phe Ile Glu Thr Asp Gln Leu Ala Arg His Arg Thr Thr Ala Phe
 65 70 75 80

Cys Leu Gly Ala Lys Arg Pro Ala Thr Asp Gly Ile Val Thr Gly Trp
 85 90 95

Gly Thr Ile Asp Gly Arg Glu Val Cys Ile Phe Ser Gln Asp Gly Thr
 100 105 110

Val Phe Gly Gly Ala Leu Gly Glu Val Tyr Gly Glu Lys Met Ile Lys
 115 120 125

Ile Met Glu Leu Ala Ile Asp Thr Gly Arg
 130 135

<210> 217

<211> 492

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(492)

<223> FRXA02850

<400> 217

gaa gag ctt ggc gga gca acc acc cac atg gtg acc gct ggt aac tcc 48
 Glu Glu Leu Gly Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser
 1 5 10 15

cac tac acc gct gcg acc gat gag gaa gca ctg gat tgg gta cag gac 96
 His Tyr Thr Ala Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp
 20 25 30

ctg gtg tcc ttc ctc cca tcc aac aat cgc tcc tac gca ccg atg gaa 144
 Leu Val Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Met Glu
 35 40 45

gac ttc gac gag gaa gaa ggc ggc gtt gaa gaa aac atc acc gct gac 192
 Asp Phe Asp Glu Glu Glu Gly Gly Val Glu Glu Asn Ile Thr Ala Asp
 50 55 60

gat ctg aag ctc gac gag atc atc cca gat tcc gcg acc gtt cct tac 240
 Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr
 65 70 75 80

gac gtc cgc gat gtc atn gaa tgc ctc acc gac gat ggc gaa tac ctg 288
 Asp Val Arg Asp Val Xaa Glu Cys Leu Thr Asp Asp Gly Glu Tyr Leu
 85 90 95

gaa atc cag gca gnc cgc gca gaa aac gtt gtt att gca ttc ggc cgc 336
 Glu Ile Gln Ala Xaa Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg
 100 105 110

atc gaa ggc cag tcc gtt ggc ttt gtt gcc aac cag cca acc cag ttc 384
 Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr Gln Phe
 115 120 125

gct ggc tgc ctg gac atc gac tcc tct gag aag gca gct cgc ttc gtc 432
 Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val
 130 135 140

cgc acc tgc gac gcg ttc aac atc cca atc gtc atg ctt gtg gac gtc 480
 Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val
 145 150 155 160

ccc ggc ttc ctc 492
 Pro Gly Phe Leu

<210> 218
 <211> 164
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 218
 Glu Glu Leu Gly Gly Ala Thr Thr His Met Val Thr Ala Gly Asn Ser
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His Tyr Thr Ala Ala Thr Asp Glu Glu Ala Leu Asp Trp Val Gln Asp
 20 25 30

Leu Val Ser Phe Leu Pro Ser Asn Asn Arg Ser Tyr Ala Pro Met Glu
 35 40 45

Asp Phe Asp Glu Glu Glu Gly Gly Val Glu Glu Asn Ile Thr Ala Asp
 50 55 60

Asp Leu Lys Leu Asp Glu Ile Ile Pro Asp Ser Ala Thr Val Pro Tyr
 65 70 75 80

Asp Val Arg Asp Val Xaa Glu Cys Leu Thr Asp Asp Gly Glu Tyr Leu
 85 90 95

Glu Ile Gln Ala Xaa Arg Ala Glu Asn Val Val Ile Ala Phe Gly Arg
 100 105 110

Ile Glu Gly Gln Ser Val Gly Phe Val Ala Asn Gln Pro Thr Gln Phe
 115 120 125

Ala Gly Cys Leu Asp Ile Asp Ser Ser Glu Lys Ala Ala Arg Phe Val
 130 135 140

Arg Thr Cys Asp Ala Phe Asn Ile Pro Ile Val Met Leu Val Asp Val
 145 150 155 160

Pro Gly Phe Leu

<210> 219
 <211> 1671
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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<222> (101)..(1648)

<223> RXA02583

<400> 219

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 Leu Ser Asn Thr Thr
 1 5

act gca gag aag cta gcg gat ctg cgc gca cgc ctg gag att gcc aaa 163
 Thr Ala Glu Lys Leu Ala Asp Leu Arg Ala Arg Leu Glu Ile Ala Lys
 10 15 20

gac cca ggt agt gaa cgc gca cgt aaa aag cgc gac gag gaa ggc cga 211
 Asp Pro Gly Ser Glu Arg Ala Arg Lys Lys Arg Asp Glu Glu Gly Arg
 25 30 35

acc acc cct cgt cag cgt att gat gct ctg ctt gat gcc gga tcc ttt 259
 Thr Thr Pro Arg Gln Arg Ile Asp Ala Leu Leu Asp Ala Gly Ser Phe
 40 45 50

gtg gag atc ggc gca cta ggc cgt acc ccg gat gaa ccc gat gcg cct 307
 Val Glu Ile Gly Ala Leu Gly Arg Thr Pro Asp Glu Pro Asp Ala Pro
 55 60 65

tac tct gac ggt gtg gtg act ggt tat ggt cgc atc gat ggt cgc cca 355
 Tyr Ser Asp Gly Val Val Thr Gly Tyr Gly Arg Ile Asp Gly Arg Pro
 70 75 80 85

gtg gcc atc tac gcc cat gac aag acc gtt tac ggt ggt tcc gtg ggc 403
 Val Ala Ile Tyr Ala His Asp Lys Thr Val Tyr Gly Gly Ser Val Gly
 90 95 100

atg act ttc gga cgt aaa gtc agc gaa gtc atg gac atg gct atc cgc 451
 Met Thr Phe Gly Arg Lys Val Ser Glu Val Met Asp Met Ala Ile Arg
 105 110 115

att ggt tgc cca gtt atc ggt att cag gat tcc ggc gga gcc cgc att 499
 Ile Gly Cys Pro Val Ile Gly Ile Gln Asp Ser Gly Gly Ala Arg Ile
 120 125 130

cag gat gcg gtg acc tcc ttg gcg atg tac tca gag atc gcg cgt cgt 547
 Gln Asp Ala Val Thr Ser Leu Ala Met Tyr Ser Glu Ile Ala Arg Arg
 135 140 145

cag ctt ccg ctg tct ggc cgc agc cct cag att tcc atc atg ctg ggt 595
 Gln Leu Pro Leu Ser Gly Arg Ser Pro Gln Ile Ser Ile Met Leu Gly
 150 155 160 165

aaa tcg gca ggt ggc gca gtg tat gca cct gtg acc act gac ttt gtt 643
 Lys Ser Ala Gly Gly Ala Val Tyr Ala Pro Val Thr Thr Asp Phe Val
 170 175 180

atc ggc gtt gat ggt gaa aca gaa atg tat gtc acc ggc cca gcc gtg 691
 Ile Gly Val Asp Gly Glu Thr Glu Met Tyr Val Thr Gly Pro Ala Val
 185 190 195

atc aag gaa gtc acc ggc gag cag atc act tcc gca gac ctc ggt ggc 739
 Ile Lys Glu Val Thr Gly Glu Gln Ile Thr Ser Ala Asp Leu Gly Gly
 200 205 210

ggt gcg cag cag atg caa aac ggc aac att tcc tat ttg gcg tcc tct Gly Ala Gln Gln Met Gln Asn Gly Asn Ile Ser Tyr Leu Ala Ser Ser 215 220 225	787
gaa gaa gag gcc ctg aat atg gtc aag gat ttg ctc gac ttc ctg cct Glu Glu Glu Ala Leu Asn Met Val Lys Asp Leu Leu Asp Phe Leu Pro 230 235 240 245	835
ttg acc tgc aat gat cca gcc cct gtg ttt gca gca cca acg gat gaa Leu Thr Cys Asn Asp Pro Ala Pro Val Phe Ala Ala Pro Thr Asp Glu 250 255 260	883
gag atc gcc tac gac gaa gct ctg aac tcg ttc atg cct gac gac act Glu Ile Ala Tyr Asp Glu Ala Leu Asn Ser Phe Met Pro Asp Asp Thr 265 270 275	931
aac cag ggc tac gac atg cat gac ctg ctg gac aag ctt ttc gac gac Asn Gln Gly Tyr Asp Met His Asp Leu Leu Asp Lys Leu Phe Asp Asp 280 285 290	979
gcc aac ctg ctg gaa atc caa gag gag tac gcc ccc aac ctg atc act Ala Asn Leu Leu Glu Ile Gln Glu Glu Tyr Ala Pro Asn Leu Ile Thr 295 300 305	1027
acc ttc gcc cgc gtt gat ggc aag gca gtc ggt gtg gtg gcc aac caa Thr Phe Ala Arg Val Asp Gly Lys Ala Val Gly Val Val Ala Asn Gln 310 315 320 325	1075
cca atg gat aag gca ggc tgc atc gac gct gac gcc gcc gac aag ggc Pro Met Asp Lys Ala Gly Cys Ile Asp Ala Asp Ala Ala Asp Lys Gly 330 335 340	1123
gcc cgc ttc atc cgt atc tgc gac gcc tac aac atc ccg atc atc ttc Ala Arg Phe Ile Arg Ile Cys Asp Ala Tyr Asn Ile Pro Ile Ile Phe 345 350 355	1171
gtc gtg gac acc cct ggc tac ctg cct ggc gtg gac caa gag aag gtc Val Val Asp Thr Pro Gly Tyr Leu Pro Gly Val Asp Gln Glu Lys Val 360 365 370	1219
ggt ttg att cac cgt ggc gca aag cta gcc ttc gca gtg gtg gaa tcg Gly Leu Ile His Arg Gly Ala Lys Leu Ala Phe Ala Val Val Glu Ser 375 380 385	1267
acc gtc cct aag att tcc ttg atc gtg cgc aag gcc tac ggc gga gca Thr Val Pro Lys Ile Ser Leu Ile Val Arg Lys Ala Tyr Gly Gly Ala 390 395 400 405	1315
tat gcc gtg atg ggt tcc aag aac ctc acc ggt gac ctc aac ttc gca Tyr Ala Val Met Gly Ser Lys Asn Leu Thr Gly Asp Leu Asn Phe Ala 410 415 420	1363
tgg cca acc gca cag atc gcc gtg atg ggc gca gcc gca gct gtc gtg Trp Pro Thr Ala Gln Ile Ala Val Met Gly Ala Ala Ala Ala Val Val 425 430 435	1411
atg atc cag ggc aag cag ctc gaa gcc gcc cca cct gag cag cgt gaa Met Ile Gln Gly Lys Gln Leu Glu Ala Ala Pro Pro Glu Gln Arg Glu 440 445 450	1459

tac atg aag aaa ctg ttc atg gac ttc tac gat gag aac atg acc agc 1507
 Tyr Met Lys Lys Leu Phe Met Asp Phe Tyr Asp Glu Asn Met Thr Ser
 455 460 465

cca tat gtg gcc gcc gag cgt ggt tac atc gac gcc atg atc gaa cct 1555
 Pro Tyr Val Ala Ala Glu Arg Gly Tyr Ile Asp Ala Met Ile Glu Pro
 470 475 480 485

gca gag acc cgt ttg gtg ctt cgc cga gca gtc cgc cag ctg gaa acc 1603
 Ala Glu Thr Arg Leu Val Leu Arg Arg Ala Val Arg Gln Leu Glu Thr
 490 495 500

aag gct gtg cga gac ctc gac aag aag cac acg atc atg ccg atg 1648
 Lys Ala Val Arg Asp Leu Asp Lys Lys His Thr Ile Met Pro Met
 505 510 515

taacgtccaa agaattatcc aga 1671

<210> 220
 <211> 516
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 220
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 20 25 30
 Asp Glu Glu Gly Arg Thr Thr Pro Arg Gln Arg Ile Asp Ala Leu Leu
 35 40 45
 Asp Ala Gly Ser Phe Val Glu Ile Gly Ala Leu Gly Arg Thr Pro Asp
 50 55 60
 Glu Pro Asp Ala Pro Tyr Ser Asp Gly Val Val Thr Gly Tyr Gly Arg
 65 70 75 80
 Ile Asp Gly Arg Pro Val Ala Ile Tyr Ala His Asp Lys Thr Val Tyr
 85 90 95
 Gly Gly Ser Val Gly Met Thr Phe Gly Arg Lys Val Ser Glu Val Met
 100 105 110
 Asp Met Ala Ile Arg Ile Gly Cys Pro Val Ile Gly Ile Gln Asp Ser
 115 120 125
 Gly Gly Ala Arg Ile Gln Asp Ala Val Thr Ser Leu Ala Met Tyr Ser
 130 135 140
 Glu Ile Ala Arg Arg Gln Leu Pro Leu Ser Gly Arg Ser Pro Gln Ile
 145 150 155 160
 Ser Ile Met Leu Gly Lys Ser Ala Gly Gly Ala Val Tyr Ala Pro Val
 165 170 175
 Thr Thr Asp Phe Val Ile Gly Val Asp Gly Glu Thr Glu Met Tyr Val
 180 185 190

Thr Gly Pro Ala Val Ile Lys Glu Val Thr Gly Glu Gln Ile Thr Ser
 195 200 205
 Ala Asp Leu Gly Gly Gly Ala Gln Gln Met Gln Asn Gly Asn Ile Ser
 210 215 220
 Tyr Leu Ala Ser Ser Glu Glu Glu Ala Leu Asn Met Val Lys Asp Leu
 225 230 235 240
 Leu Asp Phe Leu Pro Leu Thr Cys Asn Asp Pro Ala Pro Val Phe Ala
 245 250 255
 Ala Pro Thr Asp Glu Glu Ile Ala Tyr Asp Glu Ala Leu Asn Ser Phe
 260 265 270
 Met Pro Asp Asp Thr Asn Gln Gly Tyr Asp Met His Asp Leu Leu Asp
 275 280 285
 Lys Leu Phe Asp Asp Ala Asn Leu Leu Glu Ile Gln Glu Glu Tyr Ala
 290 295 300
 Pro Asn Leu Ile Thr Thr Phe Ala Arg Val Asp Gly Lys Ala Val Gly
 305 310 315 320
 Val Val Ala Asn Gln Pro Met Asp Lys Ala Gly Cys Ile Asp Ala Asp
 325 330 335
 Ala Ala Asp Lys Gly Ala Arg Phe Ile Arg Ile Cys Asp Ala Tyr Asn
 340 345 350
 Ile Pro Ile Ile Phe Val Val Asp Thr Pro Gly Tyr Leu Pro Gly Val
 355 360 365
 Asp Gln Glu Lys Val Gly Leu Ile His Arg Gly Ala Lys Leu Ala Phe
 370 375 380
 Ala Val Val Glu Ser Thr Val Pro Lys Ile Ser Leu Ile Val Arg Lys
 385 390 395 400
 Ala Tyr Gly Gly Ala Tyr Ala Val Met Gly Ser Lys Asn Leu Thr Gly
 405 410 415
 Asp Leu Asn Phe Ala Trp Pro Thr Ala Gln Ile Ala Val Met Gly Ala
 420 425 430
 Ala Ala Ala Val Val Met Ile Gln Gly Lys Gln Leu Glu Ala Ala Pro
 435 440 445
 Pro Glu Gln Arg Glu Tyr Met Lys Lys Leu Phe Met Asp Phe Tyr Asp
 450 455 460
 Glu Asn Met Thr Ser Pro Tyr Val Ala Ala Glu Arg Gly Tyr Ile Asp
 465 470 475 480
 Ala Met Ile Glu Pro Ala Glu Thr Arg Leu Val Leu Arg Arg Ala Val
 485 490 495
 Arg Gln Leu Glu Thr Lys Ala Val Arg Asp Leu Asp Lys Lys His Thr
 500 505 510
 Ile Met Pro Met

515

<210> 221
 <211> 1635
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1612)
 <223> RXA00870

<400> 221

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caacaattca cttcgagag catttaagga atttacacac atg tct gaa cca caa 115
                                         Met Ser Glu Pro Gln
                                         1      5

acc atc tcg cac tgg att gac ggc gcg att tcc cca tcc act tcc ggc 163
Thr Ile Ser His Trp Ile Asp Gly Ala Ile Ser Pro Ser Thr Ser Gly
                        10                        15                        20

aag acc gct cct gtc tac aat cct gca act ggc cag gtc acc gcc aat 211
Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly Gln Val Thr Ala Asn
                        25                        30                        35

gtt gcg ctg gct agc cag gaa gag atc gat gcc acc atc gct tct gcc 259
Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala Thr Ile Ala Ser Ala
                        40                        45                        50

acc aag gct gct aag acg tgg ggc aac ctg tct atc gct aag cgc caa 307
Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser Ile Ala Lys Arg Gln
                        55                        60                        65

gct gtg ctt ttc aac ttc cgt gag ctg ctg aat gct cgc aag ggt gag 355
Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn Ala Arg Lys Gly Glu
                        70                        75                        80                        85

ctg gcg gag atc atc act gca gag cac ggc aag gtc ttg tcc gat gcc 403
Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys Val Leu Ser Asp Ala
                        90                        95                        100

atg ggt gaa atc ctg cgc ggc cag gaa gtc gtg gag ctt gct acc ggt 451
Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val Glu Leu Ala Thr Gly
                        105                        110                        115

ttc cca cac ctg ctt aaa ggt gcg ttc aac gag aac gtc tcc acc ggc 499
Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu Asn Val Ser Thr Gly
                        120                        125                        130

att gat gtg tat tcc ttg aag cag cca ctg ggt gtt gtc ggt atc atc 547
Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly Val Val Gly Ile Ile
                        135                        140                        145

agc ccg ttc aac ttc cct gcg atg gtg ccg atg tgg ttt ttc cca atc 595
Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met Trp Phe Phe Pro Ile
                        150                        155                        160                        165

gca atc gct gca ggc aac gca gtt att ttg aag cct tca gag aag gat 643

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Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys Pro Ser Glu Lys Asp	
170 175 180	
cct tcg gca gcg ctg tgg atg gct cag atc tgg aag gaa gct ggt ctt	691
Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp Lys Glu Ala Gly Leu	
185 190 195	
cca gac ggc gta ttc aac gtg ctc cag ggc gac aag ctg gct gtt gat	739
Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp Lys Leu Ala Val Asp	
200 205 210	
ggt ttg ctg aac agc cct gat gtc tct gcg att tcc ttc gtg ggt tcc	787
Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile Ser Phe Val Gly Ser	
215 220 225	
acc cca atc gca aag tac atc tac gag act tcc gcg aag aac ggc aag	835
Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser Ala Lys Asn Gly Lys	
230 235 240 245	
cgc gtc cag gcg ttg ggc ggc gcg aag aac cac atg ctg gtg ctg cca	883
Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His Met Leu Val Leu Pro	
250 255 260	
gat gct gat ctg gat ctg gtt gcc gat cag gca atc aac gca ggt tac	931
Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala Ile Asn Ala Gly Tyr	
265 270 275	
ggc gct gcc ggt gag cgt tgc atg gct gtt tct gtg gtc ttg gct att	979
Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser Val Val Leu Ala Ile	
280 285 290	
gaa tct gtt gcc gac gag ctc att gag aag atc aag gag cgc atc gac	1027
Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile Lys Glu Arg Ile Asp	
295 300 305	
acc ctg cgc atc ggc aac ggt gcc ggc gac gag cag ggc gag ccg cac	1075
Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu Gln Gly Glu Pro His	
310 315 320 325	
ctg ggc cca cta atc acc gac gtc cac cgc gac aag gtc gct tct tat	1123
Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp Lys Val Ala Ser Tyr	
330 335 340	
gtc gac atc gct gag gcc gac ggc gcc aag atc atc gtg gac ggg cgt	1171
Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile Ile Val Asp Gly Arg	
345 350 355	
aac tgc gcc gta gac ggg cac gag gag ggc ttc ttc ttc ggc cct acg	1219
Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe Phe Phe Gly Pro Thr	
360 365 370	
ctt atc gac gac atc cca ct'c acg ttc cgc gcc tac acc gaa gaa atc	1267
Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala Tyr Thr Glu Glu Ile	
375 380 385	
ttc ggc ccg gtc ctc tct gtc gtt cgt gtc gca tcc ttc gac gag gca	1315
Phe Gly Pro Val Leu Ser Val Val Arg Val Ala Ser Phe Asp Glu Ala	
390 395 400 405	
att gag ctg atc aac tcc ggt gaa ttc ggc aac gga acc gca atc ttc	1363
Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn Gly Thr Ala Ile Phe	

	410	415	420	
acc aac gat ggt gga gcg gca cgc cgc ttc cag cat gag atc gaa gtg				1411
Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln His Glu Ile Glu Val				
	425	430	435	
ggc atg atc ggc atc aac gta cca atc cca gtg cct gtt gcg tac cac				1459
Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val Pro Val Ala Tyr His				
	440	445	450	
tcc ttc ggt ggt tgg aag aac tcc ctc ttc ggt gac gcc aag gca tat				1507
Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly Asp Ala Lys Ala Tyr				
	455	460	465	
ggc act caa ggt ttt gat ttc ttc acc agg gaa aag gcg atc acc agc				1555
Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu Lys Ala Ile Thr Ser				
	470	475	480	485
cgt tgg ctc gac cca gca acc cac ggt ggc att aac ctc ggt ttc cca				1603
Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile Asn Leu Gly Phe Pro				
	490	495	500	
cag aac gat taattgaagg agagcacagg act				1635
Gln Asn Asp				

<210> 222

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

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Pro Ser Thr Ser Gly Lys Thr Ala Pro Val Tyr Asn Pro Ala Thr Gly				
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Gln Val Thr Ala Asn Val Ala Leu Ala Ser Gln Glu Glu Ile Asp Ala				
	35	40	45	
Thr Ile Ala Ser Ala Thr Lys Ala Ala Lys Thr Trp Gly Asn Leu Ser				
	50	55	60	
Ile Ala Lys Arg Gln Ala Val Leu Phe Asn Phe Arg Glu Leu Leu Asn				
	65	70	75	80
Ala Arg Lys Gly Glu Leu Ala Glu Ile Ile Thr Ala Glu His Gly Lys				
	85	90	95	
Val Leu Ser Asp Ala Met Gly Glu Ile Leu Arg Gly Gln Glu Val Val				
	100	105	110	
Glu Leu Ala Thr Gly Phe Pro His Leu Leu Lys Gly Ala Phe Asn Glu				
	115	120	125	
Asn Val Ser Thr Gly Ile Asp Val Tyr Ser Leu Lys Gln Pro Leu Gly				
	130	135	140	
Val Val Gly Ile Ile Ser Pro Phe Asn Phe Pro Ala Met Val Pro Met				

145		150		155		160
Trp Phe Phe Pro Ile Ala Ile Ala Ala Gly Asn Ala Val Ile Leu Lys						
	165			170		175
Pro Ser Glu Lys Asp Pro Ser Ala Ala Leu Trp Met Ala Gln Ile Trp						
	180		185			190
Lys Glu Ala Gly Leu Pro Asp Gly Val Phe Asn Val Leu Gln Gly Asp						
	195		200			205
Lys Leu Ala Val Asp Gly Leu Leu Asn Ser Pro Asp Val Ser Ala Ile						
	210		215		220	
Ser Phe Val Gly Ser Thr Pro Ile Ala Lys Tyr Ile Tyr Glu Thr Ser						
225		230		235		240
Ala Lys Asn Gly Lys Arg Val Gln Ala Leu Gly Gly Ala Lys Asn His						
	245		250			255
Met Leu Val Leu Pro Asp Ala Asp Leu Asp Leu Val Ala Asp Gln Ala						
	260		265			270
Ile Asn Ala Gly Tyr Gly Ala Ala Gly Glu Arg Cys Met Ala Val Ser						
	275		280			285
Val Val Leu Ala Ile Glu Ser Val Ala Asp Glu Leu Ile Glu Lys Ile						
	290		295		300	
Lys Glu Arg Ile Asp Thr Leu Arg Ile Gly Asn Gly Ala Gly Asp Glu						
305		310		315		320
Gln Gly Glu Pro His Leu Gly Pro Leu Ile Thr Asp Val His Arg Asp						
	325		330			335
Lys Val Ala Ser Tyr Val Asp Ile Ala Glu Ala Asp Gly Ala Lys Ile						
	340		345			350
Ile Val Asp Gly Arg Asn Cys Ala Val Asp Gly His Glu Glu Gly Phe						
	355		360			365
Phe Phe Gly Pro Thr Leu Ile Asp Asp Ile Pro Leu Thr Phe Arg Ala						
	370		375			380
Tyr Thr Glu Glu Ile Phe Gly Pro Val Leu Ser Val Val Arg Val Ala						
385		390		395		400
Ser Phe Asp Glu Ala Ile Glu Leu Ile Asn Ser Gly Glu Phe Gly Asn						
	405		410			415
Gly Thr Ala Ile Phe Thr Asn Asp Gly Gly Ala Ala Arg Arg Phe Gln						
	420		425			430
His Glu Ile Glu Val Gly Met Ile Gly Ile Asn Val Pro Ile Pro Val						
	435		440			445
Pro Val Ala Tyr His Ser Phe Gly Gly Trp Lys Asn Ser Leu Phe Gly						
	450		455		460	
Asp Ala Lys Ala Tyr Gly Thr Gln Gly Phe Asp Phe Phe Thr Arg Glu						
465		470		475		480

Lys Ala Ile Thr Ser Arg Trp Leu Asp Pro Ala Thr His Gly Gly Ile
 485 490 495

Asn Leu Gly Phe Pro Gln Asn Asp
 500

<210> 223

<211> 1305

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1282)

<223> RXA01260

<400> 223

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 Val Thr Phe Asn Tyr 5
 1
 gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163
 Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly 20
 10 15
 ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211
 Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly 35
 25 30
 ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259
 Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys 50
 40 45
 gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307
 Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly 65
 55 60
 tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355
 Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val 85
 70 75 80
 tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403
 Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val 100
 90 95
 att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451
 Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly 115
 105 110
 aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt 499
 Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu 130
 120 125
 cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag 547
 Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys 145
 135 140

aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg	595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg	
150 155 160 165	
gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac	643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp	
170 175 180	
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe	
185 190 195	
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc	739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu	
200 205 210	
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc	787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val	
215 220 225	
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct	835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala	
230 235 240 245	
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly	
250 255 260	
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc	931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr	
265 270 275	
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc	979
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala	
280 285 290	
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc	1027
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe	
295 300 305	
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca	1075
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala	
310 315 320 325	
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg	1123
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu	
330 335 340	
gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag	1171
Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln	
345 350 355	
aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac	1219
Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His	
360 365 370	
cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga	1267
Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly	
375 380 385	
cac atg atc aac ttc tagaatccac ctcggttgccc ctg	1305

His Met Ile Asn Phe
390

<210> 224

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser
1 5 10 15

Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile
20 25 30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu
35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
50 55 60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
115 120 125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
130 135 140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
145 150 155 160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
165 170 175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met
180 185 190

Val Ser Val Gly Phe Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn
195 200 205

Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr
210 215 220

Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala
225 230 235 240

Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val Ala Ala
245 250 255

Glu Thr Ile Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met
260 265 270

Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr
 275 280 285

Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val
 290 295 300

Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu
 305 310 315 320

Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu
 325 330 335

Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu
 340 345 350

Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg
 355 360 365

Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala
 370 375 380

His Gly Ile Ser Gly His Met Ile Asn Phe
 385 390

<210> 225

<211> 294

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(271)

<223> RXA01261

<400> 225

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atgcacgaca atgaccact aaacacgtat ccttgaatgc gtg act gaa cat tat 115
 Val Thr Glu His Tyr
 1 5

gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163
 Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile
 10 15 20

cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac 211
 Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr
 25 30 35

tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct 259
 Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser
 40 45 50

gat caa aaa cgc tgaagttgcc cataccttta ccc 294
 Asp Gln Lys Arg
 55

<210> 226

<211> 57

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly
 1 5 10 15
 Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val
 20 25 30
 Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile
 35 40 45
 Pro Ser Lys Val Ser Asp Gln Lys Arg
 50 55

<210> 227

<211> 555

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(532)

<223> RXA01136

<400> 227

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 ctaggacctg tctactgcct tcactttgtg cgaacaccgc atg acc ttg gat tac 115
 Met Thr Leu Asp Tyr
 1 5
 ttc aag gca tcc ggc act gac tat gct ttg gga ttg gct gca gag tcg 163
 Phe Lys Ala Ser Gly Thr Asp Tyr Ala Leu Gly Leu Ala Ala Glu Ser
 10 15 20
 gaa ggg gca cga cgc act ggt atc acc ggc atg gcg agt gca ttc aag 211
 Glu Gly Ala Arg Arg Thr Gly Ile Thr Gly Met Ala Ser Ala Phe Lys
 25 30 35
 gag ttt gct ggt tgt ggt gag atc gac ctt gaa gca acc agg gta gaa 259
 Glu Phe Ala Gly Cys Gly Glu Ile Asp Leu Glu Ala Thr Arg Val Glu
 40 45 50
 ggt ggc ctc aaa gtt agt gga aag ctt cgt tgg gct tcc aac ttg tgc 307
 Gly Gly Leu Lys Val Ser Gly Lys Leu Arg Trp Ala Ser Asn Leu Cys
 55 60 65
 gaa gat cca gtg att gtg cct gct gca aag acc gca gag ggc tta caa 355
 Glu Asp Pro Val Ile Val Pro Ala Ala Lys Thr Ala Glu Gly Leu Gln
 70 75 80 85
 cta ctg ttc gca ttg ggc gca gaa aac gaa ggt gtc acc ctc ggt tct 403
 Leu Leu Phe Ala Leu Gly Ala Glu Thr Glu Gly Val Thr Leu Gly Ser
 90 95 100
 tca ctt gct cta ctc ggt ttg aac gca act gct tgc gct tgg gtg agc 451
 Ser Leu Ala Leu Leu Gly Leu Asn Ala Thr Ala Cys Ala Trp Val Ser
 105 110 115

ttt gag gat gtc ttc att cct ggg gct cag att cta agc cac gat ttc 499
 Phe Glu Asp Val Phe Ile Pro Gly Ala Gln Ile Leu Ser His Asp Phe
 120 125 130

ctt acc ttg tgg cat cgg tgc gcc caa cct tcg tgatcctacg gatctccgaa 552
 Leu Thr Leu Trp His Arg Cys Ala Gln Pro Ser
 135 140

tac 555

<210> 228

<211> 144

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Met Thr Leu Asp Tyr Phe Lys Ala Ser Gly Thr Asp Tyr Ala Leu Gly
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Leu Ala Ala Glu Ser Glu Gly Ala Arg Arg Thr Gly Ile Thr Gly Met
 20 25 30

Ala Ser Ala Phe Lys Glu Phe Ala Gly Cys Gly Glu Ile Asp Leu Glu
 35 40 45

Ala Thr Arg Val Glu Gly Gly Leu Lys Val Ser Gly Lys Leu Arg Trp
 50 55 60

Ala Ser Asn Leu Cys Glu Asp Pro Val Ile Val Pro Ala Ala Lys Thr
 65 70 75 80

Ala Glu Gly Leu Gln Leu Leu Phe Ala Leu Gly Ala Glu Thr Glu Gly
 85 90 95

Val Thr Leu Gly Ser Ser Leu Ala Leu Leu Gly Leu Asn Ala Thr Ala
 100 105 110

Cys Ala Trp Val Ser Phe Glu Asp Val Phe Ile Pro Gly Ala Gln Ile
 115 120 125

Leu Ser His Asp Phe Leu Thr Leu Trp His Arg Cys Ala Gln Pro Ser
 130 135 140

<210> 229

<211> 1140

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1117)

<223> RXN00559

<400> 229

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catgaagcat cagcctagta cgaaccgtta aagtgtccat atg tct gat aat ccg	115
Met Ser Asp Asn Pro	
1 5	
cat gag aat ccc cgt gag aat cca cac cgc tcc cca gaa gtc gtc ctt	163
His Glu Asn Pro Arg Glu Asn Pro His Arg Ser Pro Glu Val Val Leu	
10 15 20	
cgt ttc atg gct gcc cct act gac gtt ttg atg gct ggt agc cat ggc	211
Arg Phe Met Ala Ala Pro Thr Asp Val Leu Met Ala Gly Ser His Gly	
25 30 35	
gtt ggc ggt ggc cga gtc ctg gaa tgg atc gat aag gct gct tat gct	259
Val Gly Gly Gly Arg Val Leu Glu Trp Ile Asp Lys Ala Ala Tyr Ala	
40 45 50	
tgt gct acc cag tgg tct gga acc tac tgt gtc act gct tat gtt ggt	307
Cys Ala Thr Gln Trp Ser Gly Thr Tyr Cys Val Thr Ala Tyr Val Gly	
55 60 65	
cac att cac ttc act cgc cct att ccc tct ggc cac atg gtc gag gtg	355
His Ile His Phe Thr Arg Pro Ile Pro Ser Gly His Met Val Glu Val	
70 75 80 85	
cgt tcc cgc att gcg atg act ggc cgt tcc tcc atg cac atc gtg aat	403
Arg Ser Arg Ile Ala Met Thr Gly Arg Ser Ser Met His Ile Val Asn	
90 95 100	
gag gtg ctt tct gcg gat cct cgc gat ggc aac tac acc cgt gcg tgt	451
Glu Val Leu Ser Ala Asp Pro Arg Asp Gly Asn Tyr Thr Arg Ala Cys	
105 110 115	
gac tgc ttg gtt att ttc gtg gcg aag gac acc gca act ggt cgc gct	499
Asp Cys Leu Val Ile Phe Val Ala Lys Asp Thr Ala Thr Gly Arg Ala	
120 125 130	
acc cca gtt cct tca ttt acc cct aag aat gaa gaa gag cag cgc gtg	547
Thr Pro Val Pro Ser Phe Thr Pro Lys Asn Glu Glu Glu Gln Arg Val	
135 140 145	
ttg gaa gct gct aac tcc cgc atc ggg ctg cgc aag gct att gaa gcg	595
Leu Glu Ala Ala Asn Ser Arg Ile Gly Leu Arg Lys Ala Ile Glu Ala	
150 155 160 165	
gag atg gaa aag cag acg tac aac gga cct tct gag gcc cct cgt ttg	643
Glu Met Glu Lys Gln Thr Tyr Asn Gly Pro Ser Glu Ala Pro Arg Leu	
170 175 180	
att acc cgc ttc ttg gct aag cca aca gat atc aac tgg ggt ggc aag	691
Ile Thr Arg Phe Leu Ala Lys Pro Thr Asp Ile Asn Trp Gly Gly Lys	
185 190 195	
gtc cac ggt ggc act gcc atg gaa tgg atc gat gag gcg ggt gct gcg	739
Val His Gly Gly Thr Ala Met Glu Trp Ile Asp Glu Ala Gly Ala Ala	
200 205 210	
tgc acc atg gag tgg tct ggt aac cac acc gtt gcg gtt tat gct ggt	787
Cys Thr Met Glu Trp Ser Gly Asn His Thr Val Ala Val Tyr Ala Gly	
215 220 225	

ggt atc cgc ttc tac cag ccc att cag atc ggt gac ctc att gag gtg 835
 Gly Ile Arg Phe Tyr Gln Pro Ile Gln Ile Gly Asp Leu Ile Glu Val
 230 235 240 245
 gac gcc cgc atg atg cgt acc gat aag cgt tcc atg cag atg tcc atc 883
 Asp Ala Arg Met Met Arg Thr Asp Lys Arg Ser Met Gln Met Ser Ile
 250 255 260
 cac gtc cgt gcc ggt gat gct cac cgt ggc cgt gct gag cta gaa acc 931
 His Val Arg Ala Gly Asp Ala His Arg Gly Arg Ala Glu Leu Glu Thr
 265 270 275
 gct att cac gca acg gtg acc tac tta gga att gat gtc gac gga gag 979
 Ala Ile His Ala Thr Val Thr Tyr Leu Gly Ile Asp Val Asp Gly Glu
 280 285 290
 cct ttg cct gca cca cag ttt gtg cct cgt acc cct gag gat atc cag 1027
 Pro Leu Pro Ala Pro Gln Phe Val Pro Arg Thr Pro Glu Asp Ile Gln
 295 300 305
 ttg gct gag cat gca aac atc ctg agg gat ctg cgt gct gat tac acc 1075
 Leu Ala Glu His Ala Asn Ile Leu Arg Asp Leu Arg Ala Asp Tyr Thr
 310 315 320 325
 cca atg ccg ctg ttc cag cgc agg gtt cca ctg cag atc gac 1117
 Pro Met Pro Leu Phe Gln Arg Arg Val Pro Leu Gln Ile Asp
 330 335
 tagttagacc cgaaaaagcc ccc 1140

<210> 230

<211> 339

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 230

Met Ser Asp Asn Pro His Glu Asn Pro Arg Glu Asn Pro His Arg Ser
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 Pro Glu Val Val Leu Arg Phe Met Ala Ala Pro Thr Asp Val Leu Met
 20 25 30
 Ala Gly Ser His Gly Val Gly Gly Gly Arg Val Leu Glu Trp Ile Asp
 35 40 45
 Lys Ala Ala Tyr Ala Cys Ala Thr Gln Trp Ser Gly Thr Tyr Cys Val
 50 55 60
 Thr Ala Tyr Val Gly His Ile His Phe Thr Arg Pro Ile Pro Ser Gly
 65 70 75 80
 His Met Val Glu Val Arg Ser Arg Ile Ala Met Thr Gly Arg Ser Ser
 85 90 95
 Met His Ile Val Asn Glu Val Leu Ser Ala Asp Pro Arg Asp Gly Asn
 100 105 110
 Tyr Thr Arg Ala Cys Asp Cys Leu Val Ile Phe Val Ala Lys Asp Thr
 115 120 125

Ala Thr Gly Arg Ala Thr Pro Val Pro Ser Phe Thr Pro Lys Asn Glu
 130 135 140

Glu Glu Gln Arg Val Leu Glu Ala Ala Asn Ser Arg Ile Gly Leu Arg
 145 150 155 160

Lys Ala Ile Glu Ala Glu Met Glu Lys Gln Thr Tyr Asn Gly Pro Ser
 165 170 175

Glu Ala Pro Arg Leu Ile Thr Arg Phe Leu Ala Lys Pro Thr Asp Ile
 180 185 190

Asn Trp Gly Gly Lys Val His Gly Gly Thr Ala Met Glu Trp Ile Asp
 195 200 205

Glu Ala Gly Ala Ala Cys Thr Met Glu Trp Ser Gly Asn His Thr Val
 210 215 220

Ala Val Tyr Ala Gly Gly Ile Arg Phe Tyr Gln Pro Ile Gln Ile Gly
 225 230 235 240

Asp Leu Ile Glu Val Asp Ala Arg Met Met Arg Thr Asp Lys Arg Ser
 245 250 255

Met Gln Met Ser Ile His Val Arg Ala Gly Asp Ala His Arg Gly Arg
 260 265 270

Ala Glu Leu Glu Thr Ala Ile His Ala Thr Val Thr Tyr Leu Gly Ile
 275 280 285

Asp Val Asp Gly Glu Pro Leu Pro Ala Pro Gln Phe Val Pro Arg Thr
 290 295 300

Pro Glu Asp Ile Gln Leu Ala Glu His Ala Asn Ile Leu Arg Asp Leu
 305 310 315 320

Arg Ala Asp Tyr Thr Pro Met Pro Leu Phe Gln Arg Arg Val Pro Leu
 325 330 335

Gln Ile Asp

<210> 231
 <211> 313
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(313)
 <223> FRXA00559

<400> 231
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 catgaagcat cagcctagta cgaaccgtta aagtgtccat atg tct gat aat ccg 115
 Met Ser Asp Asn Pro
 1 5
 cat gag aat ccc cgt gag aat cca cac cgc tcc cca gaa gtc gtc ctt 163

His Glu Asn Pro Arg Glu Asn Pro His Arg Ser Pro Glu Val Val Leu
 10 15 20
 cgt ttc atg gct gcc cct act gac gtt ttg atg gct ggt agc cat ggc 211
 Arg Phe Met Ala Ala Pro Thr Asp Val Leu Met Ala Gly Ser His Gly
 25 30 35
 gtt ggc ggt ggc cga gtc ctg gaa tgg atc gat aag gct gct tat gct 259
 Val Gly Gly Gly Arg Val Leu Glu Trp Ile Asp Lys Ala Ala Tyr Ala
 40 45 50
 tgt gct acc cac ggg tct gga acc tac tgc gtc act gct tat gtt ggt 307
 Cys Ala Thr His Gly Ser Gly Thr Tyr Cys Val Thr Ala Tyr Val Gly
 55 60 65
 cac att 313
 His Ile
 70

<210> 232
 <211> 71
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 232
 Met Ser Asp Asn Pro His Glu Asn Pro Arg Glu Asn Pro His Arg Ser
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 20 25 30
 Ala Gly Ser His Gly Val Gly Gly Gly Arg Val Leu Glu Trp Ile Asp
 35 40 45
 Lys Ala Ala Tyr Ala Cys Ala Thr His Gly Ser Gly Thr Tyr Cys Val
 50 55 60
 Thr Ala Tyr Val Gly His Ile
 65 70

<210> 233
 <211> 802
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(802)
 <223> RXA01580

<400> 233
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 tcaactttgc tccctatcct taaaaagccc acagaaaagg atg tat aag aat atg 115
 Met Tyr Lys Asn Met
 1 5
 cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc 163
 His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr

	10	15	20	
atg acc gct ttc cag.gct gcc gcg ccc gct gac gct ttt gag ctg gat				211
Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp				
	25	30	35	
atc cac gcc acc gct gac aat cag gtc gtc gtt atc cac gac cgc acc				259
Ile His Ala Thr Ala Asp Asn Gln Val Val Val Ile His Asp Arg Thr				
	40	45	50	
gca gcg cgt gtt gcc gcg cca gat tcc ctg cac cgc gac acc ccg gtt				307
Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His Arg Asp Thr Pro Val				
	55	60	65	
gcg cgc tta agc gcc gcg caa atc aag gag ata acg ctt atc gac gga				355
Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile Thr Leu Ile Asp Gly				
	70	75	80	85
tcc ccc gta cca acc ctg gag gaa gtt cta ctc cag acg agc ctg ccg				403
Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu Gln Thr Ser Leu Pro				
	90	95	100	
atc caa gtg gaa atc aaa tct gcc ggt gca gtt cca gca gcc gca gca				451
Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val Pro Ala Ala Ala Ala				
	105	110	115	
tta ttg cag aaa tac cca gag cac ctg gag cgc ctg ctg ttc atc agt				499
Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg Leu Leu Phe Ile Ser				
	120	125	130	
ttc atc gat gca gca ctg gtg gaa atc gtg gat cga ctg cca gaa gct				547
Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp Arg Leu Pro Glu Ala				
	135	140	145	
cgc gtg gga atc ttg cgc gat gcg tcc atg gat gat ctg cgc att ctt				595
Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp Asp Leu Arg Ile Leu				
	150	155	160	165
gat tac atc ccg cta aaa aat gtg ggc gcg atc ttg ccc tcg tgg aaa				643
Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile Leu Pro Ser Trp Lys				
	170	175	180	
gca cta aac gtg gcg tca att gct gat cta cat acc aag gga atc aag				691
Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His Thr Lys Gly Ile Lys				
	185	190	195	
gtt ggc tgc tgg aca att cgg gat gaa aat gcg ttt ggg atc gca caa				739
Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala Phe Gly Ile Ala Gln				
	200	205	210	
caa gct ggc gtt gat tac ccc act gtt agc gat ccc tct cgt ttc tcg				787
Gln Ala Gly Val Asp Tyr Pro Thr Val Ser Asp Pro Ser Arg Phe Ser				
	215	220	225	
cgc cct ccc ctg ctg				802
Arg Pro Pro Leu Leu				
230				

<210> 234

<211> 234

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

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Met Tyr Lys Asn Met His Ile Val Ala His Arg Gly Ala Glu Asp Leu
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His Leu Glu Asn Thr Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp
      20           25           30

Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val
      35           40           45

Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His
      50           55           60

Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile
      65           70           75           80

Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu
      85           90           95

Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val
      100           105           110

Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg
      115           120           125

Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp
      130           135           140

Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp
      145           150           155           160

Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile
      165           170           175

Leu Pro Ser Trp Lys Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His
      180           185           190

Thr Lys Gly Ile Lys Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala
      195           200           205

Phe Gly Ile Ala Gln Gln Ala Gly Val Asp Tyr Pro Thr Val Ser Asp
      210           215           220

Pro Ser Arg Phe Ser Arg Pro Pro Leu Leu
      225           230

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<210> 235

<211> 882

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(859)

<223> RXA02677

<400> 235

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									Met	Lys	Val	Ile	Ala		5
									1						
cac	cga	ggt	tta	tcg	tct	cgc	ttt	ccc	gaa	tta	aca	gag	tct	gcg	ttt
His	Arg	Gly	Leu	Ser	Ser	Arg	Phe	Pro	Glu	Leu	Thr	Glu	Ser	Ala	Phe
				10					15					20	
cgg	gcg	gct	cta	gag	cta	ccg	att	cat	gga	att	gaa	act	gat	gtc	cgg
Arg	Ala	Ala	Leu	Glu	Leu	Pro	Ile	His	Gly	Ile	Glu	Thr	Asp	Val	Arg
			25					30					35		
ctg	act	aaa	tgt	ggc	gaa	gtg	gtt	aac	gtc	cat	gac	ccc	att	gtg	gat
Leu	Thr	Lys	Cys	Gly	Glu	Val	Val	Asn	Val	His	Asp	Pro	Ile	Val	Asp
		40					45					50			
cgc	gtg	tcg	aat	ggt	cgc	ggt	cgg	gtg	tcg	cgt	ttg	gac	ttg	gaa	tcc
Arg	Val	Ser	Asn	Gly	Arg	Gly	Arg	Val	Ser	Arg	Leu	Asp	Leu	Glu	Ser
		55				60					65				
ttg	ctg	agc	ttg	aac	ttt	gga	acc	aaa	gaa	acc	cca	gaa	aaa	gtg	ctt
Leu	Leu	Ser	Leu	Asn	Phe	Gly	Thr	Lys	Glu	Thr	Pro	Glu	Lys	Val	Leu
		70			75					80					85
act	tta	aac	aat	cta	tta	gat	att	ttt	gag	gat	tat	cca	gat	aag	cac
Thr	Leu	Asn	Asn	Leu	Leu	Asp	Ile	Phe	Glu	Asp	Tyr	Pro	Asp	Lys	His
				90					95					100	
ctt	tat	ata	gaa	acc	aag	cac	cca	atg	cgc	tac	gcg	gtc	atg	ctg	gaa
Leu	Tyr	Ile	Glu	Thr	Lys	His	Pro	Met	Arg	Tyr	Ala	Val	Met	Leu	Glu
			105					110					115		
gaa	gaa	atc	aca	aaa	atc	tta	aaa	tat	cgt	ggg	ctg	acg	gaa	gac	cca
Glu	Glu	Ile	Thr	Lys	Ile	Leu	Lys	Tyr	Arg	Gly	Leu	Thr	Glu	Asp	Pro
		120					125					130			
cgc	atc	cac	atc	att	tct	ttt	gca	ctt	ccc	gcg	atg	tat	cgc	atg	gct
Arg	Ile	His	Ile	Ile	Ser	Phe	Ala	Leu	Pro	Ala	Met	Tyr	Arg	Met	Ala
		135				140					145				
cgc	ctt	gct	cca	cag	ctt	gat	cgc	att	cat	ctg	cgc	agg	tcg	tgg	gag
Arg	Leu	Ala	Pro	Gln	Leu	Asp	Arg	Ile	His	Leu	Arg	Arg	Ser	Trp	Glu
		150			155					160					165
cgt	tgg	ggt	aat	ccg	cgc	gat	gtg	cgc	tgc	ggg	gta	ccc	acc	ggg	ttg
Arg	Trp	Gly	Asn	Pro	Arg	Asp	Val	Arg	Cys	Gly	Val	Pro	Thr	Gly	Leu
				170					175					180	
ggg	ttg	tcg	ctg	gag	cgg	gcg	aag	atg	gat	cca	agg	atg	att	ggg	gcg
Gly	Leu	Ser	Leu	Glu	Arg	Ala	Lys	Met	Asp	Pro	Arg	Met	Ile	Gly	Ala
			185					190					195		
aaa	ggg	tta	ccc	acc	tat	ctt									